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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

2. BACKGROUND

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Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, few example, diagnostics, forensics, gene mapping; identification of mutations responsible for genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases. The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NO: 1-1786 and 3573-5358. The polypeptides sequences are designated SEQ ID NO: 2n (wherein n = 1 to 20). The nucleic acids and polypeptides are provided in the Sequence Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

The nucleic acid sequences of the present invention also include, nucleic acid sequences that hybridize to the complement of SEQ ID NO:1-1786 and 3573-5358 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NO:1-1786 and 3573-5358. A polynucleotide comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO:1-1786 and 3573-5358 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358. The sequence information can be a segment of any one of SEQ ID NO:1-1786 and 3573-5358 that uniquely identifies or represents the sequence information of SEQ ID NO:1-1786 and 3573-5358.

A collection as used in this application can be a collection of only one polynucleotide. The collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection can also be provided in a computer-readable format.

This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

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full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

In a preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358; a polynucleotide comprising any of the full length protein coding sequences of SEQ ID NO:1-1786 and 3573-5358; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NO:1-1786 and 3573-5358. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (e.g. orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO:1-1786 and 3573-5358; or (b) polynucleotides that hybridize to the complement of the polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (e.g., with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (e.g. host cells) of the invention.

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The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Polynucleotides according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, e.g., in situ hybridization.

In other exemplary embodiments, the polynucleotides are used in diagnostics as expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The polypeptides according to the invention can be used in a variety of conventional procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight markers, and as a food supplement.

Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a pharmaceutically acceptable carrier.

In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

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The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (i.e., increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (e.g., bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

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PCT/US00/34263 effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2); for which they have a signature region (as set forth in Table 3); or for which they have homology to a gene family (as set forth in Table 4). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

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4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady

and continuous source of germ cells for the production of gametes. The term "primordial germ cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonculeotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30

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nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOs:1-20.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NO:1-1786 and 3573-5358. The sequence information can be a segment of any one of SEQ ID NO:1-1786 and 3573-5358 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NO:1-1786 and 3573-5358. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 420 possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome 30 with a single mismatch is calculated by multiplying the probability for a full match $(1 \div 4^{25})$ times the increased probability for mismatch at each nucleotide position (3 \times 25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

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The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements e.g. repressor genes are not contiguously linked to the coding sequence but still control transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

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The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (e.g., with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, e.g., recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

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can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, e.g., polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (e.g., nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (e.g., microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., E. coli, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

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in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed.

20 "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (e.g. Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134 -143) and factors released from damaged cells (e.g. Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol.

16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (i.e., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (i.e., washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

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In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (i.e., the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, e.g., mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more that 5% (95% sequence identity). Substantially equivalent, e.g., mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 90% sequence identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, and most preferably at least about 95% identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (e.g., via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, e.g., using the Jotun Hein method (Hein, J. (1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, e.g. by varying hybridization conditions.

The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The

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term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

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Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358; a polynucleotide encoding any one of the peptide sequences of SEQ ID NO:1787-3572 and 5359-7144; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NO:1787-3572 and 5359-7144. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO:1-1786 and 3573-5358; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NO:1787-3572 and 5359-7144. Domains of interest may depend on the nature of the encoded polypeptide; e.g., domains in receptor-like polypeptides include ligand-binding, extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

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The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, e.g., cDNA and genomic DNA, and RNA, e.g., mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO:1-1786 and 3573-5358 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpri, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length genc.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, e.g., at least about 65%, at least about 70%, at least about 75%, at least about 80%, more typically at least about 90%, and even more typically at least about 95%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, e.g. 15, 17, or 20 nucleotides or more that are selective for (i.e. specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in

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the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO:1-1786 and 3573-5358, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO:1-1786 and 3573-5358 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO:1-1786 and 3573-5358, can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altshul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by substituting first with conservative choices (e.g.,

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hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., DNA 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, Nucleic Acids Res. 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., supra, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

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Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO:1-1786 and 3573-5358, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, e.g., plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following

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vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are 15 pKK232-8 and pCM7. Particular named bacterial promoters include lacl, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable 20 markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of E. coli and S. cerevisiae TRP1 gene, and a promoter derived from a highly-expressed gene to-direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is 25 assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. 30 Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for 35

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transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID NO:1787-3572 and 5359-7144 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO:1-1786 and 3573-5358 are additionally provided.

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In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (e.g., SEQ ID NO:1-1786 and 3573-5358, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, 25 inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, 30 queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the 35

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inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier et al. (1987) Nucleic Acids Res 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue et al. (1987) Nucleic Acids Res 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue et al. (1987) FEBS Lett 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (e.g., hammerhead ribozymes (described in Haselhoff and Gerlach (1988) Nature 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be designed based upon the nucleotide sequence of a DNA disclosed herein (i.e., SEQ ID NO:1-1786 and 3573-5358). For example, a derivative of a Tetrahymena L-19 IVS RNA can be

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constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, e.g., Cech et al. U.S. Pat. No. 4,987,071; and Cech et al. U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel et al., (1993) Science 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991)

Anticancer Drug Des. 6: 569-84; Helene. et al. (1992) Ann. N.Y. Acad. Sci. 660:27-36; and Maher (1992) Bioassays 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup et al. (1996) Bioorg Med Chem 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, e.g., DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup et al. (1996) above; Perry-O'Keefe et al. (1996) PNAS 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, e.g., inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, e.g., in the analysis of single base pair mutations in a gene by, e.g., PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, e.g., S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup et al. (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, e.g., to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, e.g., RNase H and DNA polymerases, to interact with the DNA portion while the PNA

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portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn et al. (1996) Nucl Acids Res 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, e.g., 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag et al. (1989) Nucl Acid Res 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn et al. (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen et al. (1975) Bioorg Med Chem Lett 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express

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the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in coamplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, ct al., in Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, Cell 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK,

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HIL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces strains, Candida, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include Escherichia coli, Bacillus subtilis, Salmonella typhimurium, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the

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protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NO:1787-3572 and 5359-7144 or an amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358 or (b) polynucleotides encoding any one of the amino acid sequences

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set forth as SEQ ID NO:1787-3572 and 5359-7144 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NO:1787-3572 and 5359-7144 or the corresponding full length or mature protein; and "substantial equivalents" thereof (e.g., with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, typically at least about 95%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity. Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NO:1787-3572 and 5359-7144.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., Bio/Technology 10, 773-778 (1992) and in R. S. McDowell, et al., J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

The present invention also provides both full-length and mature forms (for example, without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, e.g., pharmaceutically acceptable, carrier.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

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A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, Protein Purification: Principles and Practice, Springer-Verlag (1994); Sambrook, et al., in Molecular Cloning: A Laboratory Manual; Ausubel et al., Current Protocols in Molecular Biology. Polypeptide fragments that

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retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for e.g., small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NO:1787-3572 and 5359-7144.

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

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methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, Calif., U.S.A. (the MaxBatTM kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearlTM or Cibacrom blue 3GA SepharoseTM; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

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The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, e.g., targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, e.g., antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

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4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., Nucleic Acids Research 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., J. Molec. Biol. 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., Nucleic Acids Res. vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., J. Comp. Biol., Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al., ISMB-97, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobocity prediction algorithm (J. Mol Biol, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., J. Mol. Biol. 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

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another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which
the polypeptide sequences according to the invention comprises one or more domains are fused
to sequences derived from a member of the immunoglobulin protein family. The
immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical
compositions and administered to a subject to inhibit an interaction between a ligand and a
protein of the invention on the surface of a cell, to thereby suppress signal transduction in vivo.

The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand.
Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of
proliferative and differentiative disorders, e,g., cancer as well as modulating (e.g., promoting or
inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be
used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays
to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, e.g., by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

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example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

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Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal 10 activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected ex vivo, in situ, or in vivo by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or ex vivo by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered in vivo to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (e.g., by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., ada, dhfr, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, e.g., inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

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added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

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In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

The polynucleotides of the present invention also make possible the development, through, e.g., homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4.10 USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

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polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, e.g., via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

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The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

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confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preß M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin-γ, Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 20 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 25 I pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. 30 J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

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Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells in vivo or ex vivo is expected to maintain and expand cell populations in a totipotential or pluripotential state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic fibroblast growth factor (bFGF).

Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

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layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotential/pluripotential stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source of undifferentiated totipotential/pluripotential mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition, the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., Differentiation, 48: 173-182, (1991); Klug et al., J. Clin. Invest., 98(1): 216-224, (1998)) or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering eds.* Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

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sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support e.g. as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

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Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells 5 with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of 10 stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

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4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair

useful in cosmetic plastic surgery.

A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular

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endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus,

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rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also to be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastborn et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxocol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic

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composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

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Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bowman et al., J. Virology 61:1992-1998; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

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Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E.
M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by
dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery
et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine
173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et
al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology
67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of
Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation
94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

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A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

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Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

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4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

A polypeptide of the invention may also be involved in hemostatis or thrombolysis or thrombosis. A polypucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

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Therapeutic compositions of the invention can be used in the following:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

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4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention

may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy. Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation, inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle, kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma, hemangiopericytoma and Karposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine. Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide,

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Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cisDDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Dacarbazine, Dactinomycin,
Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213),
Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide,
Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog),
Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna,
Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl,
Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate,
Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin,
Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (e.g. exposure to carcinogens) known in the art that predispose an individual to developing cancers. Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These in vitro models include proliferation assays of cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wily-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available, e.g. from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor, receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen

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recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such

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transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (i.e., increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science 282*:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, Curr. Opin. Biotechnol. 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., Mol. Biotechnol, 9(3):205-23 (1998); Hruby et al., Curr Opin Chem Biol, 1(1):114-19 (1997); Dorner et al., Bioorg Med Chem, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, e.g., ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding

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molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide e.g. a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity 10 chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (i.e., increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous 15 ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligands(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential 20 ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications i.e. phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

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Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflamation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic mylegenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

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4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of therapeutic utility, include but are not limited to nervous system injuries, and diseases or

disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

- (i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;
- (ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;
 - (iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;
 - (iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;
- (v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;
 - (vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;
 - (vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and
- (viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or

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differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or in vivo;
- (iii) increased production of a neuron-associated molecule in culture or in vivo, e.g., choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
 - (iv) decreased symptoms of neuron dysfunction in vivo.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or

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elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, e.g., differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified

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nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et at., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

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4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of

administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about $0.01\mu g/kg$ to 100 mg/kg of body weight, with the preferred dose being about $0.1\mu g/kg$ to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

15 4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), insulin-like growth factor (IGF), as well as cytokines described herein.

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The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or other active ingredient or complement its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein or other active ingredient of the invention, or to minimize side effects. Conversely, protein or other active ingredient of the present invention may be included in formulations of the particular clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

As an alternative to being included in a pharmaceutical composition of the invention including a first protein, a second protein or a therapeutic agent may be concurrently administered with the first protein (e.g., at the same time, or at differing times provided that therapeutic concentrations of the combination of agents is achieved at the treatment site). Techniques for formulation and administration of the compounds of the instant application may be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest edition. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein or other active ingredient of the present invention is administered to a mammal having a condition to be treated. Protein or other active ingredient of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co- administered with one or more cytokines, lymphokines or other hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic

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factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

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4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

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4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be

manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers

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enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations 15 of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampules or in multi-dose containers, with

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added preservative are PCT/US00/34263

an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g. polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well

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known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent.

Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable

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lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1 µg to about 10 mg, more preferably about $0.1~\mu g$ to about 1~mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic. composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions

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may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which

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modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either in vivo or ex vivo into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured ex vivo in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced in vivo for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate in vitro assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC₅₀ as determined in cell culture (i.e., the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD₅₀ (the dose lethal to 50% of the

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population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from in vitro data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations.

Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 μ g/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 μ g/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the

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invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

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Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab} , and $F_{(ab)}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG_1 , IgG_2 , and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence shown in SEQ ID NO: 1787, and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of -related protein that is located on the surface of the protein, e.g., a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte

Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each of which is incorporated herein by reference in its entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the

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target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

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5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, 15 hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized in vitro. The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego,

California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, <u>J. Immunol.</u>, <u>133</u>:3001 (1984); Brodeur et al., <u>Monoclonal Antibody Production Techniques and Applications</u>, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal. The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography; gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin

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polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5 5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-10 binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the 15 corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable 20 domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human 25 immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human 30 genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein. Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal

antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al., (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse TM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

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An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

20 5.13.4 F_{ab} Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see e.g., U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see e.g., Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab)/2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab)/2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the

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binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., 1991 EMBO J., 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to

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stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., <u>J. Immunol.</u> 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcyR), such as FcyRI (CD64), FcyRII (CD32) and FcyRIII (CD16) so as to focus cellular

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defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

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5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ²¹²Bi, ¹³¹I, ¹³¹In, ⁹⁰Y, and ¹⁸⁶Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon

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a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 or a representative fragment thereof; or a nucleotide sequence at least 95% identical to any of the nucleotide sequences of SEQ ID NO:1-1786 and 3573-5358 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and

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software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

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4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are

designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

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4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary.

Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the nucleic acid

probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

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The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (e.g., where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection). See, e.g., Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

4.18 SCREENING ASSAYS

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Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO:1-1786 and 3573-5358, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
 - (b) determining whether the agent binds to said protein or said nucleic acid.

In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

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from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

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Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from of any of the nucleotide sequences SEQ ID NO:1-1786 and 3573-5358 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent in situ hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

10 4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, i.e., small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata et al., 1985; Dahlen et al., 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller et al., 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude et al. (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, e.g., Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen et al., (1991) Anal. Biochem. 198(1) 138-42).

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The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) Nucleic Acids Res. 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) Science 251(4995)767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) Nucleic Acids Res. 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) Anal. Biochem. 169(1) 104-8; all references being specifically incorporated herein.

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To link an oligonucleotide to a nylon support, as described by Van Ness et al. (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease et al., (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected N-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook et al. (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schriefer et al. (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, $Cvi\Pi$, described by Fitzgerald et al. (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

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of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease $Cvi\Pi$ normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme ($Cvi\Pi^{**}$), yield a quasi-random distribution of DNA fragments form the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a $Cvi\Pi^{**}$ digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that $Cvi\Pi^{**}$ restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

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Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers e.g. a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

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5.1.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (e.g., 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems (ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

PCT/US00/34263 WO 01/53312

5.1.2 EXAMPLE 2

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Assemblage of Novel Nucleic Acids

The contigs or nucleic acids of the present invention, designated as SEQ ID NO: 3573-5358 were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

A polypeptide was predicted to be encoded by each of SEQ ID NO:3573-5358 as set forth below. The polypeptides was predicted using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptides based on a comparison of translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference. The predicted polypeptides are shown in Table 7.

5.2.2 EXAMPLE 3

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genebank. Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, ed-ext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS:1-327.

Table 1 shows the various tissue sources of SEQ ID NO: 1-327.

The nearest neighbor results for SEQ ID NO: 1-327 were obtained by a FASTA version 3 search against Genpept release 117, using FASTXY algorithm. FASTXY is an improved version of FASTA alignment which allows in-codon frame shifts. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1-327 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The nearest neighbor results for SEQ ID NO: 1-327 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the

signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.3.2 EXAMPLE 4

Novel Nucleic Acids

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Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genpept release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 328-1413.

Table 1 shows the various tissue sources of SEQ ID NO: 328-1413.

The nearest neighbor results for SEQ ID NO: 328-1413 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 328-1413 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in

the Sequence Listing. The nearest neighbor results for SEQ ID NO: 328-1413 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were

examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.3.2 EXAMPLE 5

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 117, gb pri 117, UniGene version 117, Genpept release 117). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1414-1652.

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Table 1 shows the various tissue sources of SEQ ID NO: 1414-1652.

The nearest neighbor results for SEQ ID NO: 1414-1652 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The nearest neighbor result showed the closest homologue for SEQ ID NO: 1414-1652 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The nearest neighbor results for SEQ ID NO: 1414-1652 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.4.2 EXAMPLE 6

30 Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 118, gb pri 118,

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UniGene version 118, Genpept release 118). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide sequences, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1653-1745.

Table 1 shows the various tissue sources of SEQ ID NO: 1653-1745.

The homology for SEQ ID NO: 1653-1745 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 118, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1653-1745 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1653-1745 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

5.5.2 EXAMPLE 7

Novel Nucleic Acids

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Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 119, gb pri 119, UniGene version 119, Genpept release 119). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1746-1768.

Table 1 shows the various tissue sources of SEQ ID NO: 1746-1768.

The homology for SEQ ID NO: 1746-1768 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 119, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1746-1768 from Genpept. The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The homologues with identifiable functions for SEQ ID NO: 1746-1768 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the PFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the PFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP VI.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

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5.6.2 EXAMPLE 8

Novel Nucleic Acids

Using PHRAP (Univ. of Washington) or CAP4 (Paracel), a full length gene cDNA sequence and its corresponding protein sequence were generated from the assemblage. Any frame shifts and incorrect stop codons were corrected by hand editing. During editing, the sequence was checked using FASTY and/or BLAST against Genbank (i.e., dbEST version 120, gb pri 120, UniGene version 120, Genpept release 120). Other computer programs which may have been used in the editing process were phredPhrap and Consed (University of Washington) and ed-ready, edext and gc-zip-2 (Hyseq, Inc.). The translated amino acid sequences for which the nucleic acid sequence encodes are shown in the Sequence Listing. The full-length nucleotide, including splice variants resulting from these procedures are shown in the Sequence Listing as SEQ ID NOS: 1769-1786.

Table 1 shows the various tissue sources of SEQ ID NO: 1769-1786.

The homology for SEQ ID NO: 1769-1786 were obtained by a BLASTP version 2.0al 19MP-WashU search against Genpept release 120 and the amino acid version of Geneseq released on October 26, 2000, using BLAST algorithm. The results showed homologues for SEQ ID NO: 1769-1786 from Genpept. The homologues with identifiable functions for SEQ ID NO: 1769-1786 are shown in Table 2 below.

Using eMatrix software package (Stanford University, Stanford, CA) (Wu et al., J. Comp. Biol., Vol. 6 pp. 219-235 (1999) herein incorporated by reference), all the sequences were examined to determine whether they had identifiable signature regions. Table 3 shows the signature region found in the indicated polypeptide sequences, the description of the signature, the eMatrix p-value(s) and the position(s) of the signature within the polypeptide sequence.

Using the pFam software program (Sonnhammer et al., Nucleic Acids Res., Vol. 26(1) pp. 320-322 (1998) herein incorporated by reference) all the polypeptide sequences were examined for domains with homology to certain peptide domains. Table 4 shows the name of the domain found, the description, the p-value and the pFam score for the identified domain within the sequence.

The nucleotide sequence within the sequences that codes for signal peptide sequences and their cleavage sites can be determine from using Neural Network SignalP V1.1 program (from Center for Biological Sequence Analysis, The Technical University of Denmark). The process for identifying prokaryotic and eukaryotic signal peptides and their cleavage sites are also disclosed by Henrik Nielson, Jacob Engelbrecht, Soren Brunak, and Gunnar von Heijne in the publication "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites" Protein Engineering, Vol. 10, no. 1, pp. 1-6 (1997), incorporated herein by

reference. A maximum S score and a mean S score, as described in the Nielson et as reference, was obtained for the polypeptide sequences. Table 5 shows the position of the signal peptide in each of the polypeptides and the maximum score and mean score associated with that signal peptide.

Table 6 is a correlation table of all of the sequences and the SEQ ID NOS.

TABLE 1

TABLE 1			
Tissue Origin	RNA Source	Hyseq Library Name	. SEQ ID NOS:
adult brain	GIBCO	AB3 001	9 19-21 50-51 65-66 72 78 80 82
44422 22421	4.500		85 87 107-108 113 116 123 138
1			140 150-152 159 169 177 192-193
1 1			202-203 212-214 225-226 235-236
}			251 258 268-269 272 280-281 295
1			298 301 321 326 331-332 334 356-
1 1			357 362 369 379 382-383 416 423
,	·		443 459-460 473 475 477 488 496
, ,			500 503 519 526 547 574 582 587
			608-609 613 618 633-634 645-646
			652 657-658 660 669-671 678 687
i i			695 697 710 715 724 731 775-777
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1	1	1	628-633 635-636 643 645-649 653
1		1	655-656 660-665 668-670 676 681
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l			773 775-778 786 789 796 799-800
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	1		861 864 869 874 878 883 897 901-
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	[}	941-942 945 955-958 963 966-969
		l	977 979-980 985-986 990 992-993
l	1	1	997-1001 1005-1007 1012 1017-
	1	1	1020 1023-1024 1029-1031 1034
			1036 1039 1050 1059 1063-1066
			1078 1081-1082 1085-1086 1089

Tissue Origin	RNA Source	Нузеф	CHA YE WAS
		Library Name	SEQ ID NOS:
			1097 1103 1107 1109 1112 1116~
			1117 1119 1121 1124 1127 1130
1			1134 1144-1145 1149 1151 1157- 1158 1167 1170 1178 1184 1188
		1	1190 1193-1194 1200 1202 1215-
			1217 1220 1226-1227 1229 1231
			1241 1243 1247 1252 1258 1263
			1267 1269 1279 1281 1284 1286-
1		ļ	1289 1293-1294 1306-1307 1312
1	}		1316-1320 1326 1333 1338 1341
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			1425-1427 1437 1443 1446 1454
			1456 1458-1459 1468 1470-1472
]		1478 1482-1483 1487-1488 1493
			1497 1499 1506 1508-1511 1517 1522-1524 1530-1533 1545-1546
	1		1548-1550 1552 1557-1559-1563
			1565 1567 1569 1571 1586 1588
			1591 1593 1595 1598-1601 1608
)			1611 1620-1621 1624-1626 1628
	1		1630-1632 1636 1640-1641 1644-
			1645 1647 1649 1653-1655 1657 1664 1667 1669 1673 1678-1681
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			1711 1719 1722-1723 1726-1727
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			1747 1749 1753 1757-1758 1760-
adult brain	Clontech	ABR001	1761 1765 1771 1785
		ADRUUL	9 29 68-69 113 115 146 152 206 223 245 277 307 320 324 330-331
	1		344 348 352 362 379 384 393 404
	}		408 414 441-442 454 469 481 490
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	1		715 799 803 833 865 871 875 880
	1		882 908 920 937 1000 1005-1006 1027 1036 1041 1043 1075 1107
	 	•	1112 1121 1127 1136-1137 1144-
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			1320 1345 1355 1361 1383-1384
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adult brain	Clontech	ABR006	5-8 15-16 168 212-213 271 278
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	1		321 326 336-338 341 352 357 359-
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Tissue Origin	RNA Source	Нувед	SEQ ID NOS:
		Library Name	208 210 214-215 218 221-226 229
		{	231-232 234-241 245-247 251-253
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			682 687 689 691-700 702 706 710 715-717 720-721 725-734 736-739
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			784-785 787-789 794 796 799 802-
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			883-884 887 889-892 894-895 897-
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			1265 1274 1324-1325 1339 1353
			1374 1377 1440-1441 1447 1504
			1549 1600 1618-1619 1631 1641
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	1		176 198 200 209 231 235-236 250
		1	272 275-276 284 306 316 321 325
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See ID Nos:	Tissue Origin	RNA Source	Hyseq	CEO TO VOO
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Genomic DNA	Research	BAC001	686 1352 1412
from BAC 63118	Genetics (CITB BAC Library)		
Genomic DNA from BAC 39316	Research Genetics (CITB BAC Library)	BAC002	1411-1412

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adult bladder	Invitrogen	BLD001	80 93 100 120-121 169 201 237
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bone marrow	Clontech	BWD001	3-8 11 13 18 29-31 33 35-36 40 43-45 47-48 50-51 57 60 65-66 75
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Tissue Origin	RNA Source	Hyseq	CEO TO WOO
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Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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Mixture of 16	Various	CTL016	401 1490 1686
tissues -	Vendors		
mRNAs	L i		
Mixture of 16	Various	CTL021	312 782 1132-1133 1403 1712 1715
tissues -	Vendors		
mRNAs*	_		
adult cervix	BioChain	CVX001	1 4-8 11 13 18-21 25-26 30-31 33
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^{*}The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphablastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

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Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
		Library Name	
			352 372 377 384 414 424 445-446 454 472 474 491 496 560 579 588 593 597 607 612 626 681 702 719 810 859 866 878 894-895 912 916 922 932 935 1046 1075 1080 1099- 1102 1113 1208 1215 1232-1233 1237 1281 1312 1385 1387 1405 1414 1424 1430 1437 1447 1505 1569 1579 1586 1600 1641 1653 1667 1671 1676-1677 1683 1691- 1692 1711 1717 1726 1772
uterus	Clontech	UTROO1	17 19 25 41 46 57-58 61 89 104 108 139 152 174 198 200-201 206 263-265 274 290 387 408 420 438 446 448 452 473 491 493 499 503 506 513 519 522 526 530 542-543 560 601 610 632 659 665 720 751 773 780 833 845 857 872 877 912 929 934 937 996 1009 1011 1018 1050 1075 1107 1124 1170 1219 1258 1279 1287 1310 1320 1323 1343-1344 1375 1437 1451-1452 1478 1481 1498 1519 1521 1536 1552 1579 1597 1602 1606 1620 1626-1627 1649 1652 1661 1670 1719 1722-1723

TRADOCS:1416191.1(%CQN01!.DOC)

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1	Y41736	Homo sapiens	Human PRO1114 protein sequence.	1398	100
2	Y66656	Homo sapiens	Membrane-bound protein PRO943.	2389	99
3	AF113136	Homo sapiens	IL-1 receptor-associated- kinase-M; IRAK-M	3043	100
	AF017806	Mus musculus	Zn-15 transcription factor	6351	77
4	X02761	Homo sapiens	fibronectic precursor	10535	98
5			fibronectic precursor	8990	89
6	X02761	Homo sapiens	fibronectin precursor	12564	99
В	X02761	Homo sapiens	Rab6 GTPase activating	5251	199
9	AJ011679	Homo sapiens	protein, GAPCenA	}	
10	W88501	Homo sapiens	Human stomach carcinoma clone HP10415-encoded protein.	2381	100
11	AF117754	Homo sapiens	thyroid hormone receptor- associated protein complex component TRAP240	11336	98
12	297630	Homo sapiens	dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G)))	896	100
13	Y58620	Homo sapiens	Protein regulating gene expression PRGE-13.	1894	98
14	AF213457	Homo sapiens	triggering receptor expressed on myeloid cells 2	1238	100
16	AF233453	Homo sapiens	RACK-like protein PRKCBP1	3124	99
17	AF201303	Homo sapiens	dhfr oribeta-binding protein	3130	98
18	AF064205	Homo sapiens	dynactin 1 p150 isoform	6377	100
19	000059	Saccharomyce s cerevisiae	Yhr121wp	174	26
20	AB032903	Homo sapiens	guanosine monophosphate reductase isolog	1801	99
21	AB032903	Homo sapiens	guanosine monophosphate reductase isolog	1485	99
22	AF140507	Homo sapiens	Ca2+/calmodulin-dependent protein kinase kinase beta	3083	99
23	AF140507	Homo sapiens	Ca2+/calmodulin-dependent protein kinase kinase beta	2300	99
24	AJ289131	Homo sapiens	chondroitin 4-0- sulfotransferase	2211	99
25	U33460	Homo sapiens	DNA-directed RNA polymerase I, largest subunit	8777	98
26	Y44488	Homo sapiens	ACRP30R2 variant protein.	1387	100
27	U43701	Homo sapiens	ribosomal protein L23a	791	100
28	U02032	Homo sapiens	ribosomal protein L23a	767	97
29	Y41324	Homo sapiens	Human secreted protein encoded by gene 17 clone	1083	99
30	W71749	Homo sapiens	Human ubiquitin conjugation system protein 2.	715	90
31	W71749	Homo sapiens	Human ubiquitin conjugation system protein 2.	631	82
32	AF231917	Homo sapiens	long-chain 2-hydroxy acid oxidase HAOX2	1811	100
33	Z29481	Homo sapiens	3-hydroxyanthranilic acid dioxygenase	1507	99
34	AB001451	Homo sapiens	Sck	2869	100
35	Y00644	Homo sapiens	precursor polypeptide (AA -34 to 287)	1667	99
36	Y00644	Homo sapiens	precursor polypeptide (AA -34 to 287)	1104	98
37	¥78795	Homo sapiens	Human antizuai-2 (AZ-2) amino	3586	78
38	¥78795	Homo sapiens	acid sequence. Human antizuai-2 (AZ-2) amino	4726	99

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	윰
ID NO:	NUMBER Y78795			WATERMAN SCORE	IDENTITY
	Y78795	Homo sapiens	Human antizuai-2 (A2-2) amino acid sequence.	3556	77
40	U93121	Homo sapiens	M-phase phosphoprotein-1	3747	100
41	¥42750	Homo sapiens	Human calcium binding protein 1 (CaBP-1).	795	100
42	AF282626	Homo sapiens	latexin	1189	100
43	G02150	Homo sapiens	Human secreted protein, SEQ ID NO: 6231.	384	94
44	U19617	Mus musculus	Elf-1	2724	88
45	U19617	Mus musculus	Elf-1	2062	86
46	AF100758 Y87591	Homo sapiens	osteoinductive factor OIF	1538	100
49	X04145	Homo sapiens	Human SPROUTY-1 protein, SEQ ID NO:24.	1737	99
	<u> </u>	Homo sapiens	T3 gamma precursor (aa -22 to 160)	942	99
51	X63547	Homo sapiens	oncogene	5845	99
52	M94043	Rattus	rab-related GTP-binding	1089	96
53	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	norvegicus	protein		
54	L31783 X83973	Mus musculus	uridine kinase	917	71
55	AF224741	Homo sapiens	transcription factor chloride channel protein 7	4486	98
56	W74805	Homo sapiens	Human secreted protein	4128	99
			encoded by gene 77 clone HOEAS24.	1491	100
57	250907	Homo sapiens	Human TBC-1 cDNA from second transcript.	4824	100
58	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	6089	99
59	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	4014	91
60	¥59738	Homo sapiens	Human normal ovarian tissue derived protein 15.	601	100
61	AB031069	Homo sapiens	protein containing CXXC domain 1	1390	100
62	Y66660	Homo sapiens	Membrane-bound protein PR0783.	2492	99
63	Y66660	Homo sapiens	Membrane-bound protein PRO783.	1709	99
64	S70011	Rattus sp.	tricarboxylate carrier	895	55
65	AF139518	Rattus norvegicus	A-kinase anchor protein	178	24
66	W29666	Homo sapiens	Homo sapiens DH1308_1 clone secreted protein.	157	30
67	AJ245738	Homo sapiens	claudin-15	1206	100
68	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4183	87
69	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4906	86
70	282059	Caenorhabdit is elegans	Similarity to Drosophila ring canal protein comes from this gene	1285	44
71	AF224278	Homo sapiens	PMEPAl protein	1282	100
72	AF126426	Homo sapiens	neurotrimin	1809	100
73	Y41652	Homo sapiens	Human MEK2 protein sequence.	2065	99
74	Y41652	Homo sapiens	Human MEK2 protein sequence.	1207	100
75	AF188622	Mus musculus	selectively expressed in embryonic epithelia protein-1	1485	74
76	AE000406	Escherichia coli	putative DNA topoisomerase	950	100
77	X99302	Homo sapiens	Pop1	655	100
78	AL136538	Schizosaccha romyces pombe	similarity to S. cerevisiae kti12 protein	210	31
79	AF129756	Homo sapiens	G4	1554	99
		Dayrens	<u> </u>	+224	フゴ

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
80	AL096768	Homo sapiens	dJ858B16.2 (phosphatidylserine	2033	100
· ·			decarboxylase (PSSC, EC 4.1.1.65))		
81	AL096768	Homo sapiens	dJ858B16.2 (phosphatidylserine decarboxylase (PSSC, EC 4.1.1.65))	1220	96
82	X57351	Homo sapiens	1-8D	677	98
83	AC005594	Homo sapiens	R26984_1	2700	98
84	X73113	Homo sapiens	fast MyBP-C	5959	99
85	AF097330	Homo sapiens	H1 chloride channel; p64H1; CLIC4	1305	99
86	AB018423	Mus musculus	SH2 domain-containing protein	1360	78
87	AF272151	Homo sapiens	adaptor protein CIKS	3084	99
88	AF196329	Homo sapiens	triggering receptor expressed on monocytes 1	1214	100
89	ЛВ016879	Arabidopsis thaliana	contains similarity to pre- mRNA splicing factor-gene id:MRB17.2	634	36
90	AJ133721	Mus musculus	homeodomain protein	654	57
91	AJ242864	Mus musculus	phtf protein	619	61
92	A61971	unidentified	MCSP	11676	99
93	Y99365	Homo sapiens	Human PRO1250 (UNQ633) amino acid sequence SEQ ID NO:86.	3890	100
94	Y87231	Homo sapiens	Human signal peptide containing protein HSPP-8 SEQ ID NO:8.	1031	100
95	AF227741	Rattus norvegicus	protein kinase WNK1	2428	95
96	AF227741	Rattus norvegicus	protein kinase WNK1	1961	94
97	Y92513	Homo sapiens	Human OXRE-10.	1626	100
98	AL021366	Homo sapiens	cICK0721Q.3 (Kinesin related protein)	3423	100
99	AC005783	Homo sapiens	R33083_1	1974	99
100	¥95293	Homo sapiens	Human GEF containing NEK-like kinase substrate sGNK.	4092	99
101	AL118501	Homo sapiens	dJil91N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069))	1509	100
102	AJ006267	Homo sapiens	ClpX-like protein .	3233	100
103	AF100753	Homo sapiens	ancient ubiquitous 46 kDa protein AUP1	2042	96
104	AB015982	Homo sapiens	serine/threonine kinase	4718	100
105	AF151074	Homo sapiens	HSPC240	831	64
106	M35522	Canis familiaris	GTP-binding protein (rab7)	354	50
107	R99800	Homo sapiens	NTII-1 nerve protein, facilitates regeneration of nerve cells.	2337	93
108	AF125533	Homo sapiens	NADH-cytochrome b5 reductase isoform	1290	93
109	AC005614	Homo sapiens	F23269_2	3369	99
110	AF064729	Homo sapiens	RAN binding protein 16	3285	100
111	X52425	Homo sapiens	interleukin 4 receptor	4496	100
112	Y41686	Homo sapiens	Human PRO274 protein sequence.	2285	100
113	W15506	Homo sapiens	Mitogen activating protein kinase BRK1.	1991	100
114	Y71071	Homo sapiens	Human membrane transport protein, MTRP-16.	1190	99
115	AL049548	Homo sapiens	dJ398G3.1 (ortholog of rat CPG2)	3497	99
116	AF189817	Mus musculus	evectin-2	1124	90
117	W30891	Homo	Human cytostatin III protein.	715	99

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SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	7 %
ID	NUMBER			WATERMAN	IDENTITY
NO:	<u> </u>			SCORE	
		sapiens			
118	AF116618	Homo sapiens	PRO1038	1469	100
119 120	Y08915	Homo sapiens	alpha 4 protein	1748	100
120	AF098070	Drosophila melanogaster	Lis1 homolog	192	39
121	AF052432	Homo sapiens	katanin p80 subunit	181	37
122	Y70743	Homo sapiens	PSEQ-1 protein encoded by	2637	98
			NSEQ gene associated with matrix remodelling.		
123	AF083246	Homo sapiens	HSPC028	2132	100
124	Y27096	Homo sapiens	Human viral receptor protein	833	99
125	M63109	Leishmania	(ACVRP). glycoprotein 96-92	172	27
		major		172	27
126	U75467	Drosophila melanogaster	Atu	935	36
127	Z68220	Caenorhabdit	Similarity to Human ADP/ATP	438	43
		is elegans	carrier protein		
128	AF095927	Rattus norvegicus	protein phosphatase 2C	1927	94
129	W92958	Homo sapiens	Human zsig44 protein.	453	
130	AF115391	Lactobacillu	ribokinase RbsK	463	100
		s sakei	TIBORINGSE ROSK	508	37
131	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	1250	100
132	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	916	87
133	W52811	Homo sapiens	Human DBI/ACBP -like protein (DBIH).	705	97
134	Y84444	Homo sapiens	Amino acid sequence of a	3230	100
			human RNA-associated protein.		
135	M69181	Homo sapiens	non-muscle myosin B	189	20
136	W74882	Homo sapiens	Human secreted protein	480	100
			encoded by gene 154 clone HE6FL83		
137	W78200	Homo sapiens	Human secreted protein	855	99
			encoded by gene 75 clone		
138	AL033520	Homo sapiens	dJ349A12.1 (similar to	424	39
139	AF020261		KIAA0701 protein)		<u></u>
139	AF020261	Santalum album	proline rich protein	119	30
140	X70394	Homo sapiens	zinc finger protein	1634	100
141	Y06439	Homo sapiens	Human protease HUPM-8.	936	100
142	268493	Caenorhabdit	predicted using Genefinder	365	42
		is elegans			
143	AB018107	Arabidopsis thaliana	ADP-ribosylation factor-like	596	65
144	AF161483	Homo sapiens	protein HSPC134	F00	
145	Y84902	Homo sapiens	A human proliferation and	580 480	51
			apoptosis related protein.	*00	100
146	AB004906	Ipomoea purpurea	tran <i>s</i> posase	146	20
147	AC007357	Arabidopsis thaliana	F3F19.18	647	31
148	W75155	Homo sapiens	Human secreted protein	1494	
		nome supports	encoded by gene 41 clone	1494	98
149	Ar056490	Homo sapiens	cAMP-specific	3710	99
150	Y58171	Homo	phosphodiesterase 8A Human hydrolase homologue	785	99
151	1110202	sapiens	HHH-7.		
	U10397	Saccharomyce s cerevisiae	Yhr146wp	515	53
152	X73478	Homo sapiens	phosphotyrosyl phosphatase activator	1719	99
153	AL049697	Homo sapiens	dJ382I10.5.1 (novel protein	2034	90
		Dupicino	Inover broceru	4034	99

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
			similar to arginyl-tRNA)		
54	AF169802	Homo sapiens	cytochrome b5 reductase b5R.2	1455	99
55	X94703	Homo sapiens	rab28	1126	99
56	Y25716	Homo sapiens	Human secreted protein encoded from gene 6.	1471	100
158	W77404	Homo sapiens	Secreted salivary polypeptide zsig32.	937	100
159	¥17248	Homo sapiens	Human protein kinase inhibitor-2 (PKI-2).	383	100
160	J04970	Homo sapiens	carboxypeptidase M precursor	2395	100
161	W54040	Homo sapiens	Human interferon-inducible protein, HIFI.	484	98
162	AL022724	Homo sapiens	dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1)	1357	100
163	AF125535	Homo sapiens	pp21 homolog	193	45
164	G03632	Homo sapiens	Human secreted protein, SEQ	463	97
165	AJ250839	Homo sapiens	serine/threonine protein kinase	1442	71
166	L09649	Zymomonas mobilis	zm2	173	100
167	¥73337	Homo sapiens	HTRM clone 1944530 protein sequence.	1204	100
168	W88645	Homo sapiens	Secreted protein encoded by gene 112 clone HUKFC71.	1084	100
169	AF214731	Homo sapiens	ATP-dependent RNA helicase conserved protein	166	27
170	AE000871	Methanobacte rium thermoautotr ophicum		821	100
171	¥27684	Homo sapiens	Human secreted protein encoded by gene No. 118.	2904	100
172	AF226044	Homo sapiens	HSNFRK	779	100
173	AJ245946	Homo sapiens	neuroglobin	3202	100
174	D43949	Homo sapiens	This gene is novel.	1205	100
175	¥07923	Homo sapiens	GTP-binding protein		100
176	W90338	Homo sapiens	Human DP1 homologue protein.	966	100
177	¥41675	Homo sapiens	Human channel-related molecule HCRM-3.	1122	100
178	Y41674	Homo sapiens	Human channel-related molecule HCRM-2.	936	99
179	AF220492	Homo sapiens	krueppel-like zinc finger protein HZF2	1240	100
180	X03084	Homo sapiens		1813	89
181	U57344	Mus musculus		1743	86
183	U57344	Mus musculus		1070	86
184 185	U57344 AF033120	Mus musculus Homo sapiens	p53 regulated PA26-T2 nuclear		58
		1	protein pantothenate kinase 1 beta	1605	82
186	AF200357 W75058	Mus musculus Homo sapiens	Human secreted protein encoded by gene 2 clone	1188	99
(HLDBG33.	2424	100
188	AJ292529	Homo sapiens		3705	100
190 191	X54134 Y22203	Homo sapiens Homo sapiens	Human calcium-binding phosphoprotein, CBPP-1,	1083	99
192	W63692	Homo	protein sequence. Human secreted protein 12.	1975	100
193	W87772	sapiens Homo sapiens	Human serum glucocorticoid- regulated kinase (H-SGK2) polypeptide.	2605	99

SEQ	ACCESSION	SPECIES	DESCRIPTION		
ID NO:	NUMBER			SMITH- WATERMAN SCORE	IDENTITY
194	AF084259	Mus musculus	bromodomain-containing protein BP75	693	54
195	Y00752	Rattus norvegicus	serine dehydratase (AA 1 - 327)	994	61
196	W95349	Homo sapiens	Human foetal brain secreted protein fh170 7.	2596	100
197	AB028859	Homo sapiens	hDj9	1890	100
198	W95633	Homo sapiens		1614	100
199	Y44277	Homo	gene clone hm236_1. Human nucleic acid methylase-	2096	99
200	AB030039	Sapiens Homo sapiens	2.		1
201	X54162	Homo sapiens		2258	100
202	G02061	Homo sapiens	Human secreted protein, SEQ	2918	99
203	X13885	Nicotiana	ID NO: 6142.	558	99
		tabacum	extensin (AA 1-620)	185	33
204	J04204	Bos taurus	32 kd accessory protein	1837	100
205	J04204	Bos taurus	32 kd accessory protein	1101	100
	Y87283	Homo sapiens	Human signal peptide containing protein HSPP-60 SEQ ID NO:60.	1318	100
208	Y02860	Homo sapiens	Fragment of human secreted protein encoded by gene 65.	936	98
209	AL121889	Homo sapiens	dJ1076E17.1 (KIAA0823 protein (continues in AL023803))	694	54
210	AF226732	Homo sapiens	NPD007	1345	76
211	X66295	Mus musculus	Clq C chair.	970	73
212	Z29328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	966	100
213	229328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	542	98
214	AJ002030	Homo sapiens	progresterone binding protein	1163	100
215	X70649	Homo sapiens	member of DEAD box protein family	3933	100
216	AF250558	Homo sapiens	claudin-2	1169	99
217	AL021453	Homo sapiens	dJ821D11.1 (PUTATIVE protein)	259	100
218	Y08565	Homo sapiens	UDP-GalNAc:polypeptide N- acetylgalactosaminyltransfera se	3331	99
219	Y94452	Homo sapiens	Human inflammation associated protein	2067	100
220	AL035521	Arabidopsis	putative protein	315	42
221	AL031786	thaliana Schizosaccha	putative proline-trna	811	41
		romyces pombe	synthetase		41
222	AL109736	Schizosaccha romyces pombe	WD repeat protein	626	40
223	X52493	Glycine max	DNA-directed RNA polymerase	136	23
224	AL035659	Homo sapiens	dJ979N1.1 (dJ979N1.1)	5199	98
225 226	AB032401	Mus musculus	mmDj4	1761	92
226 227	AB032401	Mus musculus	mmDj4	1988	92
	X83502	Saccharomyce s cerevisiae	J1007	112	26
228	X83502	Saccharomyce s cerevisiae	J1007	79	25
229	AF143723	Homo sapiens	heat shock protein HSP60	2557	99
230	Y66677	Homo sapiens	Membrane-bound protein PRO828.	982	100
231	AB027466	Homo sapiens	spondin 2	1756	99
232	W95634	Homo sapiens	Homo sapiens secreted protein.	1391	100
233	W00365	Homo sapiens	Human cyclin Bl.	-3310	
234		Homo sapiens	A GTP-binding polypeptide	2218 1017	99 100
			Porthehrine	TOT /	100

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
			designated RAQ.		
235	250749	Homo sapiens	yeast sds22 homolog	1800	100
236	Z50749	Homo sapiens	yeast sds22 homolog	1754	98
237	AB026491	Homo sapiens	PICK1	2137	100
238	AJ270205	Entodinium	putative	114	37
		caudatum	phosphatidylinositol-4-		1
	}		phosphate 5-kinase		1
239 ·	AB030189	Mus musculus	contains transmembrane (TM)	710	93
239 .	MD030103	Mus muscurus	region and ATP binding region		1
	125555		Human hedgehog interacting	3785	99
240	W5653B	Homo sapiens		3703	1 33
	1		protein (HIP).		99
241	W56538	Homo sapiens	Human hedgehog interacting	3436	99
		i	protein (HIP).	!	
242	AF155107	Homo sapiens	NY-REN-37 antigen	996	99
243	AF155107	Homo sapiens	NY-REN-37 antigen	1005	100
244	AL031320	Homo sapiens	dJ20N2.1 (novel protein	763	99
	1		similar to yeast and	Į	
		1	bacterial cytosine	i	1
	1	[deaminase)	}	
		Barra	sodium channel beta 2 subunit	162	30
245	U37026	Rattus	socium channei beca 2 subunic	102	130
		norvegicus		-	
246	AL078599	Homo sapiens	dJ991C6.1 (novel protein	2391	98
	1		similar to C. elegans		
			F55A12.9 (Tr:P91086))	L	
247	U32274	Saccharomyce	Ydr386wp; CAI: 0.12	191	37
·	33-2.1	s cerevisiae			
248	Y41719	Homo	Human PRO864 protein	1879	100
240	141/13	sapiens	sequence.		
			ghrelin precursor	611	100
249	AB029434	Homo sapiens		246	38
250	X97831	Rattus	carnitine/acylcarnitine	246	38
	ı	norvegicus	carrier protein		
251	W80993	Homo	Human RIP-interacting factor	1724	100
	}	sapiens	RIF.	l	
252	Y94873	Homo	Human protein clone HP02632.	1876	100
		sapiens		}	
253	W59878	Homo sapiens	Amino acid sequence of the	765	100
	1.550.0		cDNA clone AIF-2 (HEBGM49).	1	1
254	AL354533	Leishmania	possible adenylate kinase	265	34
234	ALISTOS	major	possible adonyrace minera		1
<u> </u>		Mus musculus	zinc transporter like 2	1916	95
255	AF233322			2247	99
256	Y78113	Homo sapiens	Human cytokine signal	2241	1 99
		}	regulator CKSR-1 SEQ ID	1	{
			NO:1.		
257	AL035539	Arabidopsis	putative amino acid transport	390	27
		thaliana	protein	}	1
258	W74787	Homo sapiens	Human secreted protein	1171	100
	1		encoded by gene 58 clone	1	i
	1		HHFHN61.	1	1
259	AL035689	Homo sapiens	dJ187J11.1 (novel protein	974	100
4 59	ADUSSERS	Homo saprens	similar to protein kinase C	1	1
	1	1		1	1
			inhibitors)	1-25-	130
260	AE000909	Methanobacte	serine/threonine protein	363	30
	1	rium	kinase related protein	1	Į
	ŀ	thermoautotr		1	1
	1	ophicum	ţ	<u> </u>	_1
261	AL050131	Homo sapiens	hypothetical protein	626	100
262	AF019661	Mus musculus	zeta proteasome chain; PSMA5	1214	100
263	AL035593	Homo sapiens	dJ310J6.1 (novel protein)	821	100
				1072	100
264	AL022318	Homo sapiens	bK150C2.3 (PUTATIVE novel	1.1012	1 200
		<u> </u>	protein similar to APOBEC1)	 	+
	AF205940	Homo sapiens	endomucin	1289	100
265			dJ500L14.1 (novel protein)	789	100
265 266	AL023583	Homo sapiens	dosessia.i (notes present	1	
266	AL023583	J		1888	99
		Homo sapiens	dJ1103G7.3 (novel protein	1	99
266	AL023583	J		1	99

No. No.	SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
Score	ID NO:	NUMBER				TDENTITY
1894 1984 1985		ARICIATO				IDENTITY.
1270 No.	L -				1884	98
AP207600 Homo sapiens Intermediate filament 1952 100					1232	96
271 APZ07500 Home sapiens ethanolamine kinase 1952 100		1120703	1	HHa5 hair keratin type I	2190	99
273 AF161483 Homo sapiens intercellular adhesion 1436 100	271	AF207600		intermediate filament		
AF161463 Homo sapiens HSFC134 S57 100	272		Homo sapiens			100
273	1	1	baptens		1436	100
274	273	AF161483	Homo sapiens	HSPC134		
100 177576 100 1	274	Y53052	Homo sapiens		1	_1
### AP077042 Homo saplens Sor ribosomal protein 762 100	276	Vancas		df202_3 protein sequence SEQ ID NO:110.	587	100
Yes Yes		"		(HCYT) (clone 2195418).	762	100
Name Name			i	30S ribosomal protein S7 homolog	1269	100
279 Y68786				ca106 19x protein sequence SEO ID NO:20	1619	98
275134 Canis familiaris Food transducin 1718 96		Y68788	Homo sapiens	Amino acid sequence of a human phosphorylation	2801	.99
275134	280	275134			1816	100
APZ49873 Homo sapiens muscle-specific protein 1395 100	281	275134	Canis	rod transducin	1718	96
ALDSOOR Home sapiens hypothetical protein 1395 100	282	AF249873				1
284 AP201931 Homo sapiens DC1 1859 99 285 AP156102 Homo sapiens Extended human secreted 1250 99 286 Y35837 Homo sapiens Extended human secreted 1250 99 287 U88964 Homo sapiens HEM45 923 100 287 288 AL050143 Homo sapiens hypothetical protein 598 100 289 AJ011098 Homo sapiens hypothetical protein 598 100 289 AJ011098 Homo sapiens telethonin 574 100 289 AF034801 Homo sapiens liprin-alpha4 2565 98 292 AF034801 Homo sapiens liprin-alpha4 2565 98 293 AL049851 Homo sapiens liprin-alpha4 2590 100 294 Y73348 Homo sapiens HTRN clone 839651 protein 1738 106 2796 AL035423 Homo sapiens dJ2013.1 (brain mitochondrial carrier protein-1 (BMCP1)) 297 AF198532 Homo sapiens liprin-alpha4 1024 79 299 AF159141 Homo sapiens Species Liprin-alpha4 2565 98 299 299 AF159141 Homo sapiens Species Liprin-alpha4 2565 98 299 299 AF159141 Homo sapiens Species Liprin-alpha4 2565 98 299 299 AF159141 Homo sapiens Species Liprin-alpha4 2565 99 299 299 200 2	283		Homo sapiens	muscle-specific protein		100
285 AF155102 Homo sapiens ELL complex EAP30 subunit 1318 99	284	AF201931	Homo sapiens	hypothetical protein		1
286 Y35897	285	AF156102	Homo sapiens			1
287 U88964 Homo sapiens HEM45 923 100	286	Y35897	Homo sapiens	Extended hyman secretari		
288 AL055143 Homo sapiens HEMAS 923 100 289 AJ011098 Homo sapiens hypothetical protein 598 100 290 Y66724 Homo sapiens telethonin 574 100 291 AF034801 Homo sapiens PRO836. 2321 100 291 AF034801 Homo sapiens liprin-alpha4 2565 98 292 AF034801 Homo sapiens liprin-alpha4 2590 100 293 AL049851 Homo sapiens dy8897228.1 (novel protein 1738 100 294 Y73348 Homo sapiens zinc finger protein 1245 99 295 L11672 Homo sapiens zinc finger protein 1694 44 296 AL035423 Homo sapiens lymphoid enhancer binding 2173 100 297 AF198532 Homo sapiens MsPc299 1147 85 299 AF161417 Homo sapiens hspeast cancer metastasis- 1236 99	300			protein sequence, SEQ ID NO.	1250	99
AD011098 Homo sapiens hypothetical protein 598 100	} ~~.		Homo sapiens		923	100
Note			Homo sapiens	hypothetical protein		
Sapiens Sapiens PRO836. PRO836. PRO836. PRO836. PRO836. PRO836. PRO836. PRO836. PRO836. PRO836. PRO836. PRO84801 Homo sapiens Liprin-alpha4 2565 98 PRO84801 Homo sapiens Liprin-alpha4 2590 100 100 2590 100 100 2590 100 100 2590 100 100 2590 100 2590 100 2590 100 2590 25					574	
AF034801 Homo sapiens Liprin-alpha4 2565 98 2590 100 2590 100 2590 100 2590 100 2590 100 2590 100 2590 100 2590 100 2590 100 2590 2590 100 2590			sapiens	PRO836.	2321	100
ALO49851 Homo sapiens Comparison Com			Homo sapiens		2565	98
100 1738 100 1738 100 1738 100 1738 100 1738 100 1738 100 1738 100 1738 100 1245 12				liprin-alpha4	2590	
Y73348	273	WID 4 2 9 2 1	Homo sapiens	dJ889J22B.1 (novel protein	1738	
295 L11672	294	¥73348	Homo sapiens	HTRM clone 839651 protein	1245	
AL035423 Homo sapiens Zinc finger protein 1694 44	295	L11672	HOMO sanda		[
297 AP198532 Homo sapiens Lymphoid enhancer binding 2173 100				zinc finger protein		
100	297		•	carrier protein-1 (BMCP1))	1024	79
299 AF159141 Homo sapiens HSPC299 1147 85				factor-1	2173	100
Suppressor 1 1236 99 1236 99 300 U26397 Rattus inositol polyphosphate 4- 160 30 30 301 AF036145 Homo sapiens meningioma-expressed antigen 3458 100 302 Z82022 Homo sapiens GlcNac-1-P transferase 2067 99 303 AF269232 Mus musculus butyrophilin-like protein 271 50 304 AJ222644 Arabidopsis thaliana asparaginyl-tRNA synthetase 659 50 305 AF054180 Homo hematopoletic cell derived 351 79 306 AJ272079 Homo sapiens APOBEC-1 stimulating protein 3056 100 309 AJ131891 Homo Human GPRW receptor 1721 100 309 AJ131891 Homo Homo Homo Homo Human GPRW receptor 1721 100 309 AJ131891 Homo Hom			Homo sapiens		1147	85
100 100			{	suppressor 1	1236	99
100 302 Z82022 Homo sapiens GlcNac-1-P transferase 2067 99			norvegicus	phosphatase	160	30
AF269232 Mus musculus butyrophilin-like protein 271 50	1			5	3458	100
AF269232 Mus musculus Butyrophilin-like protein 271 50				GlcNac-1-P transferase	2067	99
thaliana asparaginyl-tRNA synthetase 659 50 AF054180 Homo hematopoietic cell derived 351 79 sapiens zinc finger protein 351 79 AJ272079 Homo sapiens APOBEC-1 stimulating protein 3056 100 Y44486 Homo sapiens Pulman GPRW receptor polypeptide.	}		Ì	butyrophilin-like protein BUTR-1	271	
sapiens zinc finger protein 351 79 306 AJ272079 Homo sapiens APOBEC-1 stimulating protein 3056 100 Homo Sapiens Polypeptide. 1721 100 309 AJ131891 Homo Sapiens Polypeptide.	İ		thaliana		659	50
A08 Y44486 Homo sapiens APOBEC-1 stimulating protein 3056 100 Human GPRW receptor 1721 100 Sapiens polypeptide.			sapiens	hematopoietic cell derived zinc finger protein	351	79
308 Y44486 Homo Human GPRW receptor 1721 100 sapiens polypeptide.			Homo sapiens	APOBEC-1 stimulating protein	3056	700
AJ131891 Homo Sanions DWA	- 1	¥44486	Homo sapiens	Human GPRW receptor		
NA polymerase mu 2598 100	309	AJ131891		DNA polymerase mu	2599	

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:		Homo sapiens	p30 DBC	1248	92
10	111111111111111111111111111111111111111	Marc musculus	F-box protein FBL12	1501	93
12	AF176525 X57802	Homo sapiens	immunoglobulin lambda light chain	959 -	81
			Net	2048	98
113	236715	HOWO SWETCHE	HSPC047	727	100
314	AF161532	HOMO Dupadine	kelch-like protein KLHL3a	3046	100
315 316	AF208068 Y66666	Homo sapiens	Membrane-bound protein	1166	100
	1	sapiens	PRO1013.	1253	98
317	Y29666	Homo sapiens	Human Ras protein RAPR-1.	2614	99
318	AJ387747	Homo sapiens	sialin	224	40
319	AF161362	Homo sapiens	HSPC099	2243	99
320	Y68773	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-5.		
	AJ238379	Homo sapiens	putative TH1 protein	3013	100
321	AB040812	Homo sapiens	protein kinase PAK5	3792	99
322		Homo sapiens	Human secreted protein	913	100
323	¥95013		vc48_1, SEQ ID NO:66. Amino acid sequence of	1976	100
324	¥13381	Homo sapiens	protein PRO271.	2305	98
325	Y94944	Homo sapiens	Human secreted protein clone bf157_16 protein sequence SEQ ID NO:94.		99
326	Y76884	Homo sapiens	Retinoblastoma binding protein-7sequence.	6728	
327	AF198532	Homo sapiens	lymphoid enhancer binding factor-1	2173	100
328	Z78013	Caenorhabdit	Similarity to Drosophila Cadherin-related tumor	569	33
		is elegans	suppressor	484	94
329	AF212921	Mus musculus	MMTV receptor variant 1 nuclear protein SA-1	6492	99
		sapiens] >R65207 R65207 02- MAR-1995 27- AUG-1993 Human stromalin-1. [Homo			
331	AL008583	Homo sapiens	dJ327J16.3 (supported by GENSCAN, FGENES and GENEWISE)	2133	99
332	Y36104	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO.		41
122	AJ271669	Homo sapiens	putative sialoglycoprotease	1747	100
333	AF156598	Mus musculus	1 n53-regulated DDA3	997	64
334	M99058	Eimeria	em100 gene is homologous the	154	26
336	Y85564	Homo sapiens		3386	97
337	¥85564	Homo sapiens	Human homologue of UNC-53	2602	94
338	Y85564	Homo sapiens	Human homologue of UNC-53	3447	98
		Caenorhabdi	(Hs-UNC-53/1) sequence.	716	34
339	266561	is elegans	protein (PIR Acc. No.	2761	99
340	AB021643	Homo sapiens	gonadotropin inducible transcription repressor-3		98
341	G01946	Homo sapien	s Human secreted protein, SEQ	465	
	AF020591	Homo sapien	e zinc finger protein	1091	48
342	ME O COSSI	Homo sapien	The beauty about	439 .	84

NO:	ACCESSIO NUMBER	N SPECIES	DESCRIPTION VDJ region	SMITH- WATERMAN SCORE	IDENTITY
344	U10281	Sus scrofa	gastric mucin		
345	AK000404	Homo sapien	gastite mucin	279	24
346	L22557	Rattus		1177	99
		norvegicus	calmodulin-binding protein	1949	84
347	L22557	Rattus	calmodulin-binding protein	2363	
348	AL049481	norvegicus Arabidopsis	1	2363	91
		thaliana	Process	316	30
350	AJ251516	Mus musculus		1460	99
351	AK024477	Homo sapiens	protein	1230	33
352	U50133	Homo sapiens		1773	100
353	AK000625	Nomo sapiens		502	33
354	AF161420	Homo sapiens		721	100
355		Homo sapiens	HSPC302	2623	97
356	AJ010014	Homo sapiens	M96A protein	1269	_
	AF151029	Homo sapiens	HSPC195		47
357	AL022327	Homo sapiens	dJ355C18.1 (KIAA0027)	941	91
358	W78128	Homo sapiens		1911	100
			encoded by gene 3 clone	1117	100
359	X03414	Drosophila	Kr polypeptide	25.6	<u> </u>
360	AF151079	melanogaster	_ · · · · · ·	316	45
361		Homo sapiens		643	100
70T	Y53886	Homo sapiens		530	41
3.50			signalling protein designated HSCOP-6	330	41
362	AF254741	Drosophila melanogaster	Centaurin Gamma 1A	681	46
363	AF213465	Homo sapiens			
364	AF181562	Homo sapiens		2016	100
365	AF181562	Homo sapiens	prosaas	1319	100
366	U73200		proSAAS	1024	99
367	AF263744	Mus musculus	pll6Rip	884	82
368		Homo sapiens	erbb2-interacting protein ERBIN	4973	99
369	U37501	Mus musculus	laminin alpha 5 chain	5867	72
309	AF043695	Caenorhabdit	similar to the protein	549	
370	Y73440	is elegans Homo sapiens	phosphates 2c family	349	36
371		_	Human secreted protein clone yj23_1 protein sequence SEQ ID NO:102.	1484	99
372	AF272833	Homo sapiens	misato	2869	
312	AF198454	Homo sapiens	epithelial protein lost in	3927	97 100
373	Y73345	Homo sapiens	neoplasm beta HTRM clone 438283 protein		
374	AF169017	Homo sapiens	sequence.	273	80
		_	formiminotransferase cyclodeaminase	2717	98
75	A95106	unidentified	RED ALPHA	1 1 202	
76	W74828	Homo sapiens	Human secreted protein	1202	99
			encoded by gene 100 clone HLQAB52.	1012	99
77	Y32131	Homo sapiens	Human LYST-2 protein.		İ
78	M14912	**.		3556	99
79	AF090934		pol	132	86
80	X66363		PR00518		100
81		i	serine/threonine protein kinase	+	100
{		sapiens	Human PRO703 protein sequence.	2362	100
82	AF174498	Homo sapiens	GR AF-1 specific protein	7008	98
33	U64608	Caenorhabdit	phosphatase coded for by C. elegans cDNA	246	36
34	ÚS0133	15 elegans	yk173c12.5		
			ankyrin	502	33
15 1				2	
35	AU236520	Homo sapiens	putative transcription factor-like nuclear regulator	4123	7

ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:			BM-003	1375	99
87	AF208845	HOWO Sabasse	immunoglobulin lambda light	797	76
89	X57821		chain		1
90	AF182404	Homo sapiens	mitochondrial uncoupling	1670	99
91	Y85564	Homo sapiens	protein 1 Human homologue of UNC-53	3386	97
			(Hs-UNC-53/1) sequence.	3700	100
93	AF178432	******	SH3 protein cytoplasmic protein 89BC	1616	62
94	AF229928	Drosophila melanogaster	cytoplasmic protein 335c	2254	100
95	AF181721		RU2S	1626	98
96	Y69197	Homo sapiens	Amino acid sequence of a human betaIV-spectrin protein.	1620	
			zinc finger protein neuro-d4	749	60
397	U48238	Mus musculus	hymothetical protein	263	51
98	AL390137	Homo sapiens	Down syndrome cell adhesion	5337	60
399	AF217525	Homo sapiens	molecule	447	27
400	AL022599	Schizosaccha romyces	WD repeat protein		
401	AC004859	Homo sapiens	similar to 2-oxoglutarate dehydrogenase ; similar to Q02218 (PID:g1352618)	4176	78
		Mus musculus	tenascin-X	10246	62
402 403	AB010266 AL133288	Homo sapiens	dJ671D7.1 (similar to D.melanogaster CG5986	761	100
	<u> </u>		protein)	888	48
404	Z68753	Caenorhabdit is elegans	ZC518.3b	569	33
405	278013	Caenorhabdit is elegans	Cadherin-related tumor		
406	AB031230	Homo sapiens	protein containing CXXC	1196	97
	1	Homo sapiens	NV_DEN_36 antigen	1168	100
407 408	AF155106 Y57945	Homo sapiens	Human transmembrane protein HTMPN-69.	1538	99
		Ovis aries	trichohyalin	184	30
409	Z18361		RhoGEF	2733	100
410	AF249744	Homo sapiens		2072	94
411	AF176529	Mus musculus		4880	100
412	AF210842 AL031658	Homo sapiens Homo sapiens	dJ310013.7 (novel protein similar to H. roretzi HRPET-	776	98
		 	pm5 protein	6131	99
414	X57398 AB029826	Homo sapiens	3-methylcrotonyl-CoA carboxylase biotin-containing	2961 .	99
416	U43503	Saccharomyce		115	42
417	AL160493	s cerevisiae Leishmania	possible t26f17.21	239	35
		major	Human PRO331 protein.	330	29
418	Y08100	Homo sapiens		2228	54
419	U15131	Homo sapiens	p126 Link guanine nucleotide	2363	100
420	AF117946	Homo sapiens	exchange factor II	755	30
421	AF190635	melanogaster	ankyrin 2	1962	100
422	AF302150	Homo sapiens	phosphoinositol 3-phosphate- binding protein-2	433	94
423	AL137530			7269	100
424	X63753	Homo sapiens	son-a	1693	100
425	AB027249	Homo sapiens		1084	55

ID	ACCESSIO NUMBER	SPECIES	DESCRIPTION	SMITH-	\$
NO:	AF279144	Homo sapier		WATERMAN SCORE	IDENTI
430		1	precursor	1259	56
428	AE003683	Drosophila melanogaste	CG8312 gene product	149	29
429	Y07829	Homo sapien			1
430	AF096897	Drosophila	pushover	2201	99
431		melanogaste	r	4442	47
432	U41387 AF023674	Homo sapien		4021	99
433	AF146760	Homo sapien		3783	100
		sapiens	septin 2-like cell division control protein	2284	100
434	AB006697	Arabidopsis	cleft lip and palate		
		thaliana	associated transmembrane	886	42
437	Y94247	Homo sapiens	Human calcium binding protein	1704	100
438	AB040672	Homo sapiens			
		-	acetylgalactosaminyltransfera	1075	63
439	AF105228	Page 1	_ se		
440	R06463	Bos taurus Homo sapiens	tuftelin	285	33
		saprens	Derived protein of clone ICA13 (ATCC 40553).	3073	99
441	X14971	Mus musculus	alpha-adaptin (A) (AA 1-977)	14865	
442	X53773	Rattus	alpha-c large chain (AA 1-	4897 3979	98
443	Y66689	norvegicus Homo	938)	1	81
]	sapiens	Membrane-bound protein PRO1136.	3299	99
444	AC067754	Arabidopsis	unknown protein; 20348-23707	-	L
445	AF229032	thaliana		114	33
445	AF229032 AF056035	Mus musculus Rattus		2077	93
		norvegicus	s-nexilin	2662	85
447	AF132484	Mus musculus	unknown		
448	W89024	Homo sapiens	Polypeptide fragment encoded	478 528	51
449	AF161445	l Woma	by gene 156.	320	45
450	268753	Homo sapiens Caenorhabdit	HSPC327 ZC518.3b	1606	100
Tate		is elegans	2C316.3D	951	49
151	W39160	Homo sapiens	Human partial complement	155	
52	W85727	[factor H protein fragment a	155	32
	33727	Homo sapiens	Novel protein (Clone	2799	99
53	Y53629	Homo sapiens	BM46_10). A bone marrow secreted	1	
			protein designated BMS115	2810	100
54	D87438	Homo	Similar to a C.elegane	4069	100
55	AF240468	sapiens Homo sapiens	protein in cosmid Clarlo		100
56	Z15005	Homo sapiens	nicastrin CENP-E	3687	100
57	M59216	Homo	gamma-aminobutyric acid	13305	99
58	W03465	sapiens	receptor beta-1 subunit	2477	100
-6	Y73467	Homo sapiens	Human secreted protein clone	966	100
1		ļ	yd61_1 protein sequence SEO		~00
59	W67824	Homo sapiens	ID NO:156. Human secreted protein		
1	1		encoded by gene 18 clone	535	100
50	AF1623 ==		HSLFM29.		
~	AF163151	Homo sapiens	dentin sialophosphoprotein	279	19
51	D87446	Homo sapiens	precursor	- 1.	~~
	1	sabreus	Similar to a C.elegans	9196	99
			protein encoded in cosmid C27F2 (U40419)	l	
2 (G04044	Homo sapiens	Human secreted protein, SEO	486	
3 7	AC002398		ID NO: 8125.	200	3
			F25965_1	1018 1	.00
	AF223408		7acomp protein		4
		- Papiens	B99		9

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:		Homo sapiens	R99	2878	87
66	AF223408		gene trap locus-13	6336	91
67	AF104415	Mus musculus	Jun dimerization protein 1	196	4.9
68	U53450	norvegicus	JDP-1	3564	99
69	AL031297	Homo sapiens	dJ97P20.1 (novel gene)	1274	95
70	AF257077	Homo sapiens	eukaryotic translation initiation factor EIF2B subunit 3		
171	L28125	Podospora anserina	beta transducin-like protein	284	38
472	Y84903	Homo sapiens	A human proliferation and apoptosis related protein.	2337	100
173	AF144237	Homo sapiens	LOMP protein	252	44
174	Y71213	Homo sapiens	Human irritable bowel disease	838	100
		Homo sapiens	related polypeptide IMX39. Human secreted protein	3411	100
475	Y95006	Homo sapiens	vel3_1, SEQ ID NO:52.		
100	D38549	Homo sapiens	hal025 is new	6533	99
476	D38549 AF241230	Homo sapiens	TAK1-binding protein 2	3656	100
477 478	AL031534	Schizosaccha romyces pombe	putative asparagine synthase	482	40
479	128125	Podospora anserina	beta transducin-like protein	233	26
400	AF161544	Homo sapiens	HSPC059	434	77
480	AJ238248	Homo sapiens	centaurin beta2	3986	99
481		Saccharomyce	mal5, stal, len: 1367, CAI:	295	23
482	Z38061	s cerevisiae	0.3, AMYH YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)		
	AF161381	Homo sapiens	HSPC263	1404	100
483	AF223468	Homo sapiens	AD021 protein	1314	100
484	X57527	Homo sapiens	alpha 1(VIII) collagen .	4166	99
486	¥19062	Homo sapiens	39k3 protein	2475	100
487 488	¥73373	Homo sapiens	HTRM clone 921803 protein sequence.	555	56
489	AL021918	Homo sapiens	b3418.1 (Kruppel related Zinc	4184	100
490	X53773	Rattus	alpha-c large chain (AA 1-	4675	97
		norvegicus	GOK	1459	59
491 492	U52426 AL359773	Homo sapiens Leishmania	possible threonine synthase	702	45
	l	major		2929	100
493	AF226614	Homo sapiens	ferroportinl	513	96
494	Z93241	Homo sapiens	dJ222E13.1 (novel protein with some similarity to Drosophila KWAKEN)	313	
495	AF036977	Homo sapiens	unknown	1812	100
495	U93564	Homo sapiens		133	45
497	Y91405	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:126.	357	100
498	AF069781	Drosophila melanogaster	Bem46-like protein	653	43
499	Y16601	Homo sapiens	Human cell-cycle phosphoprotein CECYP-2.	1658	98
500	X70944	Homo sapiens	PTB-associated splicing factor	3883	100
501	AF027503	Mus musculus	putative membrane-associated guanylate kinase 1	205	36
502	AF282874	Homo sapiens		2856	99
502	AJ249732	Homo sapiens		669	100
504	AF208861	Homo sapiens	BM-019	1629	100
504	L09708	Homo sapiens		4022	100
505	X66285	Mus musculus	HC1 ORF	115	43
	D00189	Rattus	Na+, K+-ATPase alpha-subunit	5227	99

NO:	TOUR TOUR		DESCRIPTION	SMITH- WATERMAI SCORE	
	1949/1	Homo sapie	ns Human secreted protein clone fal71_1 protein sequence SEG		100
510	AB019038		1D NO:148.	'	
511	AB019038	Homo sapie		781	
512	AB019038	Homo sapie	15 Deta-1,4 mannosyltransforace	1347	77
513	X84908	Homo sapie	us Deta-1,4 mannosyltransferace	1520	100
514	X52851	Homo sapier	ns phosphorylase kinase	5729	99
515	AF186084	Homo sapier	as peptidylprolyl isomerace	650	99 76
	111 100003	_	epidermal growth factor	3046	99
516	G03602	Homo sapier	repeat containing protein IS Human secreted protein SEO	505	
517	U04706		1 TD NO: 7683.	1 303	99
518	G00653	Bos taurus	50 kDa protein	1749	77
	900033	Homo sapien		530	100
519	AF161475		1D NO: 4734.	1 330	100
520	¥99366	Homo sapien		1368	100
	177500	Homo sapien		3394	97
521	AF266852	Homo sapien	10010 880000000 000 000 000	1 -05.	3'
522	AE000995	Archaeoglob	S PTPLA	1295	100
	1.2000555			153	20
523	AF062249	s fulgidus	protein (smc1)	1 200	120
		monio sapiens		605	97
524	AJ223830	Rattus	variable region		13,
		norvegicus	ARE1	2950	98
525	W01535	Homo sapiens	Colles	1	
	1	Suprem	The state of the	1276	83
526	AF145658	Drosophila	BcDNA.GH10229	1	1
		melanogaster	BCDNA.GH10229	320	33
527	AF112213	Homo sapiens		ĺ	
			putative Rab5-interacting	524	79
528	D49387	Homo	NADP dependent leukotriene b4		1
	1	sapiens	1 12-hVdrovydobyd	1616	100
529	Y30819	Homo sapiens	Human secreted protein		1
530		1	encoded from gone	328	32
530	AL079335	Homo sapiens	dJ132F21.3 (72.1 KDa protein		i
	1		(UKEZP564A032 SERTOR)	1059	99
	ļ		Similar to mouse TEM-Campa		1
531	¥91506		[Induce MG11]		ļ
JJ 1	131206	Homo sapiens	Human secreted protein	1159	
	<u> </u>		sequence encoded by cone to	1139	98
532	X76116		1 SEQ 1D NO:179.		
	1 1/0116	Caenorhabdit	carrier protein (c2)	576	50
533	X76116	is elegans Caenorhabdit	}	3.0	50
	470220	is elegans	carrier protein (c2)	506	50
534	X12966	To eregans	,		30
- 1		TOWO Rabrers	3-oxoacyl-CoA thiolase	1972	100
35	¥09267	Homo sapiens	propeptide (424 AA)		100
[1	nomo sapiens	flavin-containing	2486	100
36	Z11773	Homo sapiens	monooxygenase 2	f	
37	D84224	Homo sapiens	SRE-ZBP	2201	99
38	D84224	Homo sapiens	methionyl tRNA synthetase	4741	99
39	D84224	Homo sapiens	methionyl tRNA synthetase	3887	99
40		Homo sapiens	methionyl tRNA synthetase		96
41	J03244	Bos taurus	methionyl tRNA synthetase		99
_		caurus	H+ ATPase 31kDa subunit (EC		77
	Y92514	Homo sapiens	3.6.1.3)	1	1
		Homo Sapiens	Human OXRE-11.	2301	99
	· ·	sapiens	Smad- and Olf-interacting		61
14			zinc finger protein	1	
1		rium	conserved protein	207	38
- 1		thermoautotr	{	1.	
		ophicum			1
	1 (ODIIICUM			
15 7			preTGF-betal		1

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:	Y02698	Homo sapiens	Human secreted protein	854	98
46	102030	HOMO BOFF	encoded by gene 49 clone		ŀ
			HTPCS60.		
10	AF112205	Homo sapiens	WSB-1 protein	2275	100
47	X60271	Mus musculus	c-rel	2264	74
48	AC016827	Arabidopsis	putative GTPase	810	42
49	ACU1002	thaliana			<u> </u>
	Y70400	Homo	Human cell-signalling	429	68
50	Y /0400	sapiens	protein-2.		
		Homo sapiens	NEDD4-like ubiquitin ligase 1	8290	99
51	AB048365	Homo sapiens	Human transmembrane protein	1112	95
552	Y57880	HOMO Sabiens	HTMPN-4.		
			PRO1847	265	67
553	AF119855	Homo sapiens	MHC HLA-DQ alpha precursor	1332	100
554	M17236	Homo sapiens	putative protein	540	40
555	AL078468	Arabidopsis	putative protein		
	1	thaliana	- V-lab myotoing.	515	44
556	AC006963	Homo sapiens	similar to Kelch proteins;	3-0	1
-	1	1	similar to BAA77027		1
	1	1	(PID:g4650844)	1623	98
557	AK024487	Homo sapiens	FLJ00086 protein	117	48
558	M12140	Homo sapiens	pol gene protein; Xxx		56
5 5 9	W74825	Homo sapiens	Human secreted protein	225	ء ا
9 9 9	", 4023		encoded by gene 97 clone	l	
	1	1	HAQBF73.	<u> </u>	
5.60	X56681	Homo sapiens	junD protein	373	88
560	AF003136	Caenorhabdit	contains weak similarity to	2926	54
561	AF003136	is elegans	an AMP-binding motif	i	
		Homo sapiens	ATIOGOP2.3.1 (novel PABPC)	877	100
562	AL109839	HOMO Saprens	(poly(A)-binding protein)	1	
		Drosophila	BcDNA.GH09817	289	42
563	AF181640		1.	1	
		melanogaster	gag-pol precursor polyprotein	1547	43
564	AF052723	Feline		į	i
	,	leukemia	gPr80	1	ŀ
		virus		439	44
565	AF161472	Homo sapiens	HSPC123	3338	100
566	Y28817	Homo sapiens	pt326_4 secreted protein.	1738	100
567	U09848	Homo sapiens	zinc finger protein	3603	93
569	AF155113	Homo sapiens	NY-REN-55 antigen	3951	99
570	AF155113	Homo sapiens	NY-REN-55 antigen		98
571	AL032821	Homo sapiens	dJ55C23.1 (vanin 1)	1821	99
572	M69181	Homo sapiens	non-muscle myosin B	7350	
573	M69181	Homo sapiens	non-muscle myosin B	7311	98
	¥59678	Homo sapiens		772	100
574	1270/0	TOWN SEPTEMB	E6-PL.		
	AL365234	Arabidopsis	putative protein	788	40
575	AU365234	thaliana		1	
			putative protein	788	40
576	AL365234	Arabidopsis thaliana	paddata partia	} .	
			DNA polymerase alpha-subunit	7619	99
577	X06745	Homo sapiens	(AA 1 - 1462)	1	1
l				1342	100
578	AB041642	Homo sapiens	PAR-6 similar to yeast adenylate	2446	100
	D86984	Homo sapiens	similar to yeast adenyiate		1
579	100304	1	cyclase (S56776) gamma-aminobutyric acid A	2499	99
579	D86984		I	1 - 3 - 7 -	1
579 580	AF165124	Homo sapiena	gamma-aminobecyire done	1	
			receptor gamma 2	2229	
580		Homo sapiens	receptor gamma 2 Polypeptide fragment encoded	2339	99
	AF165124		receptor gamma 2 Polypeptide fragment encoded by gene 58.		
580	AF165124 W88812	Homo sapiens	receptor gamma 2 Polypeptide fragment encoded by gene 58. novel ORF	342	100
580 581 582	AF165124 W88812 U82319	Homo sapiens	receptor gamma 2 Polypeptide fragment encoded by gene 58. novel ORF		
580	AF165124 W88812	Homo sapiens Homo sapiens Homo sapiens	receptor gamma 2 Polypeptide fragment encoded by gene 58. novel ORF	342	100
580 581 582 583	AF165124 W88812 U82319 P92219	Homo sapiens Homo sapiens (human)	receptor gamma 2 Folypeptide fragment encoded by gene 58. novel ORF CR1 protein.	342	100 99 99
580 581 582 583	AF165124 W88812 U82319 P92219 AJ223948	Homo sapiens Homo sapiens (human) Homo sapiens	receptor gamma 2 Folypeptide fragment encoded by gene 58. novel ORF CR1 protein. RNA helicase	342	100
580 581 582 583	AF165124 W88812 U82319 P92219	Homo sapiens Homo sapiens (human)	receptor gamma 2 Polypeptide fragment encoded by gene 58. novel ORF CRI protein. RNA helicase B8KDa nuclear pore complex	342 11425	100 99 99
580 581 582 583	AF165124 W88812 U82319 P92219 AJ223948 Y08612	Homo sapiens Homo sapiens Homo sapiens (human) Homo sapiens Homo sapiens	receptor gamma 2 Polypeptide fragment encoded by gene 58. novel ORF CR1 protein. RNA helicase B8kDa nuclear pore complex protein	342 11425	100 99 99
580 581 582 583	AF165124 W88812 U82319 P92219 AJ223948	Homo sapiens Homo sapiens (human) Homo sapiens	receptor gamma 2 Polypeptide fragment encoded by gene 58. novel ORF CRI protein. RNA helicase B8KDa nuclear pore complex	342 11425 6608 3874	1.00 99 99 99

NO:	NOMBER		DESCRIPTION	SMITH- WATERMA	
588	AF131775	Homo sapie		SCORE	IDEKTI
589	AJ250865			1929	99
591	Z98885	Homo sapie		2348	100
1		nomo sapie		4167	100
1			containing 1 (similar to		1 200
592	L76571	Homo sapie	peregrin, BR140))		ì
593	AF091622	Homo sapie		1355	100
594	X56807	Homo sapie		9054	100
595	AL137802	Homo sapie		4443	100
596	AL022329	Homo sapie			55
	1 - 1 - 1 - 1	sapiens	DK407F11.2 (adrenergia bet	3653	
597	AF226048			7 3033	100
598	AJ278112	Homo sapier		2009	_
	1102/0112		putative cell cycle control	335	99
		sapiens)	protein	335	23
	İ	>Y49635			
	1	Y49635 21-	1	- 1	
	}	OCT-1999 15	i-		1
		APR-1998		1	1
	1	Human sdp3.	5		
	1	protein.		1	1
	ĺ	[Homo			ŀ
599	Y59741	sapiens	}		1
	139/41	Homo sapien			
600	L36531		derived protein 18	1574	99
601	Y38458	Homo sapien	s integrin alpha 8 subunit	-	
-01	130528	Homo sapiens	Human secreted protein	5386	99
602	1 22225		encoded by ann w	895	100
603	AF218584 Y13115	Homo sapiens	GGA1		
	1 113112	Homo sapiens	serine/threonine protein	3265	100
604	AL132776		Kinase	5071	99
605	AL034452	Homo sapiens			
005	AD034452	Homo sapiens	dJ682J15.1 (nove) Collagon	2413	99
	1		triple helix renear	1979	100
606	Y14494		Containing	l	
607	AJ001981	Homo sapiens	aralari	3465	<u> </u>
508	X86098	Homo sapiens		2603	99
	A00098	Homo	binds directly to adenovirus	<u></u>	100
10	AF163572	sapiens	Lype 5 Ela protein	3069	100
	74 1035/2	Homo sapiens	Forssman glycolinid	1865	
11	AF161503		synthetase	7902	99
12	L41834	Homo sapiens		1261	
13	Y91954	Ensis minor	nuclear protein	345	97
	AJ1334	Homo sapiens	Human cytoskeleton associated	3668	30
14	AL022327		Protein 9 (CYSKP-9)	2008	100
15	X85786	Homo sapiens	dJ355C18.1 (KTAA0027)	1363	
16		Homo sapiens	binding regulatory factor	361	94
17	Y08319	Homo sapiens	kinesin-2	3203	100
18	D12644	Mus musculus	KIF2 protein	3487	99
19	U28789	Mus musculus	PACT	3609	97
-	Y35914	Homo sapiens	Extended human secreted	5936	89
- 1	1	-	protein sequence, SEQ ID NO.	1684	99
0	7004		163.	1	
.	AB046382	Mus musculus	testis-abundant finger		
1			protein	199	23
-	Y00062	Homo sapiens	precursor polypeptide (AA -23		
			to 1120)	3440	99
	AF068286	Homo sapiens	HDCMD38P	}	
	X98248	Homo sapiens	sortilin	861	100
4	X61100	Homo sapiens	75 kD2		99
			75 kDa subunit NADH		99
5	\$58544	Homo sapiens	dehydrogenase precursor	1	·
			75 kda infertility-related	2125	99
	AF151027		sperm protein	1	- 1
7 2	(14968 I		HSPC193	582	3
			RII-alpha subunit (AA 1-404)		00
1	-	-ome saptens	Human fetal brain cDNA clone vb7_1 derived protein		.00

SEQ	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:	Y50911	Homo sapiens I	Human recar brain com comment	1694	100
2.5	}		vb7_1 derived protein 17 beta-hydroxysteroid	1754	100
30	AF098786	caniens	dehydrogenase type VII	4273	100
31	AL034555		dJ134019.3 (zinc finger protein 151 (pHZ-67))	4273	100
32	W74826	Vers caniens	Himan secreted protein	794	96
32	,,,,,,,,,	-	encoded by gene 98 clone HAQBT94.		
	AF288288	Homo sapiens	HPT protein	2236	.100
33	AF041429	Vome caniens	pRGR1	823	99 100
35	X66357	Homo sapiens	serine/threonine protein kinase	1589	100
		i }_	AFX1	2571	98
536	Y11284 AB004884	Homo sapiens	PKU-alpha	3718	99
537	AJ002303	Homo sapiens	synaptogyrin 1c	1020	100
638 639	AJ002303	Homo sapiens	synaptogyrin 1b	1002	100
640	AJ002304 AJ002303	Homo sapiens	synaptogyrin 1c	933	94
641	D87682	Homo sapiens	similar to a C.elegans protein encoded in cosmid T26A5.	2676	
	M14660	Homo sapiens	ISG-K54	2473	99
642 643	X06661	Homo sapiens	calbindin (AA 1-261)	1358	100 76
644	AF119900	Homo sapiens	PRO2822	185	27
645	AB031048	Drosophila melanogaster	microtubule associated- protein orbit	738	
646	AF250842	Drosophila	multiple asters	834	29
		melanogaster	Mi-2 protein	10110	99
647 648	X86691 U67934	Homo sapiens	44.9 kDa protein C18B11	827	96
		Oryctolagus	homolog RING-finger binding protein	3830	91
649	AF236061	cuniculus	dJ914P20.2 (KIAA0784 protein	5708	100
650	AL034553	Homo sapiens	similar to Mus musculus activity-dependent neuroprotective protein (Admp))	2388	99
653	X14766	Homo sapiens	GABA-A receptor alpha 1 subunit		l
654	AC004614	Homo sapiens	similar to f-spondin proteins AB006086 (PID:g2529225)	3026	99
655	¥57908	Homo sapiens	Human transmembrane protein	608	99
			HTMPN-32.	3733	100
656	234975	Homo sapiens	dJ475B7.2 (novel protein)	1942	99
658 659	AL050306 W76734	Homo	Human mDia Rho targeting	781 .	34
		sapiens	protein. Sadl unc-84 domain protein 1	2172	100
660	AF202724	Homo sapiens	sadi unc-84 domain protein	1529	100
661	Z21966	Homo sapiens		4752	59
662	AJ242954	Mus musculus		6232	99
663 665	AF182316 AL161516	Homo sapiens Arabidopsis	hypothetical protein	209	30
		thaliana	and the same het ace	3393	99
667	X59303	Homo sapiens		3692	100
668	Y13355	Homo sapiens	protein PRO220.		52
669	AB010692	Arabidopsis thaliana	contains similarity to endo- beta-N-acetylglucosaminidase gene		
671	X56123	Mus musculus	talin	4474	76
672	AB039371	Homo sapiens	The transport of	2902	99
<u></u>	700000	Homo sapiens		806	42
673	AF269223	Mus musculus	1	4053	99
674	AF229633 L14463	Rattus	transducin	3619	92

SEQ ID NO:	ACCESSION NUMBER	NOTVEGICUS	DESCRIPTION	SMITH- WATERMAN SCORE	identit)
676	AC005757	Homo sapiens			
677	861069	Homo sapiens	R32611_1 reverse transcriptase	2779	100
678	27271300		homolog=pol (retroviral element)	252	65
	AF271388	Homo sapiens	synthase	2273	100
679	X79066	Homo sapiens		1783	100
680	AF118566	Mus musculus	protein	769	50
	Y51415	Homo sapiens	Human wild type pKe83 . protein.	2621	99
682	AL133545	Homo sapiens	bA386N14.1 (novel protein similar to a dual specificity phosphatase)	700	68
683	Y86214	Homo sapiens		5888	99
684	¥94952	Homo sapiens	Human secreted protein clone fhl16_11 protein sequence	354	98
685	AL021878	Homo sapiens	SEQ ID NO:110. dJ257120.4 (transcription factor 20 (AR1) (KIAA0292)	154	67
686	AE000198	Escherichia	(isoform 2)) orf, hypothetical protein	628	100
687	M58378	coli			
688	AF039697	Homo sapiens	synapsin I	3730	99
689	U09355	Homo sapiens	antigen NY-CO-31	508	98
690	AF155106	Oryctolagus cuniculus	protein phosphatase 2A1 B gamma subunit	2356	99
691	AC004774	Homo sapiens	NY-REN-36 antigen	265	50
692	X90530	Homo sapiens	Dlx-5	1542	100
693	X90530	Homo sapiens	ragB	1926	99
694	X90530	Homo sapiens	ragB	1405	99
695	G01563	Homo sapiens	ragB	1590	85
696	AC011810	Homo sapiens	Human secreted protein, SEQ ID NO: 5644.	330	100
697	AJ250425	Arabidopsis thaliana Rattus	Putative methionine aminopeptidase	669	52
698	AB037901	norvegicus Homo	Collybistin I	2455	98
699	Y99401	sapiens Homo sapiens	gene amplified in squamous cell carcinoma-1	5364	99
701	AF221712	Homo	Human PRO1327 (UNQ687) amino acid sequence SEQ ID NO:218.	1386	100
702	X83573	sapiens Homo sapiens	Smad- and Olf-interacting zinc finger protein ARSE	6705	100
703	AJ243274	Homo sapiens	AP-2rep protein	3184	99
704	Y71262	Homo sapiens	Human chondromodulin-like protein, Zchm1.	2078 1697	99 94
705	Y71262	Homo sapiens	Human chondromodulin-like protein, Zchml.	1736	99
06		Homo sapiens	Amino acid sequence of long human FAIM.	1060	100
. 08		Homo sapiens	bK1191B2.3 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (isoform 1))	2030	100
		Homo sapiens	AND-1 protein	5942	100
		1	Human secreted protein, SEQ ID NO: 5652.		99
	Y08698	Homo sapiens	ranbp3	2849	98
11	¥68770	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-2.		99

SEQ	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
10:			putative p150	799	59
12	U93574	Homo sapiens	Gene with similarity to DEAD	2715	99
1.3	AC004531	Homo sapiens	box helicases		}
``				538	48
14	D89016	Homo sapiens	Neurobiascoma	734	98
	Y92175	Homo sapiens	uman cardiovasculai byseem	134	
15	192175		associated protein tyrosine		1
į	i i	l	phosphatase 2.		
			bA311P8.3 (probable uracil	862	100
16	AL137013	Homo sapiens	phosphoribosyltranferase)		
			GD1 alpha/GT1a alpha/GQ1b	1696	93
717	AB035123	Mus musculus	GD1 alpha/GT1a alpha/GQ1D		
Τ,	1,000		alpha synthase	2345	85
	V96290	Homo >P40254	Human IGFAM-2 immunoglobulin.	2345	105
18	196290	P40254 25-	1		
	ł i		1		1
,		OCT-1984 09-	1		į.
		APR-1983	ļ <u></u>		1.
		Human IgD.	1		\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
	į .	[Homo	1		
	1	l -	1		
	}	sapiens	integrin beta 1 subunit	4347	99
719	X07979	Homo sapiens			l l
		-	precursor	2240	99
		Homo sapiens	tumor suppressor	2149	
720	AJ224819		transcription factor TFIIH	2373	100
721	Y07595	Homo sapiens	Clauseriperon raccor 112-1	1591	99
722	W41565	Homo	Human calpain.		1
166	441202	sapiens)			1
	1	>W41564			1
	1				ŀ
		W41564 08-	į		Į.
	1	OCT-1997 05-	1		Ì
	Į.	APR-1996		į	
	ļ	I -	1.	}	,
	ł	Human	}	!	j
	1	calpain.	\	1	. i .
	ì	[Homo		i	ì
		sapiens		7007	98
	1 777 (4 7 4 7	Homo sapiens	HSPC078	1097	
723	AF161341			1607	100
724	AF187318	Homo sapiens		1143	46
725	AC006708	Caenorhabdit	Courgins Simiating to		
		is elegans	Saccharomyces cerevisiae pre-	1	1
	1		mRNA splicing protein PRP31	1	j
		t .	(GB: Z72876)	t .	
	\	S	(GB:2/20/0/		
		V. 12 47 .	contains simlarity to	988	46
726	AC006708	Caenorhabdit	contains simlarity to	988	46
726	AC006708	Caenorhabdit	contains similarity to	988	46
726	AC006708		contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31	988	46
726	AC006708		contains simlarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GR: 272876)		
		is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)	988	46
726	AC006708	is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876)		
		is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) Contains similarity to Pfam family PROMANO (WD domain,		
		is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) Contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8,		
		is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) Contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8,	950	44
	AC024818	is elegans Caenorhabdi is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) Contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3		
		Caenorhabdi is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3	950	44
727	AC024818	is elegans Caenorhabdi is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 B JMS C Human secreted protein	950	44
727	AC024818	Caenorhabdi is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3	950	44
727	AC024818	Caenorhabdi is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JM5 Human secreted protein fragment encoded from gene	950 831 908	47 97
727	AC024818 AJ005897 Y45377	Caenorhabdiis elegans Homo sapien	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27.	950	44
727	AC024818	Caenorhabdi is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E-1.4e-20, N=3 JM5 S JM5 S Human secreted protein fragment encoded from gene 27. B Human secreted protein, SEQ	950 831 908	47 97
727 728 729	AC024818 AJ005897 Y45377	Caenorhabdi is elegans Homo sapien Homo sapien Homo sapien	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E-1.4e-20, N=3 JM5 Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012.	950 831 908	44
727 728 729	AC024818 AJ005897 Y45377 G03931	Caenorhabdi is elegans Homo sapien Homo sapien Homo sapien	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E-1.4e-20, N=3 JM5 Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012.	950 831 908	47 97
727 728 729	AC024818 AJ005897 Y45377	Caenorhabdi is elegans Homo sapien Homo sapien Homo sapien Oncorhynchu	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E-1.4e-20, N=3 JM5 Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012.	950 831 908 578 3865	44 47 97 100
727 728 729	AC024818 AJ005897 Y45377 G03931	Caenorhabdi is elegans Homo sapien Homo sapien Oncorhynchumasou	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) Contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 S JMS Human secreted protein fragment encoded from gene 27. B Human secreted protein, SEQ ID NO: 8012.	950 831 908	44
727 728 729 730	AC024818 AJ005897 Y45377 G03931	Caenorhabdi is elegans Homo sapien Homo sapien Homo sapien Oncorhynchu	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 S JM5 S Human secreted protein fragment encoded from gene 27. B Human secreted protein, SEQ ID NO: 8012. GTP-binding protein	950 831 908 578 3865	44 47 97 100
727 728 729 730	AC024818 AJ005897 Y45377 G03931 AB012720	Caenorhabdi is elegans Homo sapien Homo sapien Oncorhynchumasou	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E-1.4e-20, N=3 JM5 Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein SEQ Human secreted protein Human secreted protein	950 831 908 578 3865 862	44 47 97 100 76
727 728 729 730 731	AC024818 AJ005897 Y45377 G03931 AB012720 W73404	is elegans Caenorhabdi is elegans Homo sapien Homo sapien Oncorhynchu masou Homo sapier	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 S JM5 S Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8.	950 831 908 578 3865	44 47 97 100
727 728 729 730	AC024818 AJ005897 Y45377 G03931 AB012720	Caenorhabdi is elegans Homo sapien Homo sapien Oncorhynchumasou	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JM5 Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ	950 831 908 578 3865 862	44 47 97 100 76
727 728 729 730 731	AC024818 AJ005897 Y45377 G03931 AB012720 W73404	Caenorhabdi is elegans Homo sapien Homo sapien Homo sapien Oncorhynchumasou Homo sapier	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JM5 Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731.	950 831 908 578 3865 862 644	44 47 97 100 76
727 728 729 730 731 732 733	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650	is elegans Caenorhabdi is elegans Homo sapien Homo sapien Oncorhynchu masou Homo sapier Homo sapier	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JM5 Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731.	950 831 908 578 3865 862	44 47 97 100 76 97
727 728 729 730 731	AC024818 AJ005897 Y45377 G03931 AB012720 W73404	Caenorhabdi is elegans Homo sapien Homo sapien Homo sapien Oncorhynchu masou Homo sapier Homo sapier	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) Contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 S JM5 S Human secreted protein fragment encoded from gene 27. B Human secreted protein, SEQ ID NO: 8012. GTP-binding protein S Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. It Hypothetical protein ysaf102L.a	950 831 908 578 3865 862 644 152	44 47 97 100 76 97 97
727 728 729 730 731 732	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813	Caenorhabdi is elegans Homo sapien Homo sapien Homo sapien Oncorhynchu masou Homo sapier Homo sapier Caenorhabd is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) Contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 MMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a	950 831 908 578 3865 862 644 152	44 47 97 100 76 97
727 728 729 730 731 732 733	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650	Caenorhabdi is elegans Homo sapien Homo sapien Homo sapien Oncorhynchu masou Homo sapier Homo sapier Caenorhabd is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 S JM5 S Human secreted protein fragment encoded from gene 27. B Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. It Hypothetical protein Y54F10AL.a	950 831 908 578 3865 862 644 152	44 47 97 100 76 97 97
727 728 729 730 731 732 733	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813	Caenorhabdi is elegans Homo sapien Homo sapien Homo sapien Oncorhynchu masou Homo sapier Homo sapier Caenorhabd is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosophatidyltransferase	950 831 908 578 3865 862 644 152	44 47 97 100 76 97 97
727 728 729 730 731 732 733	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813	Caenorhabdi is elegans Homo sapien Homo sapien Homo sapien Oncorhynchu masou Homo sapier Homo sapier Caenorhabd is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) Contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 JM5 Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase for ly member protein)	950 831 908 578 3865 862 644 152 1562	44 47 97 100 76 97 97 24
727 728 729 730 731 732 733	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813	is elegans Caenorhabdi is elegans Homo sapien Homo sapien Oncorhynchu masou Homo sapier Caenorhabdi is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) Contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 S JM5 S Human secreted protein fragment encoded from gene 27. B Human secreted protein, SEQ ID NO: 8012. GTP-binding protein S Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. It Hypothetical protein y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein)	950 831 908 578 3865 862 644 152 1562	44 47 97 100 76 97 97
727 728 729 730 731 732 733 734 735	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813	is elegans Caenorhabdi is elegans Homo sapien Homo sapien Oncorhynchu masou Homo sapier Caenorhabdi is elegans Homo sapier Caenorhabdi Caenorhabdi	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) Contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 S JM5 S Human secreted protein fragment encoded from gene 27. B Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. It Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) it similar to S. cerevisiae YJU2	950 831 908 578 3865 862 644 152 1562	44 47 97 100 76 97 97 24
727 728 729 730 731 732 733	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813 AL035461	is elegans Caenorhabdi is elegans Homo sapien Homo sapien Oncorhynchu masou Homo sapier Caenorhabdi is elegans Homo sapier Caenorhabdi Caenorhabdi	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) Contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 MMS Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a MG J967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) it similar to S. cerevisiae YJUZ	950 831 908 578 3865 862 644 152 1562	44 47 97 100 76 97 97 24 98
727 728 729 730 731 732 733 734	AC024818 AJ005897 Y45377 G03931 AB012720 W73404 G02650 AC024813 AL035461	is elegans Caenorhabdi is elegans Homo sapien Homo sapien Oncorhynchu masou Homo sapier Caenorhabdi is elegans Homo sapier Caenorhabdi is elegans	contains similarity to Saccharomyces cerevisiae pre- mRNA splicing protein PRP31 (GB:Z72876) Contains similarity to Pfam family PF00400 (WD domain, G-beta repeat), score=81.8, E=1.4e-20, N=3 S JM5 S Human secreted protein fragment encoded from gene 27. B Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. It Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) it similar to S. cerevisiae YJU2	950 831 908 578 3865 862 644 152 1562	44 47 97 100 76 97 97 24

			TABLE Z		
SEQ	ACCESSIO	N SPECIES	DESCRIPTION	17	
αı	NUMBER		DESCRIPTION	SMITH-	ક
NO:			1	WATERMAN	IDENTITY
738	AJ131712	Homo sapiens	nucleolar RNA-helicase	SCORE	
739	AJ133115	Homo sapiens		2793	100
740	X98258	Homo sapiens		2054	99
741	X98258	Homo sapiens	M-phase phosphoprotein 9	953	100
742	U97191	nomo sapiens		564	74
1 1 2	09/191	Caenorhabdit		960	85
743		is elegans	sub-family of RAS proteins		03
743	X76057	Homo sapiens	phosphomannose isomerase	2191	100
744	G03209	Homo sapiens	Human secreted protein, SEQ	496	
		_	ID NO: 7290.	496	98
745	X97064	Homo sapiens	Sec23 protein		
746	W93946	Homo sapiens		4034	99
	Ī			994	100
747	¥73388	Homo sapiens	HRM-2 protein.		1
	1 273300	nomo sapiens	The species as to dear broceru	1565	99
748	M19529		sequence.		
749		Sus scrofa	follistatin A	1906	98
749	AJ249457	Trichomonas	centrin, putative	183	28
		vaginalis	1	1 103	28
750	AC004410	Homo sapiens	fos39554 1	1 3000	
751	AF074968	Homo sapiens	p47ING3 protein	2094	100
752	AF252284	Homo sapiens	transcription specificity	2167	100
		omo saprems		4005	100
753	AB049629	Homo sapiens	factor Spl		
	1-2027029	nomo sapiens		1375	99
	1	1	phosphohistidine inorganic	1	
754	D79205	 	pyrophosphate phosphatase	1	j
755		Homo sapiens	ribosomal protein L39	160	77
	AB008430	Homo sapiens	CDEP	142	29
758	L32162	Homo sapiens	transcription factor	574	
759	AF037204	Homo sapiens	RING zinc finger protein		80
760	Y44250	Homo	Human cell signalling	295	54
		sapiens	protein-13.	625	100
761	AF218586	Homo sapiens	Cide-b		1
762	U38934	Gallus	.] =	1136	100
	1	gallus	histone H2A	625	97
763	AF226053	Homo sapiens		1	1
764	X13403	Homo sapiens	HSKM-B	606	32
765	D87446	Homo sapiens	Oct-1 protein (AA 1 - 743)	3626	100
,03	D8/446	Homo sapiens	Similar to a C.elegans	568	38
	}		protein encoded in cosmid		1 30
			C27F2 (U40419)	Į.	1
766	AL023828	Caenorhabdit	Y17G7B.14	200	<u> </u>
		is elegans		200	27
767	Y82777	Homo sapiens	Human chordin related protein		
	1		(Clone dw665_4).	2551	99
768	X92475	Homo sapiens	ITBA1		
769	Y42752	Homo sapiens		1429	100
	1	ouro saprens	Human calcium binding protein	1426	100
770	X51416	Vone	3 (CaBP-3).	}	1 1
-		Homo sapiens	hormone receptor hERR1 (AA 1-	2641	97
771	7 TOOC555		521)	-	
72	AJ006591	Homo sapiens	cysteine-rich protein	1793	100
	A08695	Homo sapiens	rap2	935	100
73	Z12173	Homo sapiens	N-acetylglucosamine-6-	2970	
		-	sulphatase	29/0	100
74	Y91950	Homo sapiens			
- [Suprem	Human cytoskeleton associated	565	43
76	AL023799	Homo sapiens	protein 5 (CYSKP-5).	[
77	AL023799	omo sapiens	dJ322P7.1 (zinc finger)	855	56
78	G01880	Homo sapiens	dJ322P7.1 (zinc finger)	855	56
.	201980	Homo sapiens	Human secreted protein, SEQ	849	98
 +			ID NO: 5961.	1	1
79	AJ012590	Homo sapiens	glucose 1-dehydrogenase	4155	
80	AL078582	Homo sapiens	dJ130E4.2 (KIAAJ796)	4155	99
81	Z75955	Caenorhabdit	similar to mitochondrial	1321	68
1	ł		commiss co micochondrial	384	34
82	AL109965		carrier protein	ļ	ł
- 1			dJ1121G12.2 (SCAN domain-	900	100
33	AF061262	sapiens	Containing 1 protein)		
~		Mus	semaf cytoplasmic domain	1316	83
		musculus	associated protein 2		
34	G03873	Homo sapiens	Human secreted protein, SEQ	649	
				0-1-3	95

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:			ID NO: 7954.		
85	Y84441	Homo sapiens	Amino acid sequence of a human RNA-associated	2074	100
786	Y00918	Nomo saniens	protein. Human Rab protein, RABP-1,	1048	99
, , ,			protein sequence. ribonuclease HI large subunit	1548	99
787	Z97029	110.110	SRp25 nuclear protein	962	94
788	AB035384			2644	100
789	AF024631	HOMO Supretie	ANG2 phosphatidylinositol 3-kinase	4508	97
790	AJ006710	norvegicus		600	100
792	V00638	e lambda	reading frame eal0	819	100
793	AF049103	Homo sapiens	Huntingtin interacting protein		99
	Z26317	Homo sapiens	desmoglein 2	4810	99
795 796	¥76884	Homo sapiens	Retinoblastoma binding protein-7sequence.	5080	
797	D15155	Gallus	trypsinogen	372	37
	1197189	gallus Caenorhabdit	strong similarity to thw	227	28
798	09/109	is elegans	p13/p14 family of kinases	1 7 5 5 2	100
706	AF112201	Homo sapiens	neuronal protein NP25	1053	63
799 800	AF112201 AF234765	Rattus norvegicus	serine-arginine-rich splicing	958	
801	AF267852	Homo sapiens	placental protein 13-like protein	743	99
			BM-009	766	80
802 803	AF208851 281097	Homo sapiens Caenorhabdit is elegans	Similarity to Human retinoblastoma-binding protein RBAP46 yk662d12.5	152	27
804	G02113	Homo sapiens	comes from this gene Human secreted protein, SEQ	496	98
1 002			ID NO: 6194.	1160	100
805	AL121673	Homo sapiens	bA305P22.1 (novel protein) putative GTPase activator	264	30
806	AC013483	Arabidopsis thaliana	protein	264	3C
807	AC013483	Arabidopsis thaliana	putative GTPase activator protein		100
	AB0138B5	Homo sapiens	beta-ureidopropionase	1494	99
808	AF078842	Homo sapiens		1581	96
809	AF161421	Homo sapiens	HSPC303	2134	100
810	AF261689	Homo sapiens	DNA polymerase epsiton pi/	734	
812	274029	Caenorhabdit is elegans	Similarity to C.elegans alcohol dehydrogenase comes from this gene	610	71
813	273497	Homo sapiens	CU240C2.2 (Core histone	324	100
814	W87689	Homo	Human HTXFT19 polypeptide.	1484	99
815	X16282	sapiens Homo	zinc finger protein (217 AA) (1 is 2nd base in codon)	1109	99
816	292539	sapiens Mycobacteriu		300	36
		m tuberculosis			27
22.0	AB030483		B9	197	
818	AB030483		hypothetical protein	321	94
819			R26660 2, partial CDS	865	97
820	AC005328 G03951	Homo sapien		700	99
822	L34807	Musca domestica	transposase	174	20
823	G02928	Homo sapien	l to No: 7009.	·	78
1	Z99531	Schizosacch	death	184	29

SE II NO	NUMBER	ON SPECIE	DESCRIPTION	SMITH- WATERMAI SCORE	N IDENTI
		compces	protein 1	- SCORE	
825	AJ006692	Homo sapi			ĺ
826	U23037	Oryctolag		693	68
1	1	cuniculus	us eIF-2Bepsilon	3406	90
827	G03412	Homo sapi		1	1 30
		nomo sapi		464	100
828	Y30327	- Home	1 ID NO: 7493	100	100
	"""	Homo sapie		113	44
829	Y32199	77	encoded from gene 17		44
1	102133	Homo sapie	ns Human receptor molegula /prov	1012	
1		1	encoded by Incyte class	1012	100
830	W78279		2022379.	•	
1	1110219	Homo sapie		1051	
832	3700		I Drotein angeded to	1264	99
833	AB011542	Homo sapie	IS I MELLEY		
033	G02639	Homo sapie	ns Human secreted protein, SEQ	2097	100
834			ID NO. 6720	223	70
0.34	AF119664	Homo sapie	ns transcriptional regulator		1
			protein HCMCP	1574	100
835	AF119664	Homo sapie	transcriptional regulator		1
L		1	Drotein Howan	1144	89
836	AF119664	Homo sapie	s transcriptions		
<u> </u>		1	protein HCMCD	1448	94
837	X12517	Homo sapier	s C protein (AA 1-159)		l
838	U32865	Drosophila		918	100
	.	melanogaste	linotte protein	164	24
839	AF067730	Homo sapier)	1
840	U27831	Homo sapier		631	56
841	AF286366	Homo sapier		2840	98
842	G02309	Homo sapien	S Camki-like protein kinage	1796	100
		"OWE SEPTED	numan secreted protein cro	278	98
843	AE003615	Drosophila	1 TO NO: 6390	1	1 30
		melanogaste	ade3 gene product	113	48
844	G01350	Homo sapien			**
		nomo sapien		629	100
845	U27838	Mus musculu	1D NO: 5431.	123	100
		Mas mascara		3305	96
	1	}	inositol-anchored protein	7505	1 30
847	Y87788	Homo sapiens	(nomolog		
848	AF164794	Homo sapiens		2026	100
849	U41315	Homo sapiens		2398	100
850	AF192784	Homo sapiens	ZNF127-Xp	2458	93
851	Y58628	Homo sapiens		2062	
	1	Homo sapiens		1548	97
852	Z22968	Vome -	expression PRGE-21	~740	100
953	222971	Homo sapiens	M130 antigen	6205	100
-	/1	Homo sapiens	M130 antigen extracellular	6380	100
954	G03362	170-00-	variant	9380	100
_		Homo sapiens	Human secreted protein, SEQ	330	
55	G03362	ļ	ID NO: 7443.	330	96
	-00302	Homo sapiens	Human secreted protein cro	303	
56	AF285118	¥*	1D NO: 7443.	203	100
57	AC006069	Homo sapiens	CGI-203	452	
		Arabidopsis	putative cleavage and		100
- 1		thaliana	polyadenylation specific	1383	55
58	ALOSTES		tactor		
	AL021546	Homo sapiens	Cytochrome C Oxidase		
į	İ		Polypeptide VIa-liver	593	100
59	T 030		precursor (EC 1.9.3.1)	j	I
	L02956	Xenopus	ribonucleony-t-		
		laevis	1	.664	85
	AF201947	Homo sapiens	MEK binding partner 1 6		I
	L31783	Mus musculus	uriding king		100
	AF161472	Homo sapiens	HSPC123		2
3	249068	Caenorhabdit	mitochondrial carrier protein 3		3
4	AF154108	is elegans	desired brocesu 3	70 4	3

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	1DENTITY
10:	NOMBER	•		SCORE	<u> </u>
			receptor associated protein	230	32
55	AE001530	Helicobacter pylori J99	putative		\
6	X57807	Homo sapiens	immunoglobulin lambda light	699	91
	AL031673	Homo sapiens	dJ694B14.1 (PUTATIVE novel	4066	99
57	AL031673	HOURS SAPTEME	KRAB box protein with 18 C2H2 type Zinc finger domains)		1
			phosphate cyclase	238	1.00
68	Y11652	Homo sapiens	high-glucose-regulated	3041	99
69	AF192968	Homo sapiens	protein 8		
70	AB020648	Homo sapiens	KIAA0841 protein	3237	59
71	AL031427	Homo sapiens	dJ167A19.1 (novel protein)	1608	100
72	AF151534	Homo sapiens	core histone macroH2A2.2	1866	100
73	AL021331	Homo sapiens	dJ366N23.1 (putative C. elegans UNC-93 (protein 1, C46F11.1) LIKE protein)	1129	
374	X14608	Homo sapiens	propionyl-CoA carboxylase	3579	100
375	AL117334	Homo sapiens	dJ687F11.1 (novel protein	306	100
			(part of translation of cDNA	1	
			DKFZp434N061, Em:AL110249))	446	35
376	X79489	Saccharomyce	E-925 protein	1	} -
877	Y53001	s cerevisiae Homo sapiens	Human secreted protein clone dn834_1 protein sequence SEQ	811	100
	l		CHMP1.5	957	100
878	AF231064	Homo sapiens	40S ribosomal protein S12	687	100
879	X79417	Sus scrofa Saccharomyce	Soilp	478	28
880	AF001317	s cerevisiae	_	1	
881	Y87275	Homo sapiens	Human signal peptide containing protein HSPP-52 SEO ID NO:52.	2547	100
	l		C1-inhibitor	598	77
882	M14036	Homo sapiens	calcium-independent	2903	100
883	AB041261	Homo saptems	phospholipase A2		
884	AF020313	Mus musculus	proline-rich protein 48	999	84
885	Y10936	Homo sapiens	hypothetical protein	1104	99
886	AF073997	Mus musculus	myotubularin related protein	866	36
887	¥57893	Homo sapiens	Human transmembrane protein	1099	94
000	AL117635	Homo sapiens	hypothetical protein	929	99
888	AF210317	Homo sapiens	facilitative glucose	2046	99
869	WE TATA	1.0.10	transporter family member		
	1,00000	Homo sapiens	Extended human secreted	583 .	100
890	Y36031	HOWO Sapters	protein sequence, SEQ ID NO.		
		A	Extended human secreted	192	57
891	¥36031	Homo sapiens	protein sequence, SEQ ID NO.	_	
892	AF237631	Homo sapiens		1798	100
893	AF090929	Homo sapiens	PRO0477p	653	99
893	AL031228	Homo sapiens	dJ1033B10.2 (WD40 protein	3196	100
034	ALOSTEE		BING4 (similar to S. cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1)		
895	AL031228	Homo sapiens	BING4 (similar to S. cerevisiae YER082C, M. sexta	2825	96
i	- 1	1	MNG10 and C. elegans F28D1.1)		
896	AF171102	Homo sapiens	retinal degeneration B beta	1302	95
896	AE003551		CG18176 gene product	633	33
1001	1-200555	melanogaster		1	1

NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	\$ EDENMAR
898				SCORE	IDENTI
899	AJ237946	Homo sapien	s DEAD Box Protein 5	2443	100
900	Z97184	Homo sapien	s F.KE2	624	100
900	Z97184	Homo sapien		409	98
902	AJ245587	Homo sapien		1942	100
902	AF091034	Homo sapien	S GTP-binding protein RAB22A	1011	100
903	R95953	Homo sapien	Eukaryotic cell growth	414	
<u> </u>			inhibiting factor.	414	96
904	L04733	Homo sapiens	kinesin light chain	1936	
905	AE003540	Drosophila	CG10984 gene product		72
		melanogaste	c }	446	33
906	M55542	Homo sapiens	guanylate binding protein	- 	
L			isoform T	2993	98
907	M55542	Homo sapiens	guanylate binding protein		
	1	_	isoform I	2901	96
908	W84085	Homo sapiens	Human membrane fusion protein		
	1		WDProl.	1889	100
909	AF168676	Homo			1
		sapiens	TNF intracellular domain-	647	100
910	AB029150	Homo sapiens	interacting protein		ł
		adptens	KRAB zinc finger protein HFB101L	2196	100
911	G02871	Homo sapiens			1
		"TOMO Sapiens		521	100
912	G03162	Homo sapiens	ID NO: 6952.		I
	-03202	nouto sapiens		387	87
913	AJ243721	Homo	ID NO: 7243.	į	1
	10243/21	1	dTDP-4-keto-6-deoxy-D-glucose	1710	100
		sapiens)	4-reductase		
	1	>Y92508 Y92508 13-	i	1	1
		192508 13-			
	İ	APR-2000 06-		i	· ·
	1	OCT-1998		}	1
		Human OXRE-		İ	İ
	1	5. [Homo	·	İ	ļ
914	U24189	sapiens		İ	
714	024189	Caenorhabdit	hypothetical protein 1207-1;	244	41
		is elegans	Method: conceptual		1 **
		ļ	translation supplied by		ŀ
915	Y02591		authors	1	
	102331	Homo sapiens	A human progesterone receptor	843	99
916	AE000984		complex p23-like protein	1	7,7
	I AEURUSKA		dinitrogenace mediate		
310	1	Archaeoglobu	drintingenase reductase	177	36
919		s fulgidus	dinitrogenase reductase activating glycohydrolase	171	26
		s fulgidus	activating glycohydrolase (draG)	171	26
	M23159	s fulgidus Cricetus	activating glycohydrolase (draG)		
918	M23159	s fulgidus Cricetus cricetus	activating glycohydrolase	171	30
		S fulgidus Cricetus cricetus Caenorhabdit	activating glycohydrolase (draG)	163	30
918	M23159	Cricetus cricetus cricetus Caenorhabdit is elegans	activating glycohydrolase (draG) DHFR-coamplified protein		
918 919 920	M23159	s fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens	activating glycohydrolase (draG) DHFR-coamplified protein putative	163	30
918 919 920	M23159	s fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antiqen SLP-8p	163 1232 1260	30 41 97
918	M23159 L12018 AF102177	Cricetus cricetus cricetus Caenorhabdit is elegans	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dJ744I24.2 (similar to a	163	30
918 919 920 921	M23159 L12018 AF102177	s fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dJ744124.2 (similar to a novel human gene mapping to	163 1232 1260	30 41 97
918 919 920	M23159 L12018 AF102177	s fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens Homo sapiens	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dJ744I24.2 (similar to a novel human gene mapping to Activator)	163 1232 1260 1017	30 41 97
918 919 920 921	M23159 L12018 AF102177 AL096712	s fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens Homo sapiens	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dJ744124.2 (similar to a novel human gene mapping to	163 1232 1260	30 41 97
918 919 920 921	M23159 L12018 AF102177 AL096712 AL161495	s fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens Homo sapiens Arabidopsis thaliana	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dJ744124.2 (similar to a novel human gene mapping to Activator) putative WD-repeat protein	163 1232 1260 1017	30 41 97 78
918 919 920 921	M23159 L12018 AF102177 AL096712	s fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens Homo sapiens Arabidopsis thaliana Arabidopsis	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dJ744I24.2 (similar to a novel human gene mapping to Activator)	163 1232 1260 1017	30 41 97 78
918 919 920 921 922	M23159 L12018 AF102177 AL096712 AL161495 AL161495	cricetus cricetus Caenorhabdit is elegans Homo sapiens Homo sapiens Arabidopsis thaliana Arabidopsis	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dJ744124.2 (similar to a novel human gene mapping to Activator) putative WD-repeat protein putative WD-repeat protein	163 1232 1260 1017	30 41 97 78
918 919 920 921	M23159 L12018 AF102177 AL096712 AL161495	s fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens Homo sapiens Arabidopsis thaliana Arabidopsis thaliana Caenorhabdit	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dJ744124.2 (similar to a novel human gene mapping to Activator) putative WD-repeat protein putative WD-repeat protein	163 1232 1260 1017	30 41 97 78
918 919 920 921 922 923	M23159 L12018 AF102177 AL096712 AL161495 AL161495 U97001	s fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens Arabidopsis thaliana Arabidopsis thaliana Caenorhabdit is elegans	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dU744124.2 (similar to a novel human gene mapping to Activator) putative WD-repeat protein putative WD-repeat protein similar to Schizosaccharomyces pombe	163 1232 1260 1017 866	30 41 97 78 42 36
918 919 920 921 922 922 923 924	M23159 L12018 AF102177 AL096712 AL161495 AL161495 U97001 X71978	s fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens Arabidopsis thaliana Arabidopsis thaliana Caenorhabdit is elegans	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dJ744124.2 (similar to a novel human gene mapping to Activator) putative WD-repeat protein putative WD-repeat protein similar to Schizosaccharomyces pombe Fif	163 1232 1260 1017 866 442	30 41 97 78 42 36
918 919 920 921 922 923	M23159 L12018 AF102177 AL096712 AL161495 AL161495 U97001 X71978 M92288	s fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens Arabidopsis thaliana Arabidopsis thaliana Caenorhabdit is elegans Mus musculus Drosophila	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dU744124.2 (similar to a novel human gene mapping to Activator) putative WD-repeat protein putative WD-repeat protein similar to Schizosaccharomyces pombe	163 1232 1260 1017 866 442 605	30 41 97 78 42 36 51
918 919 920 921 922 923 924 25	M23159 L12018 AF102177 AL096712 AL161495 AL161495 U97001 X71978 M92288	s fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens Homo sapiens Arabidopsis thaliana Arabidopsis thaliana Caenorhabdit is elegans Mus musculus Drosophila melanogaster	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dJ744124.2 (similar to a novel human gene mapping to Activator) putative WD-repeat protein putative WD-repeat protein similar to Schizosaccharomyces pombe Fif	163 1232 1260 1017 866 442 605	30 41 97 78 42 36
918 919 920 921 922 922 923 924	M23159 L12018 AF102177 AL096712 AL161495 AL161495 U97001 X71978 M92288	s fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens Arabidopsis thaliana Arabidopsis thaliana Caenorhabdit is elegans Mus musculus Drosophila melanogaster	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dJ744124.2 (similar to a novel human gene mapping to Activator) putative WD-repeat protein putative WD-repeat protein similar to Schizosaccharomyces pombe Fif beta-spectrin	163 1232 1260 1017 866 442 605 1503 290	30 41 97 78 42 36 51 95
918 919 920 921 922 923 924 925 926 927	M23159 L12018 AF102177 AL096712 AL161495 AL161495 U97001 X71978 M92288 Y27575	S fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens Arabidopsis thaliana Arabidopsis thaliana Caenorhabdit is elegans Mus musculus Drosophila melanogaster Homo sapiens	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dJ744124.2 (similar to a novel human gene mapping to Activator) putative WD-repeat protein putative WD-repeat protein similar to Schizosaccharomyces pombe Fif beta-spectrin Human secreted protein	163 1232 1260 1017 866 442 605 1503 290	30 41 97 78 42 36 51
918 919 920 921 922 923 924 25	M23159 L12018 AF102177 AL096712 AL161495 AL161495 U97001 X71978 M92288 Y27575	S fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens Homo sapiens Arabidopsis thaliana Arabidopsis thaliana Caenorhabdit is elegans Mus musculus Drosophila melanogaster Homo sapiens	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dJ744124.2 (similar to a novel human gene mapping to Activator) putative WD-repeat protein putative WD-repeat protein similar to Schizosaccharomyces pombe Fif beta-spectrin Human secreted protein encoded by gene No. 9.	163 1232 1260 1017 866 442 605 1503 290	30 41 97 78 42 36 51 95 51
918 919 920 921 922 923 924 925 926 927 928	M23159 L12018 AF102177 AL096712 AL161495 AL161495 U97001 X71978 M92288 Y27575	S fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens Arabidopsis thaliana Arabidopsis thaliana Caenorhabdit is elegans Mus musculus Drosophila melanogaster Homo sapiens	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dJ744I24.2 (similar to a novel human gene mapping to Activator) putative WD-repeat protein putative WD-repeat protein similar to Schizosaccharomyces pombe Fif beta-spectrin Human secreted protein encoded by gene No. 9. Human secreted protein	163 1232 1260 1017 866 442 605 1503 290	30 41 97 78 42 36 51 95
918 919 920 921 922 923 924 925 926 927	M23159 L12018 AF102177 AL096712 AL161495 AL161495 U97001 X71978 M92288 Y27575 Y22499	S fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens Arabidopsis thaliana Arabidopsis thaliana Caenorhabdit is elegans Mus musculus Drosophila melanogaster Homo sapiens	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dJ744124.2 (similar to a novel human gene mapping to Activator) putative WD-repeat protein putative WD-repeat protein similar to Schizosaccharomyces pombe Fif beta-spectrin Human secreted protein encoded by gene No. 9. Human secreted protein sequence clone mh703 1.	163 1232 1260 1017 866 442 605 1503 290 1392 2249	30 41 97 78 42 36 51 95 51
918 919 920 921 922 923 924 925 926 927	M23159 L12018 AF102177 AL096712 AL161495 AL161495 U97001 X71978 M92288 Y27575 Y22499	S fulgidus Cricetus cricetus Caenorhabdit is elegans Homo sapiens Arabidopsis thaliana Arabidopsis thaliana Caenorhabdit is elegans Mus musculus Drosophila melanogaster Homo sapiens Homo sapiens	activating glycohydrolase (draG) DHFR-coamplified protein putative tumor antigen SLP-8p dJ744I24.2 (similar to a novel human gene mapping to Activator) putative WD-repeat protein putative WD-repeat protein similar to Schizosaccharomyces pombe Fif beta-spectrin Human secreted protein encoded by gene No. 9. Human secreted protein	163 1232 1260 1017 866 442 605 1503 290 1392 2249	30 41 97 78 42 36 51 95 51

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
			cm21c7	210	25
32	AL080065	Homo sapiens	hypothetical protein		98
33	G01884		Human secreted protein, SEQ ID NO: 5965.	767	
34	AJ276485	-	integral membrane transporter protein	1200	100
35	AL035681	Homo sapiens	dJ756G23.3 (novel protein similar to drosophila transcriptional repressor)	1142	80
		Mus musculus	synaptotagmin XI	2142	95
36	AB026808		HRIHFB2216	2601	99
37	AB015345	Homo sapiens	ORF2	498	100
38	X65724	Homo sapiens	Polypeptide fragment encoded	1487	100
39	W89024	Homo sapiens	by gene 156.	117	100
40	G04047	Homo sapiens	Human secreted protein, SEQ ID NO: 8128.		100
941	AF094583	Homo sapiens	putative HIV-1 infection related protein	452	
942	AC024200	Caenorhabdit is elegans	contains similarity to several zinc finger proteins but not to the zinc finger	350	69
	ļ		domains	-	100
943	AF129756	Homo sapiens	G5c	273	1
944	M23765	Rattus norvegicus	alpha-tropomyosin	133	96
945	AC009917	Arabidopsis thaliana	Contains similarity to	583	47
	77222450	Homo sapiens	AD021 protein	551	44
946	AF223468	Homo sapiens	GAGE-8	273	51
947	AF055473		protein kinase C mu	2019	68
948	X75756	Homo sapiens	coronin-2	2300	93
949 950	AF143956 Y36729	Mus musculus Homo	Human PG1 protein sequence.	1861	99
951	W49041	sapiens Homo sapiens	Human low density lipoprotein binding protein LBP-2.	282	67
952	AB016881	Arabidopsis	gene_id:MXC17.7~	203	46
953	Y01785	thaliana Homo sapiens	Human ubiquitin-conjugating enzyme >Y25341 Y25341 01-JUL- 1999 12-AUG-1998 Human NCE-2 protein.	365 .	100
954	AF145615	Drosophila melanogaster	BcDNA.GH03377	823	46
OFF	U09410	Homo sapiens	zinc finger protein ZNF131	2483	99
955	109410	Homo sapiens	zinc finger protein ZNF131	1853	99
956 957	AF195623	Homo sapiens	cholinephosphotransferase 1	2126	99
958	X94917	Drosophila	head-elevated expression in	155	32
959	U54807	melanogaster Rattus	GTP-binding protein	1167	97
		norvegicus	GTP-binding protein rah	606	97
960	AF058807	Bos taurus	CEO	471	100
961	G03244	Homo sapiens	ID NO: 7325.		40
962	AF078850	Homo sapiens		1 3 3 7 7	30
963	AP001754	Homo sapiens	transient receptor potential- related channel 7, a novel putative Ca2+ channel protein	1	30
964	AL035419	Homo sapiens		1129	100
965	X61381	Rattus	interferon-induced protein	202	46
966	D38169	Homo	inositol 1,4,5-trisphosphate	3278	100
	1	sapiens	3-kinase isoenzyme dJ465N24.2.1 (PUTATIVE novel	893	100

969 A 970 A 971 U 972 A 973 A 974 U 975 A 976 A 977 G 978 A 979 U 980 S 981 Y 982 A 983 X6	J79275 J79275 J79275 J79275 J79275 J79275 J79275 J79275 J79275 J79275 J79275 J79275 J79275 J79277 J7927	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Caenorhabdit is elegans Leishmania major Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Kenopus laevis Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	guanine nucleotide exchange factor (long isoform) exosome component Rrp46 weak similarity over a phort region to myosin heavy chain L8840.12 LNV Tax1 binding protein huntingtin-interacting protein HYPA/FBP11 HSPC182 Human secreted protein, SEQ ID NO: 8101	\$CORE 611 2752 1186 536 589 544 852 1390 1040 626 908 795 2029 2501 827 964	100 99 100 23 53 85 98 97 100 100 97 100 100
970 A 971 U 972 A 973 A 974 U 975 A 976 A 977 G 978 A 979 U 980 S 981 Y 982 A 983 X6	AF281134 J53336 AC018749 AF188504 J25801 AF049523 AF161530 AF164797 F16479 F1	Homo sapiens Caenorhabdit is elegans Leishmania major Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Kenopus laevis Homo sapiens Homo sapiens Kenopus laevis Homo sapiens	guanine nucleotide exchange factor (long isoform) exosome component Rrp46 weak similarity over a phort region to myosin heavy chain L8840.12 LNV Taxl binding protein huntingtin-interacting protein HYPA/FBP11 HSPC182 Human secreted protein, SEQ ID NO: 8101. ribosomal protein L17 isolog transcription factor XLMO1 calmitine; calsequestrine Human protein clone HP01462. heat shock protein PSST subunit of the NADH.	2752 1186 536 589 544 852 1390 1040 626 908 795 2029 2501	99 100 23 53 85 98 97 100 100 100 97 100 100
971 U 972 A 973 A 974 U 975 A 976 A 977 G 978 A 979 U 980 S 981 Y 982 A 983 X6	F188504 F188504 F25801 F049523 F161530 04020 F164797 94991 73775 94888 F243191	Homo sapiens Caenorhabdit is elegans Leishmania major Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Kenopus laevis Homo sapiens Homo sapiens Homo sapiens Homo sapiens	factor (long isoform) exosome component Rrp46 weak similarity over a short region to myosin heavy chain L8840.12 LNV Taxl binding protein huntingtin-interacting protein HYPA/FBP11 HSPC182 Human secreted protein, SEQ ID NO: 8101. ribosomal protein L17 isolog transcription factor XLMO1 calmitine; calsequestrine Human protein clone HP01462. heat shock protein PSST subunit of the NADH.	1186 536 589 544 852 1390 1040 626 908 795 2029 2501	100 23 53 85 98 97 100 100 100 97
971 U 972 A 973 A 974 U 975 A 976 A 977 G 978 A 979 U 980 S 981 Y 982 A 983 X6	F188504 F188504 F25801 F049523 F161530 04020 F164797 94991 73775 94888 F243191	Caenorhabdit is elegans Leishmania major Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Kenopus laevis Homo sapiens Homo sapiens Homo sapiens Homo sapiens	weak similarity over a short region to myosin heavy chain L8840.12 LNV Taxl binding protein huntingtin-interacting protein HYPA/FBP11 HSPC182 Human secreted protein, SEQ ID NO: 8101. ribosomal protein L17 isolog transcription factor XLMO1 calmitine; calsequestrine Human protein clone HP01462. heat shock protein PSST subunit of the NADH.	536 589 544 852 1390 1040 626 908 795 2029 2501	23 53 85 98 97 100 100 100 97
972 A 973 A 974 U 975 A 976 A 977 G 978 A 979 U 980 S 981 Y 982 A 983 X6	P188504 P188504 P25801 P049523 F161530 04020 F164797 94991 73775 94888 7243191 65020	is elegans Leishmania major Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Kenopus Laevis Homo sapiens Homo sapiens Homo sapiens Homo sapiens	region to myosin heavy chain L8840.12 LNV Tax1 binding protein huntingtin-interacting protein HYPA/FBP11 HSPC182 Human secreted protein, SEQ ID NO: 8101. ribosomal protein L17 isolog transcription factor XLMO1 calmitine; calsequestrine Human protein clone HP01462. heat shock protein PSST subunit of the NADH.	589 544 852 1390 1040 626 908 795 2029 2501	53 85 98 97 100 100 100 97 100 100
973 A 974 U 975 A 976 A 977 G 978 A 979 U 980 S 981 Y 982 A 983 X6	F188504 F188504 F25801 F049523 F161530 04020 F164797 94991 73775 94888 F243191 55020	major Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Kenopus laevis Homo sapiens Homo sapiens Homo sapiens	LNV Tax1 binding protein huntingtin-interacting protein HYPA/FBP11 HSPC182 Human secreted protein, SEQ ID NO: 8101. ribosomal protein L17 isolog transcription factor XLMO1 calmitine; calsequestrine Human protein clone HP01462. heat shock protein PSST subunit of the NADH.	544 852 1390 1040 626 908 795 2029 2501	85 98 97 100 100 100 97 100 100
974 U 975 A 976 A 977 G 978 A 979 U 980 S 981 Y 982 A 983 X6	25801 F049523 F161530 04020 F164797 94991 73775 94888 7243191	Homo sapiens Homo sapiens Homo sapiens Homo sapiens Kenopus laevis Homo sapiens Homo sapiens	Taxl binding protein huntingtin-interacting protein HYPA/FBP11 HSPC182 Human secreted protein, SEQ ID NO: 8101. ribosomal protein L17 isolog transcription factor XLM01 calmitine; calsequestrine Human protein clone HP01462. heat shock protein PSST subunit of the NADH.	852 1390 1040 626 908 795 2029 2501	98 97 100 100 100 97 100 100
975 A 976 A 977 G 978 A 979 U 980 S 981 Y 982 A 983 X6	F161530 04020 F164797 94991 73775 94888 J243191 65020	Homo sapiens Homo sapiens Homo sapiens Kenopus laevis Homo sapiens Homo sapiens Homo sapiens Homo sapiens	huntingtin-interacting protein HYPA/FBP11 HSPC182 Human secreted protein, SEQ ID NO: 8101. ribosomal protein L17 isolog transcription factor XLM01 calmitine; calsequestrine Human protein clone HP01462. heat shock protein PSST subunit of the NADH.	852 1390 1040 626 908 795 2029 2501	98 97 100 100 100 97 100 100
976 A. 977 G 978 A. 979 U 980 S 981 Y 982 A. 983 X6	F161530 04020 F164797 94991 73775 94888 J243191 65020	Homo sapiens Homo sapiens Kenopus laevis Homo sapiens Homo sapiens Homo sapiens Homo sapiens	huntingtin-interacting protein HYPA/FBP11 HSPC182 Human secreted protein, SEQ ID NO: 8101. ribosomal protein L17 isolog transcription factor XLM01 calmitine; calsequestrine Human protein clone HP01462. heat shock protein PSST subunit of the NADH.	1390 1040 626 908 795 2029 2501	97 100 100 100 97 100 100
977 G: 978 A: 979 U: 980 S: 981 Y: 982 A: 983 X: 6	04020 F164797 94991 73775 94888 7243191	Homo sapiens Homo sapiens Xenopus laevis Homo sapiens Homo sapiens Homo sapiens	HSPC182 Human secreted protein, SEQ ID NO: 8101. ribosomal protein L17 isolog transcription factor XLM01 calmitine; calsequestrine Human protein clone HP01462. heat shock protein PSST subunit of the NADH.	908 795 2029 2501	100 100 97 100 100
978 Ai 979 US 980 ST 981 YS 982 Ai 983 X6	F164797 94991 73775 94888 7243191 85020	Homo sapiens Homo sapiens Xenopus laevis Homo sapiens Homo sapiens Homo sapiens	Human secreted protein, SEQ ID NO: 8101. ribosomal protein L17 isolog transcription factor XLMO1 calmitine; calsequestrine Human protein clone HP01462. heat shock protein PSST subunit of the NADH.	908 795 2029 2501	100 100 97 100 100
979 US 980 ST 981 YS 982 Ad 983 X6 984 Ad	94991 73775 94888 7243191 85020	Homo sapiens Xenopus laevis Homo sapiens Homo sapiens Homo sapiens	ID NO: 8101. ribosomal protein L17 isolog transcription factor XLMO1 calmitine; calsequestrine Human protein clone HP01462. heat shock protein PSST subunit of the NADH.	908 795 2029 2501 827	100 97 100 100
979 US 980 ST 981 YS 982 Ad 983 X6 984 Ad	94991 73775 94888 7243191 85020	Xenopus laevis Homo sapiens Homo sapiens Homo sapiens	ribosomal protein L17 isolog transcription factor XLMO1 calmitine; calsequestrine Human protein clone HP01462. heat shock protein PSST subunit of the NADH.	795 2029 2501 827	97 100 100
980 ST 981 YS 982 AZ 983 X6	73775 94888 J243191	Xenopus laevis Homo sapiens Homo sapiens Homo sapiens	transcription factor XLMO1 calmitine; calsequestrine Human protein clone HP01462. heat shock protein PSST subunit of the NADH.	795 2029 2501 827	97 100 100
981 Y9 982 A2 983 X6 984 AJ	94888 7243191 65020	laevis Homo sapiens Homo sapiens Homo sapiens	calmitine; calsequestrine Human protein clone HP01462. heat shock protein PSST subunit of the NADH.	2029 2501 827	100
981 Y9 982 A2 983 X6 984 AJ	94888 7243191 65020	Homo sapiens Homo sapiens	Human protein clone HP01462. heat shock protein PSST subunit of the NADH.	2501 827	100
982 A3 983 X6	7243191 65020	Homo sapiens Homo sapiens	Human protein clone HP01462. heat shock protein PSST subunit of the NADH.	2501 827	100
983. X6	55020	sapiens Komo sapiens	heat shock protein PSST subunit of the Name.	827	
983. X6	55020	Homo sapiens	PSST subunit of the NADH.	_1_	96
984 AJ		Bos taurus	PSST subunit of the NADH.	_1_	96
	7249207	Jos caaras	ubiquinone oxidoreductase	964	
	7249207		I apridations OXIGOLEGISCLES	1	85
	243207	DL-J-	complex		
985 73		Rhodococcus sp. AD45	putative racemase	351	43
	30093	Homo sapiens	basic transcription factor 2, 35 kD subunit	1576	99
986 AB	030835	Homo sapiens	contains two glutamine rich	4500	
987 AF		•	domains, three zinc-finger domains, and matrin 3 homologous domain 3 (MH3)	4697	99
	227258	Bos taurus	RPGR-interacting protein-1	1262	38
	1	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	4048	99
_ 1	022238	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	2321	99
990 AF	161426	Homo sapiens	HSPC308		
991 AF	161426	Homo sapiens	HSPC308	448	92
992 AF:	161426	Homo sapiens	HSPC308	448	92
993 AL	023859	Schizosaccha	trna-splicing endonuclease	453	92
		romyces pombe	subunit	172	42
	049631	Homo sapiens	dJ513M9.1 (novel Homeobox domain protein)	241	47
	005253	Homo sapiens	R26445_1	1000	
	265206		MOG1 isoform A	902	100
997 AJZ	248285		sarcosine oxidase, subunit		100
98 AE0		abyssi	beta (soxB)		28
	T.	melanogaster	BG:DS00941.3 gene product	218	58
		sapiens	Secreted protein of clone CR930_1.	1340	98
			similar to bovine ADP/ATP translocase T1 mRNA with GenBank Accession Number M24102.1	1543	100
001 Y73	381 H	lomo sapiens	HTRM clone 1877278 protein sequence.	1668	L00
	08844 H		BM-002	400	
003 AEO	04944 P		hypothetical protein		100
004 ALO3	a	eruginosa	<u> </u>	134	5
005 S453				2058 1	.00
	, -	anis amiliaris	Compt top and a		.00

022158	familiaris Mus musculus Homo sapiens	chaperonin containing TCP-1 epsilon subunit Fragment of human secreted protein encoded by gene 38. Kruppel-type zinc finger protein K01H12.1 Kruppel-type zinc finger protein RING1 Human secreted protein, SEQ ID NO: 6922. BcDNA.GH10333 Fragment of human secreted protein encoded by gene 65. A human progesterone receptor complex p23-like protein. Human PRO1759 (UNQ832) amino acid sequence SEQ ID NO:374. n-chimaerin microtubule-associated proteins 1A/1B light chain 3 sex-regulated protein janus-a qdgl-1 putative protein	1315 2649 1282 1671 269 1671 2017 332 1244 664 772 2323 1710 631 674 638 155 2483 2243	98 96 97 58 67 58 100 93 52 67 97 100 100 96 37 100 100 100
022158 6332 6011414 68218 3011414 14000 02841 F145659 02860 02591 99448 667250 1F183417 1F164795 1F190625 1F193363 1F190625	Mus musculus Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Homo sapiens Trosophila melanogaster Homo sapiens Homo sapiens Homo sapiens Homo sapiens Coturnix coturnix Arabidopsis thaliana Homo sapiens	epsilon subunit Fragment of human secreted protein encoded by gene 38. Kruppel-type zinc finger protein K01H12.1 Kruppel-type zinc finger protein RING1 Human secreted protein, SEQ ID NO: 6922. BcDNA.GH10333 Fragment of human secreted protein encoded by gene 65. A human progesterone receptor complex p23-like protein. Human PR01759 (UNQ832) amino acid sequence SEQ ID NO:374. n-chimaerin microtubule-associated proteins 1A/1B light chain 3 sex-regulated protein janus-a qdgl-1 putative protein WD-repeat like sequence	1282 1671 269 1671 2017 332 1244 664 772 2323 1710 631 674 638 155	97 58 67 58 100 93 52 67 97 100 97 100 100 96 37
6332 6011414 68218 6011414 14000 02841 F145659 02860 02591 99448 667250 1F183417 AF164795 AF190625 AL133363 AB034912	Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Drosophila melanogaster Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens Coturnix coturnix Arabidopsis thaliana Homo sapiens	Fragment of human secreted protein encoded by gene 38. Kruppel-type zinc finger protein K01H12.1 Kruppel-type zinc finger protein RING1 Human secreted protein, SEQ ID NO: 6922. BcDNA.GH10333 Fragment of human secreted protein encoded by gene 65. A human progesterone receptor complex p23-like protein. Human PR01759 (UNQ832) amino acid sequence SEQ ID NO:374. n-chimaerin microtubule-associated proteins 1A/1B light chain 3 sex-regulated protein janus-a qdgl-1 putative protein WD-repeat like sequence	1671 269 1671 2017 332 1244 664 772 2323 1710 631 674 638 155	58 67 58 100 93 52 67 97 100 97 100 96 37 100
8218 3011414 14000 02841 F145659 02860 02591 99448 67250 AF164795 AF190625 AL133363 AB034912	Homo sapiens Caenorhabdit is elegans Homo sapiens Homo sapiens Homo sapiens Drosophila melanogaster Homo sapiens Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens Coturnix coturnix Arabidopsis thaliana Homo sapiens	Kruppel-type zinc finger protein K01H12.1 Kruppel-type zinc finger protein RING1 Human secreted protein, SEQ ID NO: 6922. BcDNA.GH10333 Fragment of human secreted protein encoded by gene 65. A human progesterone receptor complex p23-like protein. Human PR01759 (UNQ832) amino acid sequence SEQ ID NO:374. n-chimaerin microtubule-associated proteins 1A/1B light chain 3 sex-regulated protein janus-a qdgl-1 putative protein WD-repeat like sequence	269 1671 2017 332 1244 664 772 2323 1710 631 674 638 155	67 58 100 93 52 67 97 100 97 100 37 100
3011414 14000 02841 F145659 02860 02591 99448 67250 AF183417 AF164795 AF190625 AL133363	is elegans Homo sapiens Homo sapiens Homo sapiens Drosophila melanogaster Homo sapiens Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens Coturnix coturnix Arabidopsis thaliana Homo sapiens	Kruppel-type zinc finger protein RING1 Human secreted protein, SEQ ID NO: 6922. BcDNA.GH10333 Fragment of human secreted protein encoded by gene 65. A human progesterone receptor complex p23-like protein. Human PRO1759 (UNQ832) amino acid sequence SEQ ID NO:374. n-chimaerin microtubule-associated proteins 1A/1B light chain 3 sex-regulated protein janus-a qdgl-1 putative protein WD-repeat like sequence	1671 2017 332 1244 664 772 2323 1710 631 674 638 155	58 100 93 52 67 97 100 97 100 100 96 37
14000 02841 F145659 02860 02591 99448 667250 F183417 AF164795 AF190625 AL133363	Homo sapiens Homo sapiens Homo sapiens Drosophila melanogaster Homo sapiens Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens Coturnix coturnix Arabidopsis thaliana Homo sapiens	protein RING1 Human secreted protein, SEQ ID NO: 6922. BcDNA.GH10333 Fragment of human secreted protein encoded by gene 65. A human progesterone receptor complex p23-like protein. Human PR01759 (UNQ832) amino acid sequence SEQ ID NO:374. n-chimaerin microtubule-associated proteins 1A/1B light chain 3 sex-regulated protein janus-a qdgl-1 putative protein WD-repeat like sequence similar to Homo sapiens	2017 332 1244 664 772 2323 1710 631 674 638 155	100 93 52 67 97 100 97 100 100 96 37 100
02841 F145659 02860 02591 99448 67250 AF183417 AF164795 AF190625 AL133363	Homo sapiens Drosophila melanogaster Homo sapiens Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens Coturnix coturnix Arabidopsis thaliana Homo sapiens	RING1 Human secreted protein, SEQ ID NO: 6922. BcDNA.GH10333 Fragment of human secreted protein encoded by gene 65. A human progesterone receptor complex p23-like protein. Human PR01759 (UNQ832) amino acid sequence SEQ ID NO:374. n-chimaerin microtubule-associated proteins 1A/1B light chain 3 sex-regulated protein janus-a qdgl-1 putative protein WD-repeat like sequence	332 1244 664 772 2323 1710 631 674 638 155	93 52 67 97 100 97 100 100 96 37 100
02841 F145659 02860 02591 99448 67250 AF183417 AF164795 AF190625 AL133363	Homo sapiens Drosophila melanogaster Homo sapiens Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens Coturnix coturnix Arabidopsis thaliana Homo sapiens	Human secreted protein, SEQ ID NO: 6922. BcDNA.GH10333 Fragment of human secreted protein encoded by gene 65. A human progesterone receptor complex p23-like protein. Human PR01759 (UNQ832) amino acid sequence SEQ ID NO:374. n-chimaerin microtubule-associated proteins 1A/1B light chain 3 sex-regulated protein janus-a qdgl-1 putative protein WD-repeat like sequence similar to Homo sapiens	1244 664 772 2323 1710 631 674 638 155	52 67 97 100 97 100 100 96 37
F145659 02860 02591 99448 67250 AF164795 AF190625 AL133363 AB034912	Drosophila melanogaster Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens Coturnix coturnix Arabidopsis thaliana Homo sapiens	ID NO: 6922. BcDNA.GH10333 Fragment of human secreted protein encoded by gene 65. A human progesterone receptor complex p23-like protein. Human PR01759 (UNQ832) amino acid sequence SEQ ID NO:374. n-chimaerin microtubule-associated proteins 1A/1B light chain 3 sex-regulated protein janus-a qdgl-1 putative protein WD-repeat like sequence similar to Homo sapiens	664 772 2323 1710 631 674 638 155	67 97 100 97 100 100 96 37 100
02860 02591 99448 67250 AF183417 AF164795 AF190625 AL133363	melanogaster Homo sapiens Homo sapiens Homo sapiens Rattus norvegicus Homo sapiens Coturnix coturnix Arabidopsis thaliana Homo sapiens	Fragment of human secreted protein encoded by gene 65. A human progesterone receptor complex p23-like protein. Human PRO1759 (UNQ832) amino acid sequence SEQ ID NO:374. n-chimaerin microtubule-associated proteins 1A/1B light chain 3 sex-regulated protein janus-a qdgl-1 putative protein WD-repeat like sequence similar to Homo sapiens	772 2323 1710 631 674 638 155	97 100 97 100 100 96 37
02591 99448 67250 F183417 AF164795 AF190625 AL133363	Homo sapiens Rattus norvegicus Homo sapiens Homo sapiens Coturnix coturnix Arabidopsis thaliana Homo sapiens	protein encoded by gene 65. A human progesterone receptor complex p23-like protein. Human PRO1759 (UNQ832) amino acid sequence SEQ ID NO:374. n-chimaerin microtubule-associated proteins 1A/1B light chain 3 sex-regulated protein janus-a qdgl-1 putative protein WD-repeat like sequence similar to Homo sapiens	772 2323 1710 631 674 638 155	100 97 100 100 96 37
99448 67250 F183417 AF164795 AF190625 AL133363	Rattus norvegicus Homo sapiens Homo sapiens Coturnix coturnix Arabidopsis thaliana Homo sapiens	complex p23-like protein. Human PR01759 (UNQ832) amino acid sequence SEQ ID NO:374. n-chimaerin microtubule-associated proteins 1A/1B light chain 3 sex-regulated protein janus-a qdgl-1 putative protein WD-repeat like sequence similar to Homo sapiens	2323 1710 631 674 638 155	97 100 100 96 37
AF164795 AF190625 AL133363	Rattus norvegicus Homo sapiens Homo sapiens Coturnix coturnix Arabidopsis thaliana Homo sapiens	acid sequence SEQ ID NO:374. n-chimaerin microtubule-associated proteins 1A/1B light chain 3 sex-regulated protein janus-a qdgl-1 putative protein WD-repeat like sequence similar to Homo sapiens	1710 631 674 638 155	97 100 100 96 37
F183417 AF164795 AF190625 AL133363 AB034912	norvegicus Homo sapiens Homo sapiens Coturnix coturnix Arabidopsis thaliana Homo sapiens	microtubule-associated proteins 1A/1B light chain 3 sex-regulated protein janus-a qdgl-1 putative protein WD-repeat like sequence similar to Homo sapiens	631 674 638 155	100 100 96 37
AF164795 AF190625 AL133363 AB034912	Homo sapiens Homo sapiens Coturnix coturnix Arabidopsis thaliana Homo sapiens	proteins 1A/1B light chain 3 sex-regulated protein janus-a qdgl-1 putative protein WD-repeat like sequence similar to Homo sapiens	674 638 155 2483	100 96 37
AF190625 AL133363 AB034912	Homo sapiens Coturnix coturnix Arabidopsis thaliana Homo sapiens	sex-regulated protein janus-a qdgl-1 putative protein WD-repeat like sequence similar to Homo sapiens	638 155 2483	96 37
AF190625 AL133363 AB034912	Coturnix coturnix Arabidopsis thaliana Homo sapiens	qdgl-1 putative protein WD-repeat like sequence	155 2483	37
AL133363 AB034912	coturnix Arabidopsis thaliana Homo sapiens	putative protein WD-repeat like sequence similar to Homo sapiens	2483	100
AB034912	thaliana Homo sapiens	WD-repeat like sequence		
	Homo sapiens	similar to Homo sapiens		
	Homo sapiens	similar to Homo sapiens	2243	
	1	hexakisphosphate kinase 2 (IP6K2) mRNA with Ge		
X69910	Homo sapiens		2958	99
V80736	Homo sapiens		1657	54
AB029333	Halocynthia roretzi	HrPET-1	1048	
AB032931	Homo sapiens	isolog	1045	100
G01797	Homo sapiens	Human secreted protein, SEQ	749	98
G01797	Homo sapiens	000	749	98
AF193795	Homo sapiens		960	100
	Mus musculus		120	30
AJ222968 281317	Schizosaccha romyces		685	31
¥41519	pombe Homo sapiens	s Fragment of human secreted	1321	99
			1709	77
AJ276004 AF025459	Caenorhabdi		190	30
Ú37251		protein; this is a splicing	r 196	43
	Homo	Human membrane protein	1921	97
W74580	sapiens	BA0306.	331	80
	281317 Y41519 AJ276004 AF025459	Z81317 Schizosacch romyces pombe Y41519 Homo sapien AJ276004 Mus musculu AF025459 Caenorhabdi is elegans U37251 Homo sapien	Schizosaccha romyces protein Y41519 Homo sapiens Fragment of human secreted protein encoded by gene 75. AJ276004 Mus musculus Paxneb protein AF025459 Caenorhabdit is elegans U37251 Homo sapiens Description: KRAB zinc finge protein; this is a splicing supplied by author W74580 Homo sapiens BA0306.	Z81317 Schizosaccha romyces protein Y41519 Homo sapiens Fragment of human secreted protein encoded by gene 75. AJ276004 Mus musculus Paxneb protein 1709 AF025459 Caenorhabdit is elegans Description: KRAB zinc finger protein; this is a splicing supplied by author W74580 Homo sapiens Human membrane protein 1921 BA0306.

SEQ	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-	
NO:				WATERMAN	
	AF290204	Homo sapiens	blood group carrier molecule	1637	99
1041	Y96730	Homo sapiens	PRO539, a Costal-2 homologue.	162	22
1042	AF140683	Mus musculus	F-box protein FWD2		
1043	AF151023	Homo sapiens	HSPC189	2397	98
1044	AF181631	Drosophila	BcDNA.GH04929	1104	100
1045	¥77985	melanogaster	:	204	37
1046	AJ243972	1	sequence.	1940	100
1047	AB035863	Homo sapiens		1317	100
1048		Homo sapiens	synthetase beta subunit precursor	2324	99
	AL034550	Homo sapiens	similar to nucleolar protein 4 (NOL4) (NOLP))	981	92
1049	AF163825	Homo sapiens	pre-B lymphocyte pyobain 2	634	
1050	AF201949	Homo sapiens	60S ribosomal protein L30	868	100
1061	-	1	isolog	000	100
1051 1052	AF190624	Mus musculus	····-3= =	236	85
1022	AE003529	Drosophila	CG6151 gere product	160	85
1053	G01191	melanogaster Homo sapiens	Human secreted protein, SEQ		44
1054	AL162756	Neisseria	ID NO: 5272.	646	98 .
1055		meningitidis	Glu-tRNA(Gln) amidotransferase subunit A	682	44
1055	AF181856	Rattus norvegicus	tRNA selenocysteine associated protein	1525	99
1056	U89649	Chlamydomona	Mr19,000 outer arm dynein		}
Ş		s reinhardtii	light chain	244	34
1057	AF159141	Homo sapiens	breast cancer metastasis- suppressor 1	663	53
1058	AF230929	Homo sapiens	keratinocyte annexin-like	1710	99
1059	AJ270952	Homo sapiens	protein pemphaxin		
1050	AF224263	Heterodontus	putative membrane protein	1363	100
		francisci	HOXUS	742	83
1061	X63417	Homo sapiens	IRLB		
1062	AL079345	Streptomyces	hypothetical protein	1037	100
		coelicolor A3(2)		143	27
1063	Y71112	Homo sapiens	Human Hydrolase protein-10	2547	100
1064	AF263614	Homo sapiens	(HYDRL-10).		-
1065	Y13356	Homo sapiens	acetyl-CoA synthetase	3493	99
		odprens	Amino acid sequence of protein PRO221.	1363	100
1066	AC006153	Homo sapiens	similar to Aquifex aeolicus		
		j	GTP-binding protein; similar to AE000771 (PID:g2984292)	662	98
.067	Y18930	Sulfolobus	hypothetical protein		
068	R65969	solfataricus		162	29
069		sapiens T98G	Glioblastoma-derived polypeptide.	887	100
		Homo sapiens	Human secreted protein	863	96
070		Rattus norvegicus	CDK5 activator-binding	1995	86
071	AF245505		protein	_	
072			adlican alpha glucosidase II, beta		99
073		[subunit ·		36
		1 :	Human secreted protein, SEQ ID NO: 7970.	698	98
		Homo sapiens	970	380	
75	Y13392		Amino acid sequence of		28

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:			protein PRO328.		L
076	AF161457	Homo sapiens	HSPC339	571	100
.077	¥79509	Homo sapiens	Human carbohydrate-associated protein CRBAP-5.	2151	98
070	AF223466	Homo sapiens	HT015 protein	831	66
.078	AL132965	Arabidopsis thaliana	putative WD-40 repeat-protein	286	29
	AB024937	Homo sapiens	LUNX	1284	100
.080 L081	Y14768	Homo sapiens	V-ATPase G-subunit like	579	100
L082	AF016416	Caenorhabdit is elegans	F29A7.4 gene product	141	31
		Homo sapiens	ADP-ribosylarginine hydrolase	802	45
1083	L13291	Mus musculus	unnamed protein product	151	44
1084	AB041541 G01922	Homo sapiens	Human secreted protein, SEQ ID NO: 6003.	202	97
			H-REV107 protein homolog	833	100
1086 1087	AB030814 AF151638	Homo sapiens	phosphatidylcholine transfer protein	1142	100
1088	Y84432	Homo sapiens	Amino acid sequence of a human RNA-associated protein.	2783	100
1089	¥94867	Ното	Human protein clone HP10563.	613	100
		sapiens	unnamed protein product	130	49
1090	AK023982	Homo sapiens	unnamed protein product	1103	81
1091	AB041586	Mus musculus Homo sapiens	Human Zlipo3 protein.	606	100
1092 1093	¥71277 U34973	Mus musculus	protein tyrosine phosphatase- like	1131	95
1094	Y66677	Homo	Membrane-bound protein	522	56
1095	Y87276	Sapiens Homo sapiens	Human signal peptide containing protein HSPP-53	1029	99
1096	¥87276	Homo sapiens	SEQ ID NO:53. Human signal peptide containing protein HSPP-53	863	98
	l	_	SEQ ID NO:53.	742	98
1097	AF161455	Homo sapiens	HSPC337	242	39
1098	U80029	Caenorhabdit is elegans			99
1099	AJ005866	Homo sapiens	Sqv-7-like protein	1321	99
1100	AJ005866	Homo sapiens	Sqv-7-like protein	891	99
1101	AJ005866	Homo sapiens	Sqv-7-like protein	1016	99
1102	AJ005865	Homo sapiens	Sgy-7-like protein	299	31
1103	AL110244	Homo sapiens	hypothetical protein	147	52
1104	AF242194	Drosophila melanogaster	brakeless-B	968	100
1105	AL031010	Homo sapiens	protein similar to C. elegans (C02C2.5)		87
1106	U28016	Mus musculus	(phosphotriesterase) -related	1624	
1107	AJ278150	Homo sapiens	putative lipid kinase	2207	99
1107	G03733	Homo sapiens	000	495	98
1109	AF217287	Drosophila melanogaster	G protein RhoBTB	834	54
1110	Y28921	Homo	Human regulatory protein	941	48
1111	Y28921	sapiens Homo	Human regulatory protein HRGP-7.	1331	51
		sapiens		2027	99
1112	AF176704		glioma tumor suppressor	2418	100
1113	AF182076	sapiens	candidate region protein 2		

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-	
NO:	NUMBER		1	WATERMAN SCORE	IDENTI
1115	77000		ID NO: 8120.	SCORE	
1116	AF229439	Mus musculus		1697	91
	L40357	Homo sapiens	thyroid receptor interactor	509	
1117	L40357	Homo sapiens	thyroid receptor interactor	404	100
1118	A12155	Homo sapiens	Human X5L cDNA.	1673	85
1119	AL161542	Arabidopsis	isomerase like protein	607	100 53
1120	AL023754	thaliana Homo sapiens	dJ272L16.1 (Rat		_1
			Ca2+/Calmodulin dependent	2341	98
			Protein Kinase LIKE protein)		
1121	Y57901	Homo sapiens	Euman transmembrane protein	321	36
1122	214122	Xenopus	ETMPN-25.		36
		laevis	XLCL2	455	77
1123	AF225418	Homo sapiens	lipase		
1124	Y06518	Homo sapiens		1531	97
			protein ZIP.	3227	100
1125	AL035690	Homo sapiens	dJ202I21.1 (novel protein)	050	
1126	AJ000217	Homo sapiens	CLIC2	952	100
1127	AB030505	Mus musculus	UBE-1c2	1286	99
1128	Y73375	Homo sapiens		1069	79
		1	HTRM clone 1427838 protein sequence.	874	100
1129	Y78941	Homo sapiens	Cyclophilin-type pentidyl	877	
	1	1	prolyl cis/trans isomerase	10//	100
]	amino acid sequence.	1	1
1130	AL023553	Homo sapiens	dJ347H13.4 (novel protein)	+	
1131	Y91945	Homo sapiens	Human chaperone protein 6	557	100
1132	Z68197		(HCHP-6).	1408	100
	40019/	Schizosaccha	putative nuclear pore protein	596	39
	1	romyces	1		139
1133	268197	pombe	·	1	ļ
	20019/	Schizosaccha	putative nuclear pore protein	389	35
	1	romyces			1
134	AF180681	pombe		1	1
	70091	Homo sapiens	guanine nucleotide exchange	3597	100
.135	AF079765	Mus misculus	factor	}	l -
136	M62419		enhancer of polycomb	264	41
137	AJ006219	Mus musculus	clathrin-associated protein	2189	99
'	-10000219	Drosophila	clathrin-associated protein	1254	78
138	Y76218	melanogaster	•		
	1,0210	Homo sapiens	Human secreted protein	440	98
139	W88104		encoded by gene 95.		90
	700104	Homo	A Rab protein designated	1065	99
140	Y13401	sapiens	HRABS-2.		25
-=0	113401	Homo sapiens	Amino acid sequence of	3979	98
141	W85026	054	protein PRO339.		90
	103020	Chimeric -	Green fluorescent protein-	3309	100
142	¥13402	Homo sapiens	Zap70 fusion product.		200
	113402	Homo sapiens	Amino acid sequence of	1694	99
143	G03875	Rome	protein PRO310.	1	
	-550,5	Homo sapiens	Human secreted protein, SEQ	660	99
44	¥12917		ID NO: 7956.	İ	
			Amino acid sequence of a	750	98
45	Y12917	Homo co	human secreted peptide.	Í	
_		Homo sapiens	Amino acid sequence of a	1096	100
46	AL022157	·	human secreted peptide.	1	
- 1		nomo sapiens	SPIN (SPINDLIN HOMOLOG	1233	100
47	AL022157	Home on	(PROTEIN DXF34))	1	
'		Homo sapiens :	SPIN (SPINDLIN HOMOLOG	1233	100
48 (G02548		(PROTEIN DXF34))		
	102340	Homo sapiens I	Human secreted protein, SEQ	370	98
49	V73330		ID NO: 6629.		J ()
1	¥73338	Homo sapiens F	TRM clone 2019742 protein	1492	100
	ľ	i s	sequence.		100
50 - 1 -	174943				
50 W	V74841 I	lomo sapiens	duman secreted protein encoded by gene 113 clone	228	55

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:			HEAAR60.		
	AF044201	Rattus	neural membrane protein 35;	1570	92
151	AF044201	norvegicus	NMP35		
	AF156774	Homo	lysophosphatidic acid	1855	99
152	AF156//4	sapiens	acultransferase-gammal		<u> </u>
		Homo sapiens	dJ1191N16.1 (A novel protein	872	64
153	AL118501	NOMO Bapicino	(translation of the cDNA		
İ		ļ j	DKFZp566A0946, Em:AL050069))		1
			Unknown	473	100
.154	AF131852	Homo sapiens	Human PRO352 protein	1381	97
155	¥41705	Homo			
		sapiens	Human secreted protein, SEQ	607	99
1156	G04036	Homo sapiens		1	
			ID NO: 8117.	287	43
1157	AF112444	Lupinus	L-asparaginase	1 207	1
		luteus			32
1158	AF151848	Homo sapiens	CGI-90 protein	232	100
	AJ272267	Homo sapiens	choline dehydrogenase	2449	
1159	AB001773	Ciona	PEM-6	196	33
1160	WEGGT 1/3	savignyi			
	1.000	Homo sapiens	Human signal peptide	746	83
1161	¥87330	nomo saprems	containing protein HSPP-107	1	1
	(1	SEQ ID NO:107.	1	
	<u></u>	1	Human signal peptide	746	83
1162	Y87330	Homo sapiens	containing protein HSPP-107	1	1
			SEQ ID NO:107.		1
				2723	96
1163	AF113534	Homo sapiens	HP1-BP74 protein	191	41
1164	AF232226	Danio rerio	Deddl	1051	71
1165	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	1001	1 '-
2200		1	(translation of the cDNA		}
			DKFZp566A0946, Em:AL050069))	 	75
1166	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	945	/"
1100	ADITOSOX	1100	(translation of the CDNA	1	1 .
			DKFZp566A0946, Em:AL050069))		
	37107733	Homo sapiens	syntaphilin	831	42
1167	AF187733	Homo sapiens	phospholipase	951	55
1168	AB019435		VEO3 protein	324	33
1169	AF064604	Homo sapiens		1191	100
1170	¥01164	Homo sapiens	by gene 6.	l	i
ì				180	22
1171	L03188	Saccharomyce		1	1
İ		s cerevisiae		3941	81
1172	AF113751	Mus musculus	nuclear pore membrane	1	}
	Ĭ.	_	glycoprotein POM210	794	100
1173	AJ245417	Homo sapiens		1285	100
1174	AL022238	Homo sapiens	dJ1042K10.3 (novel protein)		28
1175	U41278	Caenorhabdit		332	20
1 77 /2	0412,0	is elegans	i		_
1175	Maccan	Homo sapiens	T-cell receptor V-alpha-J-	284	83
1176	M35617	Tionic Suprem	alpha region	L	
		Arabidopsis	putative protein phosphatase	209	37
1177	AC012680	thaliana	2C: 55455-56414	1	
L			CRO	692	99
1178	G01345	Homo sapiens	ID NO: 5426.	[1
	<u> </u>			1342	100
1179	AL096767	Homo sapiens	similar to worm, Arabidopsis	1	1
1	1		SIMITAL CO WOLM' WIGHT MODEL	1	1
1	1		and pine proteins)	496	55
1180	AF039716	Caenorhabdit		} = 75	
1	1	is elegans	chain	1000	97
1181	Y11710	Homo sapiens	collagen type XIV	1048	100
1182		Homo	T cell leukemia/lymphoma 1	617	1 -00
1 1185	A02270	sapiens)			ł
1	1	>R94974			1
1		R94974 09-			1
1	{		_	ł	1
1		MAY-1996 27		1	1
1	-	OCT-1994		1	1
1		Human TCL-1		l l	ĺ
1	polypeptide	- 1			

		_	TABLE 2		
SEQ ID NO:	ACCESSION NUMBER		DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1		[Homo sapiens			
1183	U42841	Caenorhabdit is elegans		161	33
1185	AJ131613	Homo sapiens	similarity to collagen dicarboxylate carrier protein		
1186	L27645	Danio rerio	growth-associated protein	1470	99
1187	Y02738	Homo sapiens	Human secreted protein	636	36
			encoded by gene 89 clone	038	100
1188	AF217544	Xenopus laevis	ornithine decarboxylase-2	1459	60
1189	AL136307	Homo sapiens	protein which promotes	182	33
1190	X89602	Homo sapiens	neurite outgrowth)		ļ
1191	U32828	Haemophilus	ribosomal protein S6	197	100
		influenzae Rd	modification protein (rimK)	268	31
1192	AF154831	Rattus	PV-1	1403	
1193	1	norvegicus		1403	60
1193	Y50926	Homo sapiens	Human fetal brain cDNA clone vc16_1 derived protein.	918	100
1174	AF026530	Rattus	stathmin-like-protein splice	1093	97
1195	U35244	norvegicus Rattus	variant RB3''		1
1196	¥70470	norvegicus Homo sapiens	vacuolar protein sorting homolog r-vps33a	2981	96
1197	AF157318	Homo sapiens	Human p53 target molecule, PRG3 protein. AD-017 protein	1680	100
1198	AF125443	Caenorhabdit	contains similarity to S.	912	47
1.00		is elegans	pombe phosphatidyl synthase (GB:Z28295)	460	39
1199 1200	AF201934	Homo sapiens	DC12	1649	88
1200	AL031775	Homo sapiens	dJ30M3.3 (novel protein similar to C. elegans Y63D3A.4)	1902	100
1201	M21103	Ovis aries	BIIIB4 high-sulfur keratin		
1202	285986	Homo sapiens	dJ108k11.3 (similar to yeast	1143	82
			suppressor protein SRP40)	1143	75
1203	U18762	Rattus norvegicus	retinol dehydrogenase type I	890	52
1204	U35730	Mus musculus	jerky	2235	76
1205	AB002327 AB019233	Homo sapiens	KIAA0329	151	24
		Arabidopsis thaliana	ubiquinone/menaquinone biosynthesis methyltransferase-like	762	56
1207	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a protein which promotes	742	100
1208	AF207989	Homo sapiens	neurite outgrowth) orphan G-protein coupled receptor	2326	100
209	297630	Homo sapiens	dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3.	181	44
.210	U21549		node of Ranvier (ankyrin G)))		
211	Y27700	Mus musculus	Ac39/physophilin	1280	68
212	AF117814		Human secreted protein encoded by gene No. 12.	1267	100
213	AF277233		odd-skipped related 1 protein	945	66
	D14849	fowleri	calcineurin B		39
			meiosis-specific nuclear structural protein 1		77
	272510		Human secreted protein, SEQ ID NO: 7103.		100
			similarity to yeast UTR3	634	49

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:			protein (Swiss Prot accession yk677h11.5 comes from this gene		
217	Z49703	Saccharomyce	unknown	134	22
218	AC013430	Wrantochara	F3F9.18	199	29
		thaliana	splicing factor	1026	71
1219	L10910		similar to vanadate	965	58
1220	Z70750	Caenorhabdit is elegans	resistance protein transmembranous comes from this gene		
1221	AL163815	Arabidopsis thaliana	putative protein	653	61
1222	AF155100	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	100
1223	J05071	Bos taurus	GTP-binding regulatory protein gamma-6 subunit	356	100
1224	¥73364	Homo sapiens	HTRM clone 2765991 protein sequence.	1169	99
	31050150	Homo sapiens	hypothetical protein	714	100
1225	AL050170	Homo sapiens	RAP74	2661	99
1226	X64002	Homo sapiens	catalase	2846	100
1227	X04085 AJ005620	Mus musculus	skeletal muscle-specific gene	1416	90
1228 1229	AF045564	Rattus norvegicus	development-related protein	1715	93
		Mus musculus	HCMV-interacting protein	479	96
1230	X97571	Homo sapiens	located at OATL1	2274	100
1231	L08239 AF121863	Homo sapiens	sorting nexin 14	1964	100
1232	AF121863	Homo sapiens	sorting nexin 14	1203	84
1233 1234	AC024805	Caenorhabdit is elegans	contains similarity to	744	31
1235	AC006634	Caenorhabdit is elegans	contains similarity to Saccharomyces cerevisiae probable membrane protein YLR418C (GB:U20162)	357 1559	87
1236	Y18101	Mus musculus	tyrosine-phosphorylated protein		
1237	AB042646	Homo sapiens		1224	100
1237	AB026264	Homo sapiens		1694	100
1238	AB026264	Homo sapiens	IMPACT	1123	100
1240	G00429	Homo sapiens	Human secreted protein, SEQ ID NO: 4510.	324	,
1241	Y76144	Homo sapiens	Human secreted protein encoded by gene 21.	1363	53
1242	AL035602	Arabidopsis thaliana	putative protein	499	28
1243	X76483	Gallus gallus	Yes-associated protein (65kDa)	574	48
1244	AF220186	Homo sapiens	protein HT012	503	100
1245	AL021453	Homo sapiens	dJ821D11.3 (PUTATIVE protein)	856	100
1245	AJ276003	Homo sapiens	GAR1 protein	1216	98
1247	Y57910	Homo sapiens	Human transmembrane protein		100
1248	AC004874	Homo sapiens	s similar to N- acetylgalactosaminyltransfers se; similar to Q07537 (PID:g1171989)		100
1249	AF199597	Homo sapiens	A-type potassium channel modulatory protein 1	1139	
1250	Y13148	Rattus	PAG608	1350	88
1251	M24852	Rattus norvegicus	neuron-specific protein PEP-	124	46

SEQ	ACCESSIO	N SPECIES			
ID	NUMBER		DESCRIPTION	SMITH-	क्षे
NO:	AF146738	Rattus		WATERMAN SCORE	IDENTI
1253	G02725	norvegicus	testis specific protein	771	83
		Homo sapier	ID NO: 68C6	419	97
1254	W44375	Homo sapien	s Human ubiquitin-conjugating	1045	99
1255	AC006538	Homo sapien	enzyme polypeptide. s BC41195 1		-
1256	AB004316	Bos taurus	mitochondrial methionyl-tRNA	831	78
		İ	[Cransformylace	1556	88
1257	235094	Homo sapien	s SURF-2		
1258	Y13362	Homo sapien		1354 2383	97
1259	70000014		protein PRO214	2363	100
1233	AC006014	Homo sapien	similar to RFP transforming protein; similar to P14373	1299	100
1260	AC005099	Homo sapiens	(PID:g132517) s match to AI222572		
	_		(NID:g3804775)	469	100
1261	V00507	Homo sapiens	coding sequence of DHFR (1 is		
1262	X15443		1st base in codon) (561 is 3rd base in codon)	984	100
2202	A15443	Rattus sp.	gamma-glutamyltranspeptidase	697	32
1263	AF173871	Mus musculus	(AA 1-568) neuronal PAS3	_1	1
1264	AF178983	Homo sapiens		977	94
1265	¥70473	Homo sapiens		433	97
1266			associated protein-1 (CNAP-	2785	99
1200	Y41738	Homo	Human PRO541 protein	1622	100
1267	AF061346	sapiens Mus musculus	sequence.	1	1 200
1268	U97006	Caenorhabdit		1077	64
		is elegans	Cl3F10.4 gene product	154	23
1269	AF233582	Mus musculus	GTPase Rab37		1
1270	AF195951	Homo sapiens	signal recognition particle	942	95
1271		1	68	3127	98
1271	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	1150	<u> </u>
1272	AF201933	Homo sapiens	DC11	650	55
1274	AF201933 AL021710	Homo sapiens	DC11	346	100 98
	AL021/10	Arabidopsis	putative protein	348	49
1275	AC004449	thaliana Homo sapiens			1 3 2
276	Y86295	Homo sapiens	R33683_3	556	100
]		nomo saptens	Human secreted protein	1920	100
1277	Y71111	Homo sapiens	HL2AG87, SEQ ID NO:210. Human Hydrolase protein-9	<u>i</u>	ł
			(HYDRL-9).	1576	99
278	S94421	Homo sapiens	T cell receptor eta-exon	100	
279	¥66695	Homo	Membrane-bound protein	478	100
280	D 127. C 1 7.00	sapiens	PRO1344.	1909	100
281	AF161380 Y48610	Homo sapiens	HSPC262	772	100
	740010	Homo sapiens	Human breast tumour-	779	100
282	AC015446	Arabidopsis	associated protein 71.		100
I		thaliana	Similar to AIG1 protein	405	35
	AK024432	Homo sapiens	FLJ00022 protein	.]	
284	W96153	Homo sapiens	Human FADD-interacting	403	35
			protein (FIP).	1825	81
	AJ001019	Homo sapiens	ring finger protein		_
			procetti	1301	100
	AE003823	Drosophila	CG13178 gene product	105	
286	AE003823	Drosophila melanogaster	CG13178 gene product	195	29
286	AE003823 AF178632	Drosophila melanogaster Homo sapiens	FEM-1-like death receptor		100
286	AE003823 AF178632 AC006033	Drosophila melanogaster Homo sapiens	FEM-1-like death receptor binding protein similar to MIN 64; similar to	3261	100
286	AE003823 AF178632 AC006033	Drosophila melanogaster Homo sapiens Homo sapiens	FEM-1-like death receptor binding protein similar to MIN 64; similar to I38027 (PID:92135214)	3261	_
286	AE003823 AF178632 AC006033	Drosophila melanogaster Homo sapiens Homo sapiens Homo	FEM-1-like death receptor binding protein	3261	100

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO: 1291	273424	Caenorhabdit	C44B9.1	235	36
1292	Y94871	is elegans Homo	Human protein clone HP02551.	1222	100
1293	AF180425	sapiens Homo sapiens	retinoblastoma-associated protein RAP140	489	29
1294	G03856	Homo sapiens	Human secreted protein, SEQ ID NO: 7937.	538	99
	AF133670	Mus musculus	ARL-6 interacting protein-2	367	51
1295 1296	AJ249735	Homo sapiens	claudin-6	1142	100
1297	X57560	Escherichia coli	pspE protein	535	100
1298	AF169284	Homo sapiens	LIM and cysteine-rich domains protein 1	1997	100
1299	U41023	Caenorhabdit is elegans	coded for by C. elegans cDNA yk61f1.3; coded for by C. yk109h8.5	324	2.9
1300	AB024523	Homo sapiens	basic kruppel like factor	1206	100
1301	X55989	Homo sapiens	eosinophil cationic-related protein	737	99
1302	AF007151	Homo sapiens	unknown	1481	100
1303	X52904	Escherichia coli	open reading frame (AA 1-65)	359	100
1304	U19577	Escherichia coli	galactonate dehydratase	242	93
1305	AF266508	Mus musculus	NELF protein	1409	97
1306	Y57901	Homo sapiens	Human transmembrane protein HTMPN-25.	932	100
1307	U58750	Caenorhabdit is elegans	similar to the mitochondrial carrier family	365	54
1308	AF044774	Homo sapiens	breakpoint cluster region protein 2	2681	99
1309	AL078593	Homo sapiens		267	34
1310	X82693	Homo sapiens	E48 antigen	620 283	35
1311	Z82263	Caenorhabdit is elegans	C47A4.1	1493	100
1312	AF131218	Homo sapiens	chromosome 16 open reading frame 5	1636	100
1313	Y41763	Homo sapiens	Human PRO938 protein sequence.	2239	100
1314	AF196972	Homo sapiens	JM24 protein	228	97
1315	AF053356	Homo sapiens	insulin receptor substrate like protein	1909	100
1316	Y66695	Homo sapiens	Membrane-bound protein PRO1344.	2442	89
1317	AF153127	Gallus gallus	SAPK interacting protein	1477	83
1318	AF153127	Gallus gallus	SAPK interacting protein	1651	86
1319	AF153127	Gallus gallus	SAPK interacting protein 23 kD highly basic protein	1044	100
1320	X56932	Homo sapiens	F-box protein Fbx25	1467	70
1321	AF174605	Homo sapiens] >Y83086 Y83086 09- MAR-2000 28- AUG-1998 F- box protein FBP-18. [Homo			
1322	M61732	sapiens Trypanosoma cruzi	neuraminidase	214	24
1323	¥17013	porcine	pol	304	64

1324 AL138655 Arabidopsis Putative protein 1174 37 1325 AL138655 Arabidopsis Putative protein 1174 37 1325 AL138655 Arabidopsis Putative protein 1474 37 1326 AL13215 Homo sapiens Sanidar to rat tricarboxylate 1322 39 1326 AL13215 Homo sapiens Sanidar to rat tricarboxylate 1327 AF161541 Homo sapiens HTRM clone 6.36698 protein 785 96 1328 1330 Homo sapiens HTRM clone 6.36698 protein 785 96 1328 1330 AF146568 Homo sapiens Putative protein 1352 39 1331 W87772 Homo sapiens Putative protein 1352 39 1331 W87772 Homo sapiens Putative protein 1350 AF146568 Homo sapiens Putative protein 1350 AF146568 Homo sapiens Putative protein 1350 AF146568 Homo sapiens Putative protein 1350 AF146568 Homo sapiens Putative protein 1360 100 1333 AF235005 Homo sapiens Sapien	SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	· · · · · · · · · · · · · · · · · · ·
No.	ID	NUMBER		223CKIT I TON		* TDENTTON
1324	NO:					IDENTITY
1326			retrovirus	<u> </u>	- COME	
1325	1324	AL138655		putative protein	1174	37
thaliana tha				_	1	13'
1326	1325	AL138655		putative protein	946	35
1327 AF161541 Some saplems Similar to rat tricarboxylate 1327 AF161541 Some saplems INSPECSS 1328 Y73346 Home saplems INSPECSS 1329 L10910 Some saplems Sequence 1329 L10910 Some saplems Mill protein 1936 100	1					1
Similar to rat tricarboxylate Carriers	1326	AL133215	Homo sapiens		1322	99 3
1327 AF161541 Homo sapiens HENCIONE 619699 protein 785 96	i		1	similar to rat tricarboxylate	1	
1328	1355					
1329			Homo sapiens		1357	99
1329	1328	Y73346	Homo sapiens		785	96
1330	1330	710010	<u> </u>			
1331 N87772 Homo sapiens Ruman serum glucocorticoid-regulated kinase (H-SGK2) 232 33 33 37 37 37 37 3					912	82
1332 Y41741 Homo sapiens Human phosphatase 178 1		_1 -			1936	100
1332 Y41741	1 1331	W0///2	Homo sapiens		232	39
1332 Y41741 Homo sapiens Human PRO704 protein Sapiens Sapiens Sapiens Sapiens Sapiens Sapiens Sapiens Sapiens Sapiens Sapiens Sapiens Sapiens Sapiens Sapiens Similarity to Mouse kinensin- 1ke protein K174 Comes from this gene Similarity to Mouse kinensin- 1ke protein K174 Comes from this gene Similarity to Mouse kinensin- 1ke protein K174 Comes from this gene Similarity to Mouse kinensin- 1ke protein K174 Comes from this gene Similarity to Mouse kinensin- 1ke protein K174 Comes from this gene Similarity to Mouse kinensin- 1ke protein K174 Comes from this gene Conserved protein 290	ı					1
1333 AF295096 Homo sapiens Sequence. 1860 100	1333	V41241	177		-	
1333 AF295996 Homo sapiens Zinc-finger protein ZBRK1 411 91	1332	141/41			1860	100
1334 Z82271 Caemorhabdit Similarity to Mouse kinemsin- 1ike protein XIF4 comes from this gene 1335 AE000810 Methanobacte rium thermoautotr ophicum 1336 Y68779 Homo sapiens Amino acid sequence of a human phosphorylation 1337 AE027003 Mus musculus Protein phosphatase 378 84 1338 U64856 Caemorhabdit Is elegans 1339 AE001394 Plasmodium Flacmodium Falciparum 1340 X76717 Homo sapiens MF-11 protein 204 89 1341 AC011914 Arabidopsis C7881 AE127017 Homo sapiens AF187016 Homo sapiens AF187016 Homo sapiens Similar to BAA77027 AF187016 Homo sapiens Similar to Kelch proteins; simila	1333	AF295096				1
1335 AE000810 Methanobacte rium this gene Conserved protein 290 43			Constant			91
1335 AE000810 Methanobacte conserved protein 290 43	1	2022/1			578	44
1335 AE000810 Nethamobacte rium thermoautotr ophicum oph			is elegans	like protein KIF4 comes from	ĺ	i
1336 Y68779 Komo sapiens Amino acid sequence of a human phosphorylation effector PHSP-11. 1337 AB027003 Mus musculus Protein phosphatase 378 84 1338 1338 1338 1348 AF161548 Homo sapiens Amino acid sequence of a human phosphorylation effector PHSP-11. 1339 AB027003 Mus musculus Protein phosphatase 378 84 1339 AB001394 Plasmodium falciparum Protein of the YMR7 family 170 29 1340 X76717 Homo sapiens MT-11 protein 204 89 1341 AC011914 Arabidopsis Challana Arabidopsis Challana AF187016 Homo sapiens AF187016 Homo sapiens MT-11 protein 2303 39 2122 100 2124	1335	AE000810	Mathanahaaka			1
1336 Y68779 Komo sapiens Amino acid sequence of a human phosphorylation effector PRSP-11.		1.2000310		conserved protein	290	43
1336 Y68779 Homo sapiens Amino acid sequence of a human phosphorylation effector PHSP-11. 1337 AB027003 Mus musculus protein phosphatase 378 84 1338 U64856 Caenorhabdit is elegans Total protein phosphatase 215 40 40 40 40 40 40 40 4	1		,			1
1336 Y68779	J					ľ
human phosphorylation effector PHSP-11.	1336	Y68779		Amino agid gomenes of	· ·	
1337 AB027003 Mus musculus Protein phosphatase 378 84 1338 U64856 Caenorhabdit is elegans weak similarity to TPR 215 40 1339 AE001394 Plasmodium protein of the YMR7 family 170 29 1340 X76717 Homo sapiens MT-11 protein 204 89 1341 AC011914 Arabidopsis putative mutT protein; 68398- 289 45 1342 AJ276171 Homo sapiens ASPIC 2122 100 1343 AF187016 Homo sapiens ASPIC 2122 100 1344 AC006963 Homo sapiens myosin regulatory light chain 2303 99 1344 AC006963 Homo sapiens similar to Kelch proteins; similar to BAA77027 (PID:94650844) 1345 AF257466 Homo sapiens N-acetylneuraminic acid 1880 99 1346 Y25896 Homo sapiens N-acetylneuraminic acid 1880 99 1347 AJ272073 Torpedo male sterility protein 2-like 1664 58 1348 AF161548 Homo sapiens Human secreted protein 1117 100 1351 GO2144 Homo sapiens Human secreted protein 1117 100 1353 Al2029 Homo sapiens Human secreted protein 1117 100 1353 Al2029 Homo sapiens MRP-14 613 100 1354 AC005328 Homo sapiens MRP-14 613 100 1355 AC024876 Caenorhabdit contains similarity to 829 61 1356 AF077226 Homo sapiens Copine III 1876 64 1359 AF217188 Mus musculus YIPIB 801 63 1360 AC074331 Homo sapiens Copine III 1876 64 1360 AC074331 Homo sapiens Copine III 1876 64 1360 AC074331 Homo sapiens Copine III 1876 64 1360 AC074331 Homo sapiens Copine III 1876 64 1360 AC074331 Homo sapiens Copine III 1876 64 1360 AC074331 Homo sapiens Copine III 1876 64 1360 AC074331 Homo sapiens Copine III 1876 64 1360 AC074331 Homo sapiens Copine III 1876 64 1360 AC074331 Homo sapiens Copine III 1876 64 1360 AC074331 Homo sapiens Copine III 1876 64 1360 AC074331 Homo sapiens Copine III Copine III Copine	1	1		human phosphorelation	1019	91
1337 AB027003 Mus musculus Protein phosphatase 378 84 1338 U64856 Caenorhabdit is elegans Weak similarity to TPR 215 40 1339 AE001394 Plasmodium protein of the YMR7 family 170 29 1340 X76717 Homo sapiens MT-11 protein 204 89 1341 AC011914 Arabidopsis thaliana 67881 45 1342 AJ276171 Homo sapiens ASPIC 2122 100 1343 AF187016 Homo sapiens MSPIC 2122 100 1344 AC006963 Homo sapiens Similar to Kelch proteins; 894 35 1345 AF257466 Homo sapiens Similar to Kelch proteins; 894 35 1346 Y25896 Homo sapiens Human secreted protein 1148 100 1347 AJ272073 Torpedo male sterility protein 2-like 1664 58 1348 AF161548 Homo sapiens Human secreted protein 1117 100 1351 G02144 Homo sapiens Human secreted protein 1117 100 1353 Al2029 Homo sapiens Human secreted protein 1117 100 1353 Al2029 Homo sapiens Reference Refere	ļ	1		effector PHSP-11		
1338	1337	AB027003	Mus musculus		370	<u> </u>
1339 AE001394 Plasmodium Protein of the YMR7 family 170 29	1338	U64856	Caenorhabdit	Weak similarity to TPP		1
1339 AE001394 Plasmodium falciparum Flasmodium falciparum Flasmodium falciparum Flasmodium falciparum Flasmodium falciparum Flasmodium falciparum Flasmodium falciparum Flasmodium falciparum Flasmodium falciparum Flasmodium falciparum Flasmodium falciparum Flasmodium falciparum Flasmodium falciparum Flasmodium falciparum Flasmodium falciparum Flasmodium falciparum Flasmodium falciparum falciparum Flasmodium falciparum f			is elegans		1 213	40
1340 X76717 Homo sapiens MT-11 protein 204 89	1339	AE001394			170	30
1341 AC011914 Arabidopsis Putative mutT protein; 68398- 289 45	<u></u>		falciparum	- and a second s	1 - 70	29
1341 AC011914 Arabidopsis Examination Arabidopsis C7881				MT-11 protein	204	89
Chaliana 67881 1342 AJ276171 Homo sapiens ASPIC 1343 AF187016 Homo sapiens Myosin regulatory light chain interacting protein MIR 2303 99 1344 AC006963 Homo sapiens Similar to Kelch proteins; 894 35 Similar to BAA77027 (PID:g4650844)	1341	AC011914		putative mutT protein; 68398-		1 '
1343 AF187016 Homo sapiens Msylotin regulatory light chain 2303 99				67881		
1344 AC006963 Homo sapiens myosin regulatory light chain interacting protein MIR 1344 AC006963 Homo sapiens Similar to Kelch proteins; 894 35 35 35 35 35 36 35 36 36					2122	100
1344 AC006963 Homo sapiens Similar to Kelch proteins; 894 35	1343	AF187016	Homo sapiens	myosin regulatory light chain	2303	
1345 AF257466 Homo sapiens N-acetylneuraminic acid phosphate synthase 1148 100	1244	1 2000 50 50 50		interacting protein MIR		
1345 AF257466 Homo sapiens N-acetylneuraminic acid phosphate synthase 1480 99	1344	AC006963	Homo sapiens	similar to Kelch proteins;	894	35
1345 AF257466 Homo sapiens N-acetylneuraminic acid phosphate synthase 1880 99		1				i
1346 Y25896	1345	AF257466	Home cond-	(PID:g4650B44)		
1346 Y25896		.223,400	nomo sapiens	N-acetylneuraminic acid	1880	99
1347	1346	¥25896	Homo saniona	phosphate synthase		
1347 AJ272073 Torpedo marmorata protein 2-like 1664 58 1348 AF161548 Homo sapiens HSPC063 1018 98 1349 W78128 Homo sapiens Human secreted protein 1117 100 1351 G02144 Homo sapiens Human secreted protein, SEQ 418 100 1352 D90669 Escherichia similar to 2047 100 1353 A12029 Homo sapiens MRP-14 613 100 1354 AC005328 Homo sapiens R26660 1, partial CDS 870 74 1355 AC024876 Caenorhabdit contains similarity to is elegans SW:RPB1_CRIGR 1356 AF077226 Homo sapiens Copine III 1876 64 1359 AF217188 Mus musculus YIP1B 801 63 1360 AC074331 Homo sapiens ZNF234 3869 100			omo Bapiens	frament annual frament	1148	100
1347]	1		64.	1 1	
Marmorata Protein 1664 58	1347	AJ272073	Torpedo			
1348				protein	1664	58
1349 W78128 Homo sapiens Human secreted protein 1117 100	1348	AF161548			1010	
encoded by gene 3 clone HOSB196. 1351 G02144 Homo sapiens Human secreted protein, SEQ 418 100 1352 D90863 Escherichia similar to 2047 100 1353 A12029 Homo sapiens MRP-14 613 100 1354 AC005328 Homo sapiens R26660 1, partial CDS 870 74 1355 AC024876 Caenorhabdit is elegans SW:RPB1_CRIGR 1356 AF077226 Homo sapiens Copine III 1876 64 1359 AF217188 Mus musculus YIP1B 801 63 1360 AC074331 Homo sapiens ZNF234 3869 100	1349	W78128	Homo sapiens		<u> </u>	
HOSBI96. Homo sapiens Human secreted protein, SEQ 418 100				encoded by gene 3 clone	1111/	100
1351 G02144 Homo sapiens Human secreted protein, SEQ 418 100 1352 D90669 Escherichia similar to 2047 100 1353 A12029 Homo sapiens MRP-14 613 100 1354 AC005328 Homo sapiens R26660 1, partial CDS 870 74 1355 AC024876 Caenorhabdit is elegans SW:RPB1_CRIGR 1356 AF077226 Homo sapiens Copine III 1876 64 1359 AF217188 Mus musculus YIP1B 801 63 1360 AC074331 Homo sapiens ZNF234 3869 100			İ			
ID NO: 6225.	1351	G02144	Homo sapiens		410	700
1352 D90869 Escherichia similar to 2047 100				ID NO: 6225.	-10	100
Coli	1352	D90869	Escherichia	similar to	2047	100
1354 AC005328 Homo sapiens R26660 1, partial CDS 870 74			:	•	/	-00
1354 AC005328 Homo sapiens R26660 1, partial CDS 870 74 1355 AC024876 Caenorhabdit contains similarity to 829 61 1356 AF077226 Homo sapiens Copine III 1876 64 1359 AF217188 Mus musculus YIP1B 801 63 1360 AC074331 Homo sapiens ZNF234 3869 100				MRP-14	613	100
1355 AC024876 Caenorhabdit contains similarity to 829 61 1356 AF077226 Homo sapiens copine III 1876 64 1359 AF217188 Mus musculus YIP1B 801 63 1360 AC074331 Homo sapiens ZNF234 3869 100			Homo sapiens	R26660 1, partial CDS		
1356 AF077226 Homo sapiens Copine III 1876 64 1359 AF217188 Mus musculus YIP1B 801 63 1360 AC074331 Homo sapiens ZNF234 3869 100	1355	AC024876	Caenorhabdit	Contains similarity to		
1356 AF077226 Homo sapiens copine III 1876 64 1359 AF217188 Mus musculus YIP1B 801 63 1360 AC074331 Homo sapiens ZNF234 3869 100		<u> </u>				
1359 AF217188 Mus musculus YIP1B 801 63 1360 AC074331 Homo sapiens ZNF234 3869 100			Homo sapiens		1876	64
1360 AC074331 Homo sapiens ZNF234 3869 100						
1361 AL163279 Homo sapiens homolog to cAMP response 5035 00	1					
	1361	AL163279	Homo sapiens	homolog to cAMP response	5035	99

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:			element binding and beta		
}		ĺ	transducin family proteins		
		Homo sapiens	glucokinase regulator	3160	99
162	Z48475	Homo sapiens	glucokinase regulator	2682	97
63	Z48475		megakaryocyte-enhanced gene	2055	99 .
364	AF195764	Homo sapiens	transcript 1 protein; MEGT1 protein		
		Homo sapiens	PRO0915	581	100
365	AF116609	Homo sapiens	FRO0915	581	100
366	AF116609	Homo sapiens	dJ876B10.3 (novel protein	2581	99
367	AL117352	HOMO sapiens	similar to C. elegans T19B10.6 (Tr:Q22557))		
.368	Y34124	Homo sapiens	Human potassium channel K+Hnov15.	1342	100
369	AJ245621	Homo sapiens	CTL2 protein	3728	99
370	AF008220	Bacillus subtilis	YtaG	429	45
1371	X05562	Homo sapiens	alpha-2 chain precursor (AA - 25 to 1018) (3416 is 2nd base in codon)	5908	99
1372	Z98048	Homo sapiens	dJ408N23.4 (novel DnaJ domain protein)	1296	99
1373	AF154415	Homo sapiens	FLASH	10253	100
1374	U20286	Rattus norvegicus	lamina associated polypeptide 1C	1567	69
1375	U53445	Homo sapiens	DOC1	1645	46
1376	AL117337	Homo sapiens	bA393J16.1 (zinc finger protein 33a (KOX 31))	250	60
1377	AC005328	Homo sapiens	R26660_1, partial CDS	1126	100
1378	U35113	Homo sapiens	metastasis-associated gene	1823	69
1379	L15313	Caenorhabdit is elegans	putative	858	58
1380	¥25756	Homo sapiens	Human secreted protein encoded from gene 46.	1508	100
1381	AB037360	Homo sapiens	ANKHZN	5734	95
1382	AB037360	Homo sapiens	ANKHZN	959	97
1383	AF237676	Mus musculus	G beta-like protein GBL	1721	96
1384	AF237676	Mus musculus	G beta-like protein GBL	1043	70
1385	Y58793	Homo sapiens	Human calcium regulatory protein CaREG-1.	715	100
1386	AF212162	Homo sapiens	ninein	10369	99
1387	AL031685	Homo sapiens	dJ963K23.2 (novel protein)	337	33
1388	AC004890	Homo sapiens	similar to zinc finger proteins; similar to BAA24380 >W06316 W06316 03-OCT-1996 27-APR-1995 TRP-1 protein.	542	86
	3010000	Homo cantend	zinc finger protein ZNF223	2665	99
1389	AF187989	Homo sapiens		3459	100
1390 -	AC035150	Homo sapiens		1410	97
1391 1392	AF287894 AF282265	Homo sapiens		1794	99
1393	X90840	Homo sapiens	axonal transporter of synaptic vesicles	4584	99
1394	AF076249	Homo sapiens	zinc finger protein SBBIZ1	3208	99
1395	G02224	Homo sapiens		299	75
1396	AC004809	Arabidopsis thaliana	Similar to	130	34
1398	AF242519	Homo sapiens	zinc finger protein SBZF3	181	66
1399	AL133396	Homo sapiens	dJ1068H6.4 (prion protein like protein doppel)	962	100
1400	Y48611	Homo sapiens		817	99
1401	AC004472	Homo sapiens		280	54
	12003212			164	27
1402	X91489	Saccharomyce	putative HMG box	1 70-2	1 ~ .

ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-	
		1		WATERMAN	8
1403	¥79222			SCORE	IDENTITY
	179222	Homo sapiens	Human transferasc TRNSFS-14.	2842	100
L 1	X81058	Mus musculus	tex261	1010	99
	AB012084	Mus musculus	ĪTM	194	29
	AB030251	Homo sapiens	GTPase activating protein	3233	99
1407	AJ010585	Rattus rattus	PTB-like protein	2684	99
1408	X75760	Drosophila	LRR47	364	
1409	W7.661.0	melanogaster		364	29
	U76618 AC005578	Mus musculus	N-RAP	804	48
	AE000284	Homo sapiens	P20887_1, partial CDS	835	63
		Escherichia Coli	orf, hypothetical protein.	360	100
	X01563	Escherichia coli	L5 (rplE) (aa 1-179)	911	100
1413 V	W78279	Homo sapiens	Fragment of human secreted protein encoded by gene 33.	1264	99
1414	AB031051	Homo sapiens	organic anion transporter	3832	100
1415 N	M17466	Homo sapiens	coagulation factor XII	13455	100
	AF097994	Homo	L-kynurenine/alpha-	3455	100
		sapiens	aminoadipate aminotransferase	2202	99
	AF151077	Homo sapiens	HSPC243	1262	99
1418 Y	Y09945	Rattus	putative integral membrane	1098	61
-		norvegicus	transport protein		01
1419 U	U13152	Mesocricetus auratus	guanine nucleotide-binding	2179	76
1420 A	AL162458	Homo sapiens	protein beta 5		
	TET02430	Homo saprens	bA465L10.5 (KIAA1176 (novel protein, presumed ortholog	5696	100
1			of mouse K-Cl cotransporter	1	
1			KCC2))		
1421 Y	799426	Homo sapiens	Human PRO1604 (UNQ785) amino	152	29
			acid sequence SEQ ID NO:308.	1	2.5
1422 Y	(94923	Homo sapiens	Human secreted protein clone	4039	99
			qs14_3 protein sequence SEQ ID NO:52.	j	
1423 A	F177388	Homo	cancer-amplified		
] [sapiens	transcriptional coactivator	10748	99
		•	ASC-2		
1424 Y	48517	Homo sapiens	Human breast tumour-	1851	99
			associated protein 62.		"
	F208848	Homo sapiens	BM-006	1454	89
	F208848	Homo sapiens	BM-006	853	79
T42/ A	F112886	Bos taurus	differentiation enhancing	4693	95
1428 0	41387	Homo sapiens	factor 1	l	
	F161534	Homo sapiens	Gu protein HSPC049	1372	63
	F125043	Mus musculus	bisphosphate 3'-nucleotidase	2853	78
	66718	Homo	Membrane-bound protein	275 1886	30
		sapiens	PRO1106.	2000	100
1432 A	F193613	Homo sapiens	cell recognition molecule	568	100
1433 A	P0445-55		Caspr2		
	B044560	Mus musculus	Gliacolin	192	34
ATUT K	99900	Homo sapiens	NTII-1 nerve protein,	707	51
1	i	ľ	facilitates regeneration of		1
1435 A	F220530	Homo sapiens	nerve cells. myo-inositol 1-phosphate		
	1	_	synthase Al	2904	100
1436 X7	70944	Homo sapiens	PTB-associated splicing	1261	72
1437 AF	F271732	77	factor		
		Homo sapiens	bridging integrator-3		100
13	2011	Homo sapiens	Human secreted protein	595	98
1439 AJ	7293659		encoded from gene 1. mucolipidin		
			GGA3 long isoform		97
			GGA3 long isoform		100
			2003 200201111	3346	100

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH- WATERMAN	TDENTITY
ID	NUMBER			SCORE	IDENTITI
NO:		1		1944	100
442	AB039669	1101110 035-1	ALEX3	1914	27
443	AF237711	Drosophila	Diablo .	191	2'
		melanogaster	•	420	39
444	AJ011896	Homo sapiens	Nafl beta protein	439	98
445	X73874	Homo sapiens	phosphorylase kinase	6233	
446	AF214114	Homo sapiens	breast carcinoma-associated	3999	99
440	AL BATTE		antigen BCAA		
447	λF003924	Homo sapiens	ANC 2H01	2645	99
448	AF003136	Caenorhabdit	contains weak similarity to	2843	52
.446	Aroostso	is elegans	an AMP-binding motif		
	AF155112	Homo sapiens	NY-REN-50 antigen	1184	89
449	Y95004	Homo sapiens	Human secreted protein	985	100
450	195004	nonio saprene	Vc54 1, SEQ ID NO:48.		
	AF107203	Homo sapiens	ataxin 2-binding protein	688	57
L451		Homo sapiens	ataxin 2-binding protein	456	78
.452	AF107203	Mus musculus	DMR-N9	882	56
1453	Z38011		Protein sequence and	510	28
1454	X90568	Homo sapiens	annotation available soon via	1	
	ł		LABEIT@EMBL-Heidelberg.DE	1	
	l		dJ564M11.3 (similar to	1356	100
1455	AL035409	Homo sapiens	sialyltranferase)		
			MATH-2 protein	272	100
1456	D44480	Mus musculus	RNA helicase HDB/DICE1	478	45
1458	AF141326	Homo sapiens		945	34
1459	AF242552	Gallus	retinovin		1
	1	gallus		724	84
1460	U11036	Homo sapiens	Ibd1	545	39
1461	AB025258	Mus musculus	granuphilin-a acid sphingomyelinase-like	2428	99
1462	Y08134	Homo sapiens	acid sphingomyellnase-like	2320	.
	i		phosphodiesterase	B69	98
1463	AC004997	Homo sapiens	match to ESTS 243979	1 807	1
		Ì	(NID:g573097), R19699	1	1
	1		(NID:g774333)	869	98
1464	AC004997	Homo sapiens	match to ESTs 243979	1 800	150
			(NID:g573097), R19699		
	1		(NID:g774333)	315	50
1465	U32743	Haemophilus	fucose operon protein (fucU)	1 323	-
	1	influenzae.		1	
		Rd		2342	100
1466	Y09022	Homo sapiens	Not56-like protein	1072	99
1467	AC003034	Homo sapiens	Homolog of rat kidney-	1072	1 33
	1	Ì	specific (KS) gene		26
1468	AF071544	Spinacia	ribulose-1,5-bisphosphate	333	20
		oleracea	carboxylase/oxygenase small	§	1
	1	1 (subunit N-methyltransferase I		100
1469	Y57930	Homo sapiens		1053	100
1203	1		HTMPN-54.		
1470	AF032666	Rattus	rsec5	4504	93
17/0	1	norvegicus	<u></u>		
1471	¥70467	Homo sapiens	Human membrane charnel	452	74
-4/1	1,040,		protein-17 (MECHP-17).		
1472	AL031033	Homo sapiens	C321D2.1 (Ribosomal Large	1694	100
14/2	ADUSTUSS	20110	Subunit Pseudouridine	i	İ
l			Synthase protein)		
	NP127707	Homo sapiens		4026	98
1473	AF177292	Homo sapiens		1101	50
1474	S45936	Homo sapiens		1879	98
1475	Y86241	HOMO Baprens	HOABR60, SEQ ID NO:156.		
		Program	Sand	1278	68
1476	AJ010317	Fugu	Saulu		
		rubripes	coded for by C. elegans cDNA	846	44
1477	U42831	Caenorhabdit	yk99b4.3; similar to human	1	1
		is elegans	YK99D4.3; SIMITAL CO HUMAN	Ī	1
1			transforming protein	Į.	
}	1		(PIR:S22157)	543	61
1478	X62447	Homo sapiens	PR 264	7116	100
1479	X82209	Homo sapiens		675	84
	U10536	Pan paniscus	MHC class I A	10/2	1 ~ ~

SEQ	ACCESSION NUMBER	N SPECIES	DESCRIPTION	SMITH-	1 %
NO:	HOUBER			WATERMAN	
1481	AL078599	Homo sapiens	dJ991C6.1 (novel protein	SCORE	_
	1	July Suprom	similar to C. elegans	1274	65
			F55A12.9 (Tr:P91086))	1	}
1482	298977	Schizosaccha	putative vacuolar protein		
1	1	romyces	radiolar protein	256	29
		pombe			1
1483	AB005662	Mus musculus		4968	
1484	AL050120	Homo sapiens	hypothetical protein	716	92
1485	M27878	Homo sapiens	DNA binding protein	1006	100
1486	Y69161	Homo sapiens	Amino acid sequence of a	575	53
1487			partial protein kinase	7,3	99
1487	X84156	Saccharomyce	ATHI	341	29
1488	1270000	s cerevisiae	_]	1 - 1 -	29
1489	AF038963	Homo sapiens		446	34
1409	U56966	Caenorhabdit		620	42
		is elegans	yk30b3.5; coded for by C	020	42
1490	377000000		elegans cDNA yk30b3.3	· ·	1
1490	AE000989	Archaeoglobu	enoyl-CoA hydratase (fad-4)	533	46
1491	MODER	s fulgidus	!	1	***
1431	M80633	Rattus	adenylyl cyclase type IV	707	95
1492	107774	norvegicus		1	1 23
1432	Y73342	Homo sapiens	HTRM clone 2709055 protein	3513	99
1493	V2.5000		sequence.	7 3 3 3	1 39
1493	Y17220	Homo sapiens	Human secreted protein (clone	452	37
1494	-		[fj283-11].	***	3 /
1495	AF133670	Mus musculus	ARL-6 interacting protein-2	701	97
1432	Y94897	Homo	Human protein clone HP10574.	1371	100
1496	DYDAGGG	sapiens		-3/2	100
1496	AL049699	Homo sapiens	dJ747H23.2 (novel protein)	1550	100
1497	AF037447	Homo sapiens	ribosomal S6 protein kinase	2427	100
7430	AL445067	Thermoplasma	putative target YPL207w of	269	35
	1	acidophilum	the HAP2 transcriptional	1 203	33
1499	AB039947		complex related protein		
1500	AJ277750	Homo sapiens	X11L-binding protein 51	227	36
1501	AL050333	Homo sapiens	UBASH3A protein	3509	100
-501	m030333	Homo	dJ93K22.1 (novel protein	2439	100
1502	AF179896	sapiens	(contains DKFZP564B116))		===
1503	AF178948	Homo sapiens	TALE homeobox protein Meis2b	1140	100
1504	Y53005	Homo sapiens	TALE homeobox protein Meis2a	1177	100
	155005	Homo sapiens	Human secreted protein clone	1442	99
			pm749_8 protein sequence SEQ		
1505	X82494	Vome	ID NO:16.		
506	X98296	Homo sapiens	fibulin-2	3580	99
.507	AL034548	Homo sapiens	ubiquitin hydrolase	783	42
508	Y76144	Homo sapiens	dJ1103G7.6 (novel protein)	1098	100
		Homo sapiens	Human secreted protein	1736	100
509	AF220182	Homo gazzi au	encoded by gene 21.	1 1	
		Homo sapiens	uncharacterized hypothalamus	1181	98
510	U64601	Caenorhabdit	protein HT008		
		is elegans	Gene probably begins in the	415	58
511	AL356192	Neurospora	next cosmid		
		crassa	related to MDM1 protein	196	29
512	D17629				
j			N-acetylgalactosamine 6-	1829	100
513	AF168717	Homo sapiens	sulfate sulfatase (GALNS)		
514	AU243531		x 009 protein	694	99
515			nM15 protein	735	100
		Arabidopsis	putative C3HC4-type RING zinc	407	30
516	AF115435	nallana	finger protein	į	
		Rattus	syntaxin 17	1374	90
517	AF003140	norvegicus			
		Caenorhabdit is elegans	C44E4.5 gene product	274	31
· }		IS ALACONA	- -		
1	AB002584	Rattus	oeta-alanine-pyruvate	2238	02
518	AB002584	Rattus norvegicus	peta-alanine-pyruvate aminotransferase /east atp12 protein precursor	2238	82

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH- WATERMAN	* IDENTITY
ID	NUMBER		ļ	SCORE	
NO:			77		
		romyces	homolog		ļ
		pombe	vascular endothelial	547	100
1520	AF255910	Ното	junction-associated molecule	J 1 ,	
		sapiens		170	27
1521	D31764	Homo sapiens	KIAA0064	985	100
1522	Y66634	Homo	Membrane-bound protein	305	1 100
		sapiens	PRO190.		43
1523	¥94450	Homo sapiens	Human inflammation associated	250	43
	·		protein		
1524	AC000107	Arabidopsis	F17F8.22	277	37
1321		thaliana		_	
1525	AF109377	Mus musculus	ldlBp	1277	83
1526	AL031427	Homo sapiens	dJ167A19.4 (novel protein)	1432	99
		Mus musculus	acid sphingomyelinase-like	1496	79
1527	Y08135	Mus musculus	phosphodiesterase	<u> </u>	
			FLJ00012 protein	611	100
1528	AK024423	Homo sapiens		679	100
1529	AF154502	Homo sapiens	quiescent cell proline	1 " "	
			dipeptidase	1368	100
1530	AF205598	Homo sapiens	transposase-like protein		50
1531	AF251039	Homo sapiens	putative zinc finger protein	1420)
1532	W74805	Homo sapiens	Human secreted protein	493	57
	1	i	encoded by gene 77 clone		1
	ł	ļ	HOEAS24.		<u> </u>
1533	AF039023	Homo sapiens	Ran-GTP binding protein;	5707	99
1933	AI 033023		RanBP6	1	
1534	AC007190	Arabidopsis	F23N19.9	374	37
1534	AC007130	thaliana	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	}	
	2007564	Homo sapiens	DINB1	4482	100
1535	AB027564		Human secreted protein	377	87
1536	¥36178	Homo sapiens	Human fetal brain cDNA clone	3593	99
1537	Y50907	Homo sapiens	vb3 1 derived protein.	1 3333	1
				177	47
1538	AF017368	Mus musculus	faciogenital dysplasia	1 - / /	1 "
	i	<u> </u>	protein 2	2011	99
1539	AF266756	Homo sapiens	sphingosine kinasc	2238	100
1540	Z48804	Homo sapiens	OA1		42
1541	AF000195	Caenorhabdit	Contains similarity to Pfam	379	42
	ŀ	is elegans	domain: PF00169 (PH),	ļ	
	i		Score=20.6, E-value=1.9e-05,	ŀ	}
	1		N=1		
1542	Y71159	Homo sapiens	Human phosphodiesterase	9415	99
		1 .	interacting protein,]
	i .		myomegalin.		
1543	X76092	Homo sapiens	DNA binding protein RFX3	3327	100
1544	AB015330	Homo sapiens		631	50
-	AF198487	Homo sapiens	transcription factor LBP-1b	2822	100
1545		Caenorhabdit	Similar to BZIP transcription	518	42
1546	AF016417		factor	1 -	1
		is elegans		1106	100
1547	X55885	Homo sapiens	KDEL receptor	836	42
1548	AB035495	Carassius	ubiquitin-activating enzyme	1 555	1
		auratus	E1 (977) 2660)	12600	100
1549	AL021707	Homo sapiens	dJ508I15.4 (KIAA0668)	3688	42
1550	AJ223978	Bacillus	YvqK protein	292	42
		subtilis			
1551	AF145615	Drosophila	BcDNA.GH03377	822	44
		melanogaster			
1552	AL157734	Schizosaccha	putative mannosyltransferase	435	37
		romyces	involved in N-glycosylation	1	1
	1	pombe			
1557	AF079527	Mus musculus	IER5	691	63
1553			acetoacetyl-CoA synthetase	1099	88
1554	AB026291	Rattus	aceroacery - con symmetrase		ľ
		norvegicus	Human immune system molecule,	1780	99
1555	Y44722	Homo sapiens		1	
<u> </u>	_l		ISMO-3.	277	32
1556	AF116553	Drosophila	antennal-specific short-chain	211	1
1		melanogaster	dehydrogenase/reductase	1000	 ••
	Y71056	Homo sapiens	Human membrane transport	1975	99

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	3.
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	
1555			protein, MTRP-1.		
1558	Y71056	Homo sapiens		1975	99
1559	V21056		protein, MTRP-1.	ł	1
1223	Y71056	Homo sapiens	The state of the s	1894	97
1560	AF092050		protein, MTRP-1.	ļ	
1360	AF092050	Mus musculus	1 = / - 2.	262	44
1561	AL109827		acetylglucosaminyltransferase		1
1361	ALLU9827	Homo sapiens	dJ309K20.2 (acrosomal protein	1607	97
	1		ACR55 (similar to rat sperm		
1562	AJ131890	Homo sapiens	antigen 4 (SPAG4)))		
1563	AL035424	Homo sapiens		3002	100
	112035424	nomo saprens		3015	100
:			similar to Drosophila Kelch	1	ļ
1564	AC002400	Homo sapiens	proteins)		l
	1	-10mo saprems	Gene product with similarity to Ubiquitin binding enzyme	2790	100
1565	AC005306	Homo sapiens	R27216 1	<u> </u>	<u></u>
1566	AF000195	Caenorhabdit		919	82
	000255	is elegans	Contains similarity to Pfam domain: PF00169 (PH),	550	45
1		10 Cacgains	Score=20.6, E-value=1.9e-05,	}	ļ
1			N=1	l	1
1567	AB033281	Ното	F-box and WD-repeats protein		
		sapiens	beta-TRCP2 isoform C	2879	100
1568	D19173	Mus musculus	truncated form of Sox17	-	·
1569	AK025270	Homo sapiens	unnamed protein product	1047	78
1570	X75756	Homo sapiens	protein kinase C mu	210	91
1571	AF145713	Homo sapiens	SCHIP-1	4797	99
1572	AE003831	Drosophila	CG18445 gene product	2388 .	100
		melanogaster	CG10445 gene product	180	31
1573	AF074603	Streptomyces	NonF		
	·	griseus	, Notife	205	38
	Į	subsp.			
		griseus			
1574	U28993	Caenorhabdit	F22D3.3 gene product	144	27
		is elegans	Jane product	144	21
1575	AF129507	Homo sapiens	transcription factor ICBP90	287	68
1576	X64878	Homo sapiens	oxytocin receptor	2002	100
1577	AF237711	Drosophila	Diablo	421	54
		melanogaster		1	34
1578	G00975	Homo sapiens	Human secreted protein, SEQ	480	100
			ID NO: 5056.	1	100
1579	AF248744	Cryptosporid	thrombospondin-related	123	33
		ium parvum	adhesive protein		
1580	AL121782	Homo sapiens	dJ585I14.2 (novel protein	663	100
l			(translation of cDNA		
			Em:AK000219))	j i	
1581	AF041853	Homo comican	kinesin family member protein		
		Homo sapiens	waredan remark member brotern	I 345 I	33
1500			KIF3A	345	33
1582	AF025441	Homo sapiens	Opa-interacting protein OIP5	1198	
1582 1583		Homo sapiens Thermotoga	KIF3A		100
1583	AF025441 AE001803	Homo sapiens Thermotoga maritima	Opa-interacting protein OIPS glycerate kinase, putative	1198	100
1583 1584	AF025441 AE001803 AF252283	Homo sapiens Thermotoga maritima Homo sapiens	Opa-interacting protein OIP5 glycerate kinase, putative Kelch-like 1 protein	1198	100
1583	AF025441 AE001803	Homo sapiens Thermotoga maritima Homo sapiens Homo	Opa-interacting protein OIPS glycerate kinase, putative Kelch-like 1 protein leucine-rich repeat	1198 349	100
1583 1584 1585	AF025441 AE001803 AF252283 AF169675	Homo sapiens Thermotoga maritima Homo sapiens Homo sapiens	Opa-interacting protein OIPS glycerate kinase, putative Kelch-like 1 protein leucine-rich repeat transmembrane protein FLRT1	1198 349 3973	100
1583 1584 1585 1586	AF025441 AE001803 AF252283 AF169675 AF118274	Homo sapiens Thermotoga maritima Homo sapiens Homo sapiens Homo sapiens	Opa-interacting protein OIPS glycerate kinase, putative Kelch-like 1 protein leucine-rich repeat transmembrane protein FLRT1 DNb-5	1198 349 3973	100
1583 1584 1585 1586 1587	AF025441 AE001803 AF252283 AF169675 AF118274 X79440	Homo sapiens Thermotoga maritima Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Opa-interacting protein OIPS glycerate kinase, putative Kelch-like 1 protein leucine-rich repeat transmembrane protein FLRT1 DNb-5 NADP+-dependent malic enzyme	1198 349 3973 3494	100 34 100 99
1584 1584 1585 1586 1587 1588	AF025441 AE001803 AF252283 AF169675 AF118274 X79440 X99802	Homo sapiens Thermotoga maritima Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Opa-interacting protein OIPS glycerate kinase, putative Kelch-like 1 protein leucine-rich repeat transmembrane protein FLRT1 DNb-5 NADP+-dependent malic enzyme ZYG homologue	1198 349 3973 3494 2628	100 34 100 99
1583 1584 1585 1586 1587 1588 1589	AF025441 AE001803 AF252283 AF169675 AF118274 X79440 X99802 AF169803	Homo sapiens Thermotoga maritima Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Opa-interacting protein OIPS glycerate kinase, putative Kelch-like 1 protein leucine-rich repeat transmembrane protein FLRT1 DNb-5 NADP+-dependent malic enzyme ZYG homologue flavohemoprotein b5+b5R	1198 349 3973 3494 2628 3167	100 34 100 99 97
1584 1584 1585 1586 1587 1588	AF025441 AE001803 AF252283 AF169675 AF118274 X79440 X99802	Homo sapiens Thermotoga maritima Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Opa-interacting protein OIPS glycerate kinase, putative Kelch-like 1 protein leucine-rich repeat transmembrane protein FLRT1 DNb-5 NADP+-dependent malic enzyme ZYG homologue flavohemoprotein b5+b5R Human secreted protein clone	1198 349 3973 3494 2628 3167 3966 2563	100 34 100 99 97 99 99 99
1584 1585 1586 1587 1586 1589 1590	AF025441 AE001803 AF252283 AF169675 AF118274 X79440 X99802 AF169803 Y29861	Homo sapiens Thermotoga maritima Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Opa-interacting protein OIPS glycerate kinase, putative Kelch-like 1 protein leucine-rich repeat transmembrane protein FLRT1 DNb-5 NADP+-dependent malic enzyme ZYG homologue flavohemoprotein b5+b5R Human secreted protein clone cb98_4.	1198 349 3973 3494 2628 3167 3966	100 34 100 99 97 99
1583 1584 1585 1586 1587 1588 1589	AF025441 AE001803 AF252283 AF169675 AF118274 X79440 X99802 AF169803	Homo sapiens Thermotoga maritima Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Opa-interacting protein OIPS glycerate kinase, putative Kelch-like 1 protein leucine-rich repeat transmembrane protein FLRT1 DNb-5 NADP+-dependent malic enzyme ZYG homologue flavohemoprotein b5+b5R Human secreted protein clone	1198 349 3973 3494 2628 3167 3966 2563	100 34 100 99 97 99 99 100 47
1584 1584 1585 1586 1587 1588 1589 1590	AF025441 AE001803 AF252283 AF169675 AF118274 X79440 X99802 AF169803 Y29861	Homo sapiens Thermotoga maritima Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Opa-interacting protein OIPS glycerate kinase, putative Kelch-like 1 protein leucine-rich repeat transmembrane protein FLRT1 DNb-5 NADP+-dependent malic enzyme ZYG homologue flavohemoprotein b5+b5R Human secreted protein clone cb98_4. nuclear pore complex protein hnup153	1198 349 3973 3494 2628 3167 3966 2563 181	100 34 100 99 97 99 99 99
1584 1584 1585 1586 1587 1588 1589 1590 1591	AF025441 AE001803 AF252283 AF169675 AF118274 X79440 X99802 AF169803 Y29861 Z25535	Homo sapiens Thermotoga maritima Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Opa-interacting protein OIPS glycerate kinase, putative Kelch-like 1 protein leucine-rich repeat transmembrane protein FLRT1 DNb-5 NADP+-dependent malic enzyme ZYG homologue flavohemoprotein b5+b5R Human secreted protein clone cb98_4. nuclear pore complex protein	1198 349 3973 3494 2628 3167 3966 2563 181	100 34 100 99 97 99 99 100 47
1584 1584 1585 1586 1587 1588 1589 1590 1591	AF025441 AE001803 AF252283 AF169675 AF118274 X79440 X99802 AF169803 Y29861 Z25535 X13293 M74027	Homo sapiens Thermotoga maritima Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Opa-interacting protein OIPS glycerate kinase, putative Kelch-like 1 protein leucine-rich repeat transmembrane protein FLRT1 DNb-5 NADP+-dependent malic enzyme ZYG homologue flavohemoprotein b5+b5R Human secreted protein clone cb98_4. nuclear pore complex protein hnup153 B-myb protein (AA 1-700) mucin	1198 349 3973 3494 2628 3167 3966 2563 181 7567	100 34 100 99 97 99 99 100 47
1584 1584 1585 1586 1587 1588 1589 1590 1591	AF025441 AE001803 AF252283 AF169675 AF118274 X79440 X99802 AF169803 Y29861 Z25535	Homo sapiens Thermotoga maritima Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	Opa-interacting protein OIPS glycerate kinase, putative Kelch-like 1 protein leucine-rich repeat transmembrane protein FLRT1 DNb-5 NADP+-dependent malic enzyme ZYG homologue flavohemoprotein b5+b5R Human secreted protein clone cb98_4. nuclear pore complex protein hnup153 B-myb protein (AA 1-700)	1198 349 3973 3494 2628 3167 3966 2563 181 7567	100 34 100 99 97 99 99 100 47

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:					
		pombe	Fragment of human secreted	1318	98
595	W78324	Homo sapiens	protein encoded by gene 81.		1
			Human secreted protein clone	2236	98
596	Y94906	Homo sapiens	rb649_3 protein sequence SEQ		1
į.			TD NO:18.		l
1			ID NO:18.	1408	99
597	AF174605	Homo sapiens	F-box protein Fbx25	9676	98
598	AB032254	Homo	bromodomain adjacent to zinc	3070	1
			finger domain 2A	5568	95
599	X73114		slow MyBP-C		100
600	X82200	Homo sapiens	gpStaf50	2305	
	Y00876	Homo	Human LAPH-1 protein	1149	98
601	100876		semience.		
		Were saniens	HTRA-interacting protein 3	2821	99
1602	AJ223351		neutral sphingomyelinase	2268	99
1603	AJ222801	1,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	neutral sphingomyelinase	1601	99
1604	AJ222801	Homo sapiens	POZ/zinc finger transcription	3435	97
1605	AF185576	Mus musculus	factor ODA-8		1
				131	100
1606	AF093744	Homo sapiens	unknown	800	98
1607	A12142	synthetic	IFN-pseudo-omega 2	1 300	1
-,00,		construct		7068	100
1608	¥57949	Homo sapiens	Human transmembrane protein	1868	100
TOOR	-3/343		HTMPN-73.	L	97
	AF151044	Homo sapiens	USPC210	681	
1609		Homo sapiens	ski protein (AA 1 - 728)	3765	100
1610	X15218		rab geranylgeranyl	2976	100
1611	₹08200	Homo sapiens	transferase	Į.	
	<u> </u>	<u> </u>	B/K protein	2486	99
1612	AF220560	Homo sapiens	nodulin-like protein	371	26
1613	AC004481	Arabidopsis	DOGUTTU-TIVE DIOCETH	1	ł
	1	thaliana	he maduatage	1607	100
1614	Y09501	Homo sapiens	NADH-cytochrome-b5 reductase	3150	97
1615	Y15521	Homo sapiens	start position 1	890	62
1616	AJ010750	Rattus	Castration induced prostatic	890	02
1010	120,20	norvegicus	apoptosis related protein-1,	1	l
	1		(CIPAR-1)		-
1655	X58079	Homo sapiens	S100 alpha protein	481	100
1617		Homo	Membrane-bound protein	967	100
1618	¥66678	sapiens	PRO1009.	L	
	I		peptide methionine sulfoxide	929	100
1619	AJ242973	Homo sapiens	reductase	1 .	1
				288	100
1620	AF150733	Homo sapiens	E1B-55kDa-associated protein	4646	98
1621	AJ007509	Homo sapiens	EIB-55KDa-absociated protein	380	100
1622	X64177	Homo sapiens	metallothionein	240	36
1623	AE001045	Archaeoglobu	A. fulgidus predicted coding	240	1 -
1023		s fulgidus	region AF0859	1	34
1624	AL355013	Schizosaccha	mitochondrial carrier protein	403	34
1024	MD355013	romyces		1	
1	1	pombe		1	
	1,,,,,,,	Homo	Membrane-bound protein	1184	100
1625	Y66746	Homo sapiens	PRO1198.		
			destrin	863	100
1626	D90053	Sus scrofa		756	100
1627	¥35954	Homo sapiens	protein sequence, SEQ ID NO.		ļ
1	1	į		1	1
1			203.	470	100
1628	AL031775	Homo sapiens		286	68
1629	AF132484	Mus musculus	unknown		61
1630	AF017096	Drosophila	eimilar to C. elegans	493	0,
1030	ME07.1030	melanogaster			1
	ļ	""CTUING GOVER	YD8419.03c		
L				1704	100
1631	X03077	Homo sapiens	1	763	100
1632	AF151084			255	97
1633	AJ001874	Homo sapiens	orf	143	38
1634	AC012187	Arabidopsis	Contains weak similarity to	143	"
1		thaliana	GATA-6 DNA-binding protein		1
1		-	gb H36135, gb Z26200 come		1
1	ŀ	1	from this gene.	Į.	l

SEQ	ACCESSION	SPECIES	DESCRIPTION	CMYON	
ID	NUMBER		DDOCKIF 110N	SMITH- WATERMAN	\$ TD133000000
No:			_	SCORE	IDENTITY
1635	AF026246	Homo sapiens		111	90
1030	Y50943	Homo sapiens	Human adult brain cDNA clone	1126	95
1637	27774500		ve8_1 derived protein.		1 22
1638	AF134593	Homo sapiens	L-pipecolic acid oxidase	2068	99
1639	AJ238247 Y94942	Mus musculus	putative phosphatase subunit	1948	96
1039	¥94942	Homo sapiens	Human secreted protein clone	1320	100
1			yk251_1 protein sequence SEC) .	1 200
1640	AF235030	<u> </u>	ID NO:90.		
1641	AF233030	Homo sapiens	_1	766	99
1041	AF233288	Drosophila	WDS	358	26
1642	M19351	melanogaster			1
-012	WISSEL	Mus musculus	1 Heavy Chain	145	34
1643	Y70452		binding protein		
1 -0 13	170432	Homo sapiens		1352	100
1644	AF176520	Mus musculus	protein-2 (MECHP-2).		1
]	AF1/0520	Mus musculus		2676	88
1645	W67816	Home	protein FBW5	1	
	1.07010	Homo sapiens	Human secreted protein	1156	100
1			encoded by gene 10 clone		
1646	X67155	Homo sapiens	HCEMU42.	1	
1647	M63180	Homo sapiens		4456	99
1648	Y87342	Homo sapiens	threonyl-tRNA synthetase	1040	61
	10,342	nomo sapiens		1566	93
	1	}	containing protein HSPP-119		j
1649	R95332	Homo sapiens	SEQ ID NO:119.		
	1120332	nomo saptens	Tumor necrosis factor	4137	100
1			receptor 1 death domain ligand (clone 3TW),		
1650	AC007136	Homo sapiens			
			Putative map kinase interacting kinase	856	99
1651	AB015346	Homo sapiens	Eps15R		1
1652	AL161576	Arabidopsis	putative protein	4464	99
	1	thaliana	pucacive procein	1341	48
1653	AC005313	Arabidopsis	putative calmodulin		
		thaliana	Pacacive carmoddill	288	28
1654	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	7505	
1655	AL031428	Homo sapiens	dJ184J9.1 (KIAAO601 protein)	3526	100
1656	AB017910	Dictyosteliu	myoM	3526	100
		m discoideum	•	291	32
1657	Y28919	Homo	Human regulatory protein	2251	99
4		sapiens	HRGP-5.	2231	99
1658	AF056191	Homo sapiens	TPA inducible protein	2744	98
1659	U76846	Arabidopsis	ubiquitin-specific protease	137	35
1660		thaliana		== '	33
1000	AL078627	Schizosaccha	actin-like protein; (2 actin	320	34
		romyces	domains)		J.
1662	VE2020	pombe		!	į
1002	X52022	Homo sapiens	collagen type VI, alpha 3	16274	99
1663	AF300648		Chain	i	
1003	AE300648	Homo	guanine nucleotide binding	1811	100
1664	AF214736	sapiens	protein beta subunit 4		
-504	AF214/36	Homo sapiens	EH domain containing protein	2774	100
1665	248613		2	1	
	240013	Saccharomyce	unknown	138	26
1666	AF177385	s cerevisiae		1	
1000	•	Homo	cytochrome c oxidase assembly	1395	99
1667		sapiens	protein isoform 2	1	
1668			BC331191_1	1581	47
		Borna	P40		43
- 1		disease	j	j	
- 1		virus BDV,	·		- 1
		WT-1, Halle			
		D7 /01			
] :	B1/91, horse			!
		brain, field			
		B1/91, horse brain, field isolate, Peptide, 370			

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:		aa			
.669	Z99753	Schizosaccha	putative NOL1-NOP2-sun family nucleolar protein	569	47
		nombe		427	97
670	G03130	Homo sapiens	Human secreted protein, SEQ ID NO: 7211.		
L671	M96625	Gallus gallus	cardiac muscle tensin	1185	54
1672	AF174482	Homo sapiens	polycomb 3	2005	99
L673	Y51846 .	Homo sapiens	Human 18.1 homolog protein fragment.	233	29
1674	AF255334	Homo sapiens	EXP35	152	29
1675	Y94867	Homo sapiens	Human protein clone HP10563.	109	30
1676	Y25712	Homo sapiens	Human secreted protein encoded from gene 2.	3043	99
1677	¥25712	Homo sapiens	Human secreted protein encoded from gene 2.	1580	91
1678	AF163151	Homo sapiens	dentin sialophosphoprotein	170	17
1679	AF163151	Homo sapiens	dentin sialophosphoprotein	170	17
		<u> </u>	precursor FLJ00045 protein	1349	100
1680	AK024453	Homo sapiens Dictvosteliu	TipD	613	34
1681	AF019236	m discoideum	-	153	26
1682	AJ243459	Leishmania major	proteophosphoglycan	560	46
1683	Z69369	Schizosaccha romyces pombe	putative GTP-binding protein	560	
1684	X94910	Homo sapiens	ERp28	1334	100
1685	AF286475	Takifugu rubripes	retinitis pigmentosa GTPase regulator-like protein	196	19
	AF191298	Homo sapiens	vacuolar sorting protein 35	4087	100
1686 1687	AJ275986	Homo sapiens	transcription factor	2958	100
1688	AJ275986	Homo sapiens	transcription factor	1886	88
1689	X07311	Drosophila melanogaster	heat shock protein	138	43
1690	AF240463	Rattus	LIS1-interacting protein	1383	83
1691	AJ272078	Homo sapiens	APOBEC-1 stimulating protein	1256	68
1692	AJ272079	Homo sapiens	APOBEC-1 stimulating protein	1336	60
1693	AF177942	Xenopus laevis	katanin p60	1664	66
1694	AF263539	Homo sapiens	arginine N-methyltransferase	1774	100
1695	AF222689	Homo sapiens	protein arginine N- methyltransferase 1-variant 2	1182	81
1696	AK000193	Homo sapiens	unnamed protein product	1060	100
1697	AB041035	Homo sapiens	kidney superoxide-producing NADPH oxidase	3122	100
1698	AB041035	Homo sapiens		2181	100
1699	AF025772	Homo sapiens	C2H2 zinc finger protein	488	54
1700	Y44676	Homo sapiens		938	97
1701	AK022407	Homo sapiens	unnamed protein product	315 1172	98 100
1702	AB024574	Homo sapiens		421	52
1703	AF055078	Homo sapiens		1057	77
1704 1705	AF198092 AE003573	Mus musculus Drosophila	CG12474 gene product	161	33
1706	AB036345	melanogaster Drosophila melanogaster	aquaporin	164	24
1707	Y55927	Homo sapiens		2146	100
1708	U27121	Danio rerio	G12	212	47
1709	AL391710	Arabidopsis	putative protein	505	50

SEQ ID NO:	ACCESSIO NUMBER	N SPECIES	DESCRIPTION .	SMITH- WATERMAN	& IDENTAGE
NO:				SCORE	IDENTITY
1710	B01311	thaliana			
1711	U40750	Homo sapien:	Human PRO241 polypeptide.	1649	97
1712	AJ011118	Mus musculus		4561	85
		Mus museurus	skeletal muscle and cardiac	1490	89
1713	AF255303	Homo			1
- 1		sapiens	membrane-associated nucleic	4416	99
1714	AF255303	Homo	acid binding protein membrane-associated nucleic		
- 1	j	sapiens	acid binding protein	2960	100
1715	U08227	Rattus	Ras-related protein		
		norvegicus	ras relaced protein	511	51
1716	AF168795	Rattus	schlafen-4	1	
L		norvegicus		1129	44
1717	AF196304	Homo sapiens	SUMO-1-specific protease	5804	
1718	AL355737	Homo sapiens	HMG20A	1782	99
1719	AB029333	Halocynthia	HrPET-1	1069	100
		roretzi		1009	46
1720	AF071317	Mus musculus	1 compact subunit 10	1297	197
1721	AJ272215	Homo sapiens	HEYL protein	1681	99
1722	G01982	Homo sapiens	Human secreted protein, SEQ	718	100
1723	-		ID NO: 6063.	/10	100
1/23	AL032643	Caenorhabdit	Jamaiar to Uncharacterized	825	41
1724	G01972	is elegans	protein family UPF0034.] **
1,724	601972	Homo sapiens	Human secreted protein, SEO	586	92
1725	¥94441	+	ID NO: 6053.		
1 - 123	134441	Homo	Human Adipose Specific	1231	100
1726	AP255443	Homo sapiens	Protein 1.	}	1
1727	AF183426	Homo sapiens	CGI-201 protein	4397	99
1728	D10884	Bos taurus	HT004 protein	1810	99
1729	218529	Gallus	neurocalcin tensin	1002	99
Í		gallus	tensin	1411	84
1730	273423	Caenorhabdit	cDNA EST EMBL: Z14908 comes		
	1	is elegans	I disamus 43.4.	233	41
	<u>L</u>		gene this gene-cDNA EST this		
1732	AF090891	Homo sapiens	PRO0105	470	
1733	AJ277724	Homo sapiens	histone deacetylase 8	2015	30
1734	G04050	Homo sapiens	Human secreted protein, SEQ	503	100 95
1735			ID NO: 8131.	303	95
1735	D45913	Mus musculus	leucine-rich-repeat protein	3531	94
1,36	AF096709	Drosophila	failed axon connections	276	32
1737	AF195120	virilis	protein		32
1738	L15314	Homo sapiens	dynactin p62 subunit	2417	99
-/20	11.5514	Caenorhabdit	contains similarity to Pfam	206	37
1739	X54618	is elegans Listeria	family PF01772 N=1	!	
		monocytogene	phosphadidylinositol specific	134	27
1	ļ	s	phospholipase C	1	ĺ
1740	AL031658	Homo sapiens	d.T310013 4 (
Ì			dJ310013.4 (novel protein similar to predicted C.	123	31
1			elegans an C. intestinalis		
			proteins)	1	
1741	Y35924	Homo sapiens	Extended human secreted		
		-	protein sequence, SEQ ID NO.	1013	99
		}	173.	į į	!
1742	AC013354	Arabidopsis	F15H18.15	202	
L		thaliana		202	32
1743	W75771	Homo	Human GTP binding protein	1932	
		sapiens	APDOS.	1932	59
1744	W75771	Homo	Human GTP binding protein	1854	
1774		sapiens	APDO8.	1034	61
1745	AF221098	Homo	Ral guanine nucleotide	1224	70
172	Voor	sapiens	exchange factor RalGPS1A		70
1746	Y99372	Homo sapiens	Human PRO1430 (UNQ736) amino	1332	99
1747	Y94294		acid sequence SEQ ID NO:116.		
	174274	Homo sapiens	Human coenzyme A-utilising	842	100

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	\$ *
ID NO:	Number	1		Waterman Score	IDENTITY
		 	enzyme CoAEN-2.		
1748	AK024436	Homo sapiens	FLJ00026 protein	1619	100
1749	AE000877	Methanobacte	conserved protein	231	36
1743	ABOOOT	rium thermoautotr ophicum	-		
1750	AF101361	Orosophila melanogaster	Abnormal X segregation	193	33
1751	¥15067	Homo sapiens	ZNF232	889	100
1752	AF251038	Homo sapiens	GAP-like protein	822	100
1753	AC003093	Homo sapiens	OXYSTEROL-BINDING PROTEIN; 45% similarity to P22059 (PID:g129308)	352	57
1754	X69089	Homo sapiens	165kD protein	5703	99
1755	AL049795	Homo sapiens	dJ622L5.3 (novel protein)	1039	100
1756	AL031393	Homo sapiens	dJ733D15.1 (Zinc-finger protein)	2765	100
1757	AB040672	Homo sapians	UDP-GalNAc: polypeptide N- acetylgalactosaminyltransfera se	2020	99
1758	AL022238	Homo sapiens	dJ1042K10.4 (novel protein)	776	43
1759	AF117653	Homo sapiens	double homeobox protein	375	54
1760	¥12065	Homo sapiens	hNop56	2959	99
1761	AL049712	Homo sapiens	dJ686C3.2 (nucleolar protein hNop56)	2595	99
1762	AC002394	Homo sapiens	Gene product with similarity to dynein beta subunit	1542	51
1763	AF169017	Homo sapiens	formiminotransferase cyclodeaminase	877	100
1764	U91541	Homo sapiens	human formiminotransferase cyclodeaminase (ftcd)protein, carboxy-terminal end	596	100
1765	AB013365	Bacillus halodurans	YlqF	350	34
1766	Y38421	Homo sapiens	Human secreted protein encoded by gene No. 36.	145	71
1767	AC009176	Arabidopsis thaliana	putative ribulose-1,5- bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I	216	27
1768	AK000647	Homo sapiens	unnamed protein product	737	99
1769	AJ238982	Homo sapiens	VNN3 protein	2665	99
1770	U73522	Homo sapiens	AMSH	1214	56
1771	U89435	Mus musculus	unknown	829	86
1772	570011	Rattus sp.	tricarboxylate carrier	1604	95
1773	AL035086	Homo sapiens	dJ44A20.2 (novel protein)	2036	100
1774	Y99426	Homo sapiens	Human PRO1604 (UNQ785) amino acid sequence SEQ ID NO:308.	1057 .	99
1775	AF110330	Homo sapiens	glutaminase	3146	100
1776	AJ269529	Homo sapiens	glycerol 3-phosphate permease	2787	100
1777	Z81579	Caenorhabdit is elegans		232	31
1778	AY007239	Homo sapiens	monooxygenase X	1875	99
1779	AL109608	Schizosaccha romyces pombe	oxysterol-binding protein family	644	36
1780	AF254260	Homo sapiens	tuftelin 1	1729	100
1781	L07924	Mus musculus	guanine nucleotide dissociation stimulator	247	50
1782	AF295773	Homo sapiens	ral guanine nucleotide dissociation stimulator	142	49.
1783	AK024475	Homo sapiens	FLJ00068 protein	4333	100
1784	AK024475	Homo sapiens	FLJ00068 protein	3996	93
1785	G03933	Homo sapiens	Human secreted protein, SEQ	570	100
	· · · · · · · · · · · · · · · · · · ·	Homo sapiens	Ig lambda-like gene/beta-	247	100

TABLE 2

	SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	
	ID	NUMBER	ŀ	DESCRIPTION		- *
- [NO:				WATERMAN	IDENTITY
					SCORE	
- [glucuronidase exon 11 homolog		
			·		(1

TRADOCS:1416280.1(%CT401!.DOC)

TABLE 3

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
2	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 8.250e- 12 157-181
3	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109D 17.04 8.085e- 13 358-381
4	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.400e- 10 1129-1146 BL00028 16.07 1.257e-09 820- 837
5	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
6	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
7	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
8	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
9	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.119e- 09 863-917 PR00464D 17.40 6.182e-
10	PR00464	E-CLASS P450 GROUP II SIGNATURE	12 294-312 PR00464G 12.41 4.231e-11 377- 393
11	PR00734	GLYCOSYL HYDROLASE FAMILY 7 SIGNATURE	PR00734I 11.46 4.296e- 09 502-520
12	PF00023	Ank repeat proteins.	PF00023B 14.20 6.500e- 10 89-99 PF00023B 14.20 2.636e-09 56-66
14	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 3.848e- 09 79-113
15	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208A 12.59 9.868e- 10 517-535 PR00208A 12.59 2.233e-09 520- 538
17	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e- 14 282-295 PD00066 13.92 9.400e-14 477- 490 PD00066 13.92 6.500e-13 505-518 PD00066 13.92 9.500e- 13 254-267 PD00066 13.92 1.429e-12 393- 406 PD00066 13.92 6.571e-12 421-434
18	BL00845	CAP-Gly domain proteins.	BL00845 16.43 2.200e- 25 55-80 BL00487E 16.12 5.737e-
20	BL00487	IMP dehydrogenase / GMP reductase proteins.	26 154-199 BL00487F 18.79 8.984e-22 235- 276 BL00487G 26.82 4.082e-12 287-329
21	BL00487	<pre>IMP dehydrogenase / GMP reductase proteins.</pre>	BL00487E 16.12 5.737e- 26 154-199 BL00487F 18.79 8.984e-22 235- 276 BL00487G 26.82 4.082e-12 348-390
22	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 3.250e- 26 302-333

SEQ ID N	NO.	DESCRIPTION	RESULTS*
23	BL00107	Protein kinases ATP-	BL00107A 18.39 3.250e
25		binding region proteins.	. 26 302-333
25	BL00115	Eukaryotic RNA	BL00115T 8.45 7.273e-
		polymerase II	29 1208-1242 BL00115
	1 .	heptapeptide repeat	18.08 2.776e-21 953-
	ŀ	proteins.	983 BL00115Y 11.86
	1		8.000e-17 1604-1650
	i		DT 00335W 10 00
			BL00115M 19.19 8.130e
			16 731-774 BL00115H
		1	14.34 9.392e-16 463-
	1		496 BL00115A 15.44
	i		7.414e-15 43-82
	1		BL00115R 6.50 6.128e-
	1		14 983-1010 BL00115J
	1	·	16.71 9.289e-14 591-
	1		617 BL00115I 8.33
	1	· ·	4.336e-13 535-590
	-		BL00115L 12.25 5.939e-
		1	13 662-694 BL00115G
		1	11.65 6.011e-13 435-
	1		100 22001138 13.03
			3.417e-10 617-659
	1		BL001150 16.76 5.805e-
	i		10 863-913 BL00115P
		İ	11.54 7.538e-10 913-
	ł		953 BL00115S 18.24
	1		7.968e-10 1010-1052
•	ł		BL00115U 10.34 4.475e-
26			09 1242-1265
20	BL00420	Speract receptor repeat	BL00420A 20.42 4.109e-
	ļ	proteins domain	11 81-110 BL00420A
		proteins.	20.42 8.820e-10 84-113
27	BL00050	Ribosomal protein L23	BL00050A 23.71 9.250e-
		proteins.	27 94-127 BL00050B
		1	14.81 8.125e-12 133-
		1	147
28	PR00925	NONHISTONE CHROMOSOMAL	PR00925B 3.73 3.089e-
	1	PROTEIN HMG17 FAMILY	10 41-54
	İ	SIGNATURE	10 41-24
29	PF00756	Putative esterase.	DECORPOR
		ractive esterase.	PF00756C 14.12 1.108e-
32	BL00557	EMN damage	09 486-516
	2200337	FMN-dependent alpha-	BL00557D 17.76 5.065e-
		hydroxy acid	37 274-316 BL00557A
		dehydrogenases proteins.	35.08 8.909e-29 24-73
	1	1	BL00557C 15.59 1.000e-
	i		28 227-257 BL00557B
	f	1	21.27 8.898e-22 130-
			169
4	PR00629	SHC PHOSPHOTYROSINE	PR00629E 9.90 5.886e-
	1	INTERACTION DOMAIN	35 299-328 PR00629F
		SIGNATURE	10 0F 0 2C4- 30 55-
			10.95 8.364e-32 334-
	ł		361 PR00629B 13.66
	l		3.786e-27 224-247
	Į.		PR00629A 13.45 8.364e-
	j.	1	21 206-222 PR00629C
	į.		3.80 4.000e-12 249-261
	1	1	PR00629D 12.45 3.739e-
5	1222		11 276-286
-	PD01270	RECEPTOR FC	PD01270A 17.22 1.000e-
		IMMUNOGLOBULIN AFFIN.	40 39-79 PD01270B
			22.18 2.875e-38 94-131
		1	PD01270D 24 55
	1	1	PD01270D 24.66 3.700e-
			34 171-207 PD01270C
	1	j i	19.54 3.455e-30 137-
j	PD01270	I Dudon	166
	-2012/0	RECEPTOR FC	PD01270A 17.22 1.000e-
	j .	IMMUNOGLOBULIN AFFIN.	40 39-79 PD01270B
	•		

EQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	NO.		PD01270D 24.66 3.700e-
			34 171-207 PD01270C
		ļ	19.54 3.455e-30 137-
	1		166
7	BL00412	Neuromodulin (GAP-43)	BL00412C 10.28 9.241e-
,	LEGG 122	proteins.	10 264-298
8	BL00412	Neuromodulin (GAP-43)	BL00412C 10.28 9.241e-
8	5500-22	proteins.	10 264-298
	BL00412	Neuromodulin (GAP-43)	BL00412C 10.28 9.241e-
9	BUOGETE	proteins.	10 264-298
	PR00380	KINESIN HEAVY CHAIN	PR00380B 12.64 7.366e-
.0	PROUSEO .	SIGNATURE	14 342-360 PR00380C
			13.18 6.927e-13 375-
	ļ	1	394 PR00380D 9.93
		<u> </u>	2.180e-12 429-451
			PR00380A 14.18 5.154e-
	ł		12 143-165
		Ets-domain proteins.	BL00345B 21.28 1.000e-
14	BL00345	Ecs-domain bross-	40 239-290 BL00345A
]	1	13.96 2.452e-14 204-
			223
		Ets-domain proteins.	BL00345B 21.28 1.000e-
45	BL00345	Ets-domain procesus.	40 215-266 BL00345A
	1	•	13.96 2.452e-14 180-
	1	· ·	199
		VODA	DM01551A 15.63 3.538e-
46	DM01551	kw OSTEOINDUCTIVE YOPM	26 172-202 DM01551C
	į	MEMBRANE OUTER.	14.62 3.571e-17 232-
	1		252 DM01551B 8.84
	}		4.750e-11 214-226
			PR00876B 7.66 9.328e-
47	PR00876	NEMATODE METALLOTHIONEIN	11 246-260
	Ţ	SIGNATURE	PD01066 19.43 4.231e-
48	PD01066	PROTEIN ZINC FINGER	
	i	ZINC-FINGER METAL-	33 6-45
	l l	BINDING NU.	BL00972D 22.55 7.750e-
50	BL00972	Ubiquitin carboxyl-	19 994-1019 BL00972A
	1	terminal hydrolases	11.93 7.120e-18 216-
	İ	family 2 proteins.	234 BL00972E 20.72
			9.471e-14 1020-1042
	1		BL00972C 16.48 7.000e-
			BL00972C 16.48 7.000C
			13 360-375 BL00972B
	į		9.45 8.269e-10 302-312
51	BL00972	Ubiquitin carboxyl-	BL00972D 22.55 7.750e-
J.		terminal hydrolases	19 990-1015 BL00972A
		family 2 proteins.	11.93 7.120e-18 216-
	}		234 BL00972E 20.72
		1	9.471e-14 1016-1038
			BL00972C 16.48 7.000e-
	1		13 360-375 BL00972B
	\	i	9.45 8.269e-10 302-312
	BL01115	GTP-binding nuclear	BL01115A 10.22 3.063e-
52	BUCLIES	protein ran proteins.	14 10-54
L	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 8.500e-
53	PR00300		17 20-38 PR00988F
		1	12.23 7.828e-15 196-
l		1	210 PR00988C 13.64
	,	1	6.108e-14 104-120
			PR00988E 8.27 3.872e-
1		1	11 174-186 PR00988D
1	1	1	5.95 6.878e-10 160-171
1	1	1	PR00988B 11.60 2.915e-
1	1		09 57-69
I			PR00762C 9.29 4.682e-
55	PR00762	CHLORIDE CHANNEL	21 294-314 PR00762D
1		SIGNATURE	21 294-314 PKUU/82D
1	1		11.29 4.103e-19 509-
		Ì	530 PR00762A 14.22
	1	•	9.333e-18 199-217

SEQ ID NO:		DESCRIPTION	RESULTS*
	NO.		
			PR00762F 15.12 3.100e-
			16 563-583 PR00762B
			12.12 6.063e-16 230-
			250 PR00762E 12.07
			2.286e-15 545-562
	1		PR00762G 14.13 6.276e-
56			13 601-616
36	BL00216	Sugar transport	BL00216B 27.64 8.800e-
58		proteins.	10 153-203
58	PF00791	Domain present in ZO-1	PF00791B 28.49 2.049e-
		and Unc5-like netrin	10 1080-1135
59	PF00791	receptors.	
3.7	PF00/91	Domain present in ZO-1	PF00791B 28.49 2.049e-
	1	and Unc5-like netrin	10 1062-1117
61	PD01929	receptors.	
01	PD01929	KINASE TYPE RESISTANCE	PD01929E 10.76 9.018e-
		ANTIBIOTIC TRANSFERASE	09 206-221
68	PR00360	AM.	
00	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e-
69	PR00360		09 680-693
0.5	PR00380	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e-
70	PF00651		09 670-683
70	FF00031	BTB (also known as BR-	PF00651 15.00 8.714e-
72	DM00179	C/Ttk) domain proteins.	10 51-64
, <u>.</u>	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.304e-
73	BL00239		09 108-118
	B100239	Receptor tyrosine kinase	BL00239B 25.15 7.075e-
74	BL00790	class II proteins. Receptor tyrosine kinase	12 118-166
	2200750	class V proteins.	BL00790N 13.25 6.116e-
76	DM00471	0 PROKARYOTIC DNA	10 93-120
	51.100 17.2	TOPOISOMERASE I.	DM00471A 11.73 9.357e-
		10101BONBIGAB 1.	13 53-66 DM00471B 8.45 4.857e-12 70-81
80	PD02876	DECARBOXYLASE	
		PHOSPHATIDYLSERINE.	PD02876C 8.80 2.723e- 13 223-236 PD02876D
			12.13 2.588e-12 334-
	1		351
81	PD02876	DECARBOXYLASE	PD02876C 8.80 2.723e-
		PHOSPHATIDYLSERINE.	13 282-295 PD02876D
			12.13 2.588e-12 393-
	1		410
83	BL00708	Prolyl endopeptidase	BL00708B 24.91 7.197e-
		family serine proteins.	12 570-601
84	PR00014	FIBRONECTIN TYPE III	PR00014C 15.44 8.043e-
		REPEAT SIGNATURE	09 985-1004
86	PR00678	PI3 KINASE P85	PR00678H 9.13 1.379e-
		REGULATORY SUBUNIT	09 246-269
90		SIGNATURE	1
89	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 8.200e-
	1	REPEAT SIGNATURE	09 264-279 PR00320B
		1	12.19 8.650e-09 264-
93	Dr. 00 : 55		279
93	BL00455	Putative AMP-binding	BL00455 13.31 2.588e-
95	DY 0.01 6 5	domain proteins.	14 316-332
	BL00107	Protein kinases ATP-	BL00107A 18.39 4.000e-
96	DY 00102	binding region proteins.	10 123-154
-3	BL00107	Protein kinases ATP-	BL00107A 18.39 4.000e-
97	DEGGGG.	binding region proceins.	10 212-243
- 1	PR00081	GLUCOSE/RIBITOL	PR00081B 10.38 6.318e-
		DEHYDROGENASE FAMILY	13 134-146 PR00081A
98	DD00303	SIGNATURE	10.53 2.500e-12 54-72
	.PR00380	KINESIN HEAVY CHAIN	PR00380A 14.18 5.500e-
		SIGNATURE	24 401-423 PR00380D
		}	9.93 7.188e-20 613-635
			PR00380B 12.64 7.517e-
			16 529-547 PR00380C
			13.18 2.756e-13 560- 579

EQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
102	PR00300	ATP-DEPENDENT CLP	PR00300A 9.56 7.545e-
		PROTEASE ATP-BINDING SUBUNIT SIGNATURE	14 289-308
04	BL00479	Phorbol esters /	BL00479B 12.57 6.786e-
.0-2		diacylglycerol binding	18 298-314 BL00479A
	}	domain proteins.	19.86 4.913e-16 155-
			178 BL00479A 19.86
	4		4.300e-13 272-295
	1		BL00479B 12.57 6.294c-
	1		12 181-197
.06	BL01019	ADP-ribosylation factors	BL01019A 13.20 8.013e-
		family proteins.	12 43-83
107	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 5.000e-
		ENDOSOMAL III.	16 403-416
108	BL00191	Cytochrome b5 family,	BL00191K 17.38 4.951e-
		heme-binding domain	27 238-282 BL00191J
	1	proteins.	11.37 6.447e-17 182-
]		204
109	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 4.938e-
	1	ZINC-FINGER METAL-	37 8-47
	1	BINDING NU.	<u> </u>
110	BL01138	Scorpion short toxins	BL01138A 10.96 8.297e-
-	1	proteins.	10 38-50
113	BL00107	Protein kinases ATP-	BL00107A 18.39 5.800e-
		binding region proteins.	23 156-187 BL00107B
			13.31 9.100e-14 225-
	1	<u> </u>	241
117	BL00214	Cytosolic fatty-acid	BL00214B 26.51 1.000e-
		binding proteins.	17 46-91 BL00214A
			21.17 7.052e-11 5-31
118	BL00107	Protein kinases ATP-	BL00107A 18.39 8.560e-
110		binding region proteins.	13 36-67
119	PR00529	GONADOTROPHIN RELEASING	PRO0529C 11.03 7.506e-
		HORMONE RECEPTOR	10 158-177
		SIGNATURE	
120	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 9.400e-
		REPEAT SIGNATURE	09 80-95
121	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 9.400e-
	ļ	REPEAT SIGNATURE	09 80-95
127	BL00215	Mitochondrial energy	BL00215A 15.82 7.158e-
		transfer proteins.	13 216-241
128	BL01032	Protein phosphatase 2C	BL01032C 6.14 3.195e-
		proteins.	12 147-157 BL01032H
	ļ		11.25 5.680e-11 318-
			331 BL01032G 8.33
		<u> </u>	8.932e-11 282-296
			BL01032I 10.42 8.902e-
	t		09 379-389
129	BL01310	ATPIG1 / PLM / MAT8	BL01310 14.74 6.694e-
		family proteins.	26 28-64
130	PR00990	RIBOKINASE SIGNATURE	PR00990B 12.32 9.534e-
100	1		15 47-67 PR00990A
	1	J	16.23 5.500e-14 20-42
			PR00990C 12.62 2.412e
	1		09 119-133
133	BL00880	Acyl-CoA-binding	BL00880 17.52 5.575e-
	1	protein.	26 72-122
134	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 9.308e
274	1.0000	region RNP-1 proteins.	14 18-37
135	PR00215	NEUROMODULIN SIGNATURE	PR00215C 13.98 6.779e
133	FR00213		10 475-496
136	- Pr 03 23 0	ATPIG1 / PLM / MAT8	BL01310 14.74 2.432e-
136	BL01310	family proteins.	29 71-107
l	DYOGGG	Zinc finger, C2H2 type,	BL00028 16.07 7.882e-
140	BL00028	domain proteins.	14 214-231 BL00028
1		domarn processes.	16.07 9.471e-14 102-
1			119 BL00028 16.07
1			

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			BL00028 16.07 5.500e- 13 74-91 BL00028
			16.07 9.100e-13 186- 203 BL00028 16.07 8.043e-12 46-63
			BL00028 16.07 8.435e- 12 130-147 BL00028
			16.07 9.217e-12 270- 287 BL00028 16.07 6.192e-11 242-259
			BL00028 16.07 4.000e- 10 158-175
141	BL00501	Signal peptidases I serine proteins.	BL00501D 16.69 9.538e- 14 113-133 BL00501C
143	BP01050	SAR1 family proteins.	9.61 8.688e-10 89-101 BL01020C 15.35 7.722e- 20 79-130
146	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 6.400e- 25 335-374
149	BL00126	3'5'-cyclic nucleotide phosphodiesterases proteins.	BL00126C 22.07 1.450e- 25 509-550 BL00126E 35.22 3.951e-16 654- 709 BL00126D 25.50 1.360e-15 565-604 BL00126B 15.20 8.200e- 11 483-495 BL00126A 27.56 8.269e-11 442-
151	BL00632	Ribosomal protein S4 proteins.	479 BL00632 23.79 5.271e- 20 106-149
154	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.	BL00559I 13.63 5.304e- 19 29-58 BL00559K 13.17 2.957e-18 172- 199 BL00559J 19.63 8.385e-13 99-151 BL00559L 13.60 5.814e-
155	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	12 241-259 PR00449A 13.20 1.692e- 13 13-35
157	BL00406	Actins proteins.	BL00406D 12.58 2.547e- 18 275-330 BL00406A 9.95 5.776e-16 15-50 BL00406B 5.47 7.429e- 12 69-124 BL00406C 6.75 9.682e-12 128-183
160	BL00132	Zinc carboxypeptidases, zinc-binding region 1 proteins.	BL00132A 26.07 7.000e- 14 22-63 BL00132C 21.35 3.466e-12 104- 145
165	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 9.043e- 13 139-158
168	BL00362	Ribosomal protein S15 proteins.	BL00362 24.67 9.700e- 15 129-172
169	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	BL00039D 21.67 1.000e- 35 640-686 BL00039A 18.44 1.964e-13 212- 251 BL00039B 19.19 4.553e-13 378-404 BL00039C 15.63 8.773e-
175	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 3.721e-
178	BL01310	RAS SIGNATURE ATPIG1 / PLM / MAT8	12 14-36 BL01310 14.74 2.432e-
179	PD01066	family proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-	29 133-169 PD01066 19.43 9.455e- 36 6-45

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.	BINDING NU.	
	PR00007	COMPLEMENT CIQ DOMAIN	PR00007B 14.16 7.429e-
180	PROGOT	SIGNATURE	20 160-180 PR00007A
	1	SIGNATURE	19.33 4.938e-19 133-
	1		160 PR00007C 15.60
	,	}	1.225e-15 206-228
			PR00007D 9.64 6.885e-
	1		11 238-249
			BL00027 25.43 9.526e-
1.81.	BL00027	'Homeobox' domain	24 280-323
		proteins.	BL00027 26.43 9.526e-
182	BL00027	'Homeobox' domain	24 263-306
	1	proteins.	BL00027 26.43 9.526e-
183	BL00027	'Homeobox' domain	
	1	proteins.	24 280-323
184	BL00027	'Homeobox' domain	BL00027 26.43 9.526e-
104		proteins.	24 263-306
188	PR00929	AT-HOOK-LIKE DOMAIN	PR00929C 5.26 3.328e-
190	TROUSES	SIGNATURE	09 460-471
	PR00929	AT-HOOK-LIKE DOMAIN	PR00929C 5.26 3.328e-
189	PRUUJAJ	SIGNATURE	09 440-451
	\	Tyrosine specific	BL00383F 15.51 7.188e-
190	BF00383	protein phosphatases	17 666-682 BL00383A
			13.34 8.714e-17 162-
		proteins.	177 BL00383E 10.35
	1	1	1.000e-14 333-344
	\$		BL00383E 10.35 7.300e-
		l	14 628-639 BL00383F
•			15.51 1.720e-13 371-
	Ì		15.51 1.7208-13 371-
			387 BL00383C 10.10
			3.000e-13 217-228
		į	BL00383D 11.92 7.000e-
			13 295-308 BL00383B
			7.61 1.692e-11 187-196
	ļ	ì	BL00383C 10.10 1.750e-
]	1	09 509-520 BL00383D
	•		11.92 4.000e-09 589-
	ł		602 BL00383B 7.61
		_	8.000e-09 479-488
	PR00450	RECOVERIN FAMILY	PR00450C 12.22 7.911e-
191	PROU450	SIGNATURE	15 83-105 PR00450C
		SIGNATURE	12.22 6.286e-13 47-69
		Octicosapeptide repeat	PF00564B 24.74 6.164e-
193	PF00564		16 227-278
		proteins.	PR00503D 20.81 9.156e-
194	PR00503	BROMODOMAIN SIGNATURE	15 204-224 PR00503B
ı	1		9.96 9.571e-13 170-187
			BL00901C 20.63 3.429e-
195	BL00901	Cysteine	
		synthase/cystathionine	18 67-117
		beta-synthase P-	
		phosphate att.	
197	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 6.211e-
-5.			17 40-57 BL00636B
	İ		15.11 2.000e-13 67-88
100	PR00690	ADHESIN FAMILY SIGNATURE	
198	PROUBSU		09 463-482
		Ribosomal RNA adenine	BL01131A 26.62 2.343e-
199	BL01131	RIDOSOMAI RWA Adenime	12 84-130
		dimethylases proteins.	PR00910A 2.51 8.352e-
201	PR00910	LUTEOVIRUS ORF6 PROTEIN	12 509-522
1		SIGNATURE	DM00215 19.43 2.286e-
203	DM00215	PROLINE-RICH PROTEIN 3.	
203			10 39-72
203	- 	LOW DENSITY LIPOPROTEIN	PR00261A 11.02 4.462e
L	1 PR00261		19 65-87 PR00261C
206	PR00261	(LDL) RECEPTOR SIGNATURE	
	PR00261	(LDL) RECEPTOR SIGNATURE	11.37 9.308e-19 65-87
L	PR00261	(LDL) RECEPTOR SIGNATURE	11.37 9.308e-19 65-87
	PR00261	(LDL) RECEPTOR SIGNATURE	11.37 9.308e-19 65-87
	PR00261	(LDL) RECEPTOR SIGNATURE	11.37 9.308e-19 65-87 PR00261D 12.47 2.667e-

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			4.833e-18 143-165 PR00261D 12.47 7.500e- 18 143-165 PR00261B 14.12 5.065e-16 65-87 PR00261C 11.37 8.967e- 16 143-165 PR00261F 11.57 4.938e-13 143- 165 PR00261E 11.08 7.188e-13 65-87 PR00261F 11.57 7.188e- 13 65-87 PR00261E 11.08 1.643e-11 143-
209	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 6.143e- 13 118-173 PF00791C 20.98 7.680e-10 132-
211	PR00007	COMPLEMENT CLQ DOMAIN	171
		SIGNATURE CIQ DOMAIN	PR00007A 19.33 5.781e- 19 131-158 PR00007B 14.16 4.115e-18 158- 178 PR00007C 15.60 1.675e-15 201-223 PR00007D 9.64 7.231e-
212	BL00183	Ubiquitin-conjugating	11 233-244 BL00183 28.97 1.545e-
213	BL00183	enzymes proteins. Ubiquitin-conjugating	30 43-91 BL00183 28.97 1.545e-
215	BL00039	enzymes proteins. DEAD-box subfamily ATP- dependent helicases	30 43-91 BL00039D 21.67 1.900e-
	-	proteins.	29 568-614 BL00039A 18.44 1.871e-23 21-60 BL00039C 15.63 1.720e- 11 364-388 BL00039B 19.19 4.064e-11 277-
217	BL00100	Chloramphenicol acetyltransferase	303 BL00100D 17.22 8.484e- 09 68-106
219	PR00213	proteins. MYELIN PO PROTEIN	PR00213C 15.94 3.969e-
222	BL00678	SIGNATURE Trp-Asp (WD) repeat	11 199-227 BL00678 9.67 1.947e-09
224	PR00875	proteins proteins. MOLLUSC METALLOTHIONEIN	144-155 PR00875A 5.83 1.000e-
225	BL00636	SIGNATURE Nt-dnaJ domain proteins.	09 901-913
226	BL00636	Nt-dnaJ domain proteins.	BL00636B 15.11 8.200e- 19 18-39 BL00636A 8.07 1.000e-
229	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE	21 21-38 BL00636B 15.11 8.200e-19 45-66 PR00301F 13.98 7.563e- 13 329-346 PR00301G 13.78 4.300e-12 361-
230	BL00460	Glutathione peroxidases selenocysteine proteins.	382 BL00460A 28.67 8.773e- 20 35-70 BL00460B 9.73 7.429e-16 78-96 BL00460C 14.35 2.831e- 12 111-134 BL00460D 16.89 8.773e-11 140-
31	PR00647	SENR ORPHAN RECEPTOR	PR00647B 10.19 8.522e-
33	BL00292	Cyclins proteins.	09 273-287 BL00292B 20.31 7.429e- 27 244-275 BL00292A 22.87 7.750e-27 201-
34	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	235 PR00449A 13.20 6.308e- 13 7-29 PR00449C

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	NO.		17.27 4.462e-11 47-70 PR00449D 10.79 7.120e- 11 109-123
235	PR0 0019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300e- 10 251-265 PR00019B 11.36 5.320e-09 119- 133 PR00019B 11.36 1.000e-08 229-243
236	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PRO0019B 11.36 7.300c- 10 245-259 PR00019B 11.36 5.320e-09 113- 127 PR00019B 11.36 1.000e-08 223-237
237	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYNA.	PD00289 9.97 8.448e-09 67-81
240	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e- 10 616-635
241	PR00011	TYPE III EGF-LIKE SIGNATURE	PRO0011D 14.03 3.492e- 10 616-635
244	BL00903	Cytidire and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 8.941e- 12 54-64
245	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 8.043e- 09 124-134
248	BL00246	Wnt-1 family proteins.	BL00246D 23.97 1.000e- 40 186-239 BL00246E 20.32 1.000e-40 305- 351 BL00246B 13.69 4.176e-36 105-140 BL00246A 15.75 2.286e- 24 70-90 BL00246C 15.56 4.857e-22 150- 175
250	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927E 14.93 5.114e- 10 253-275
254	BL00674	AAA-protein family proteins.	BL00674B 4.46 1.000e- 09 223-245
255	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	PD01796 15.01 6.045e- 09 61-88
256	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 2.800e 10 421-435
258	PR00094	ADENYLATE KINASE SIGNATURE	PR00094C 12.94 2.200e- 18 87-104 PR00094D 12.52 2.731e-14 161- 177 PR00094A 10.31 5.500e-14 11-25 PR00094B 11.01 4.115e 13 39-54 PR00094E 11.25 7.333e-13 178- 193
259	BL00892	HIT family proteins.	BL00892A 18.17 5.500e 13 60-91 BL00388A 23.14 1.000e
262	BL00388	Proteasome A-type subunits proteins.	40 8-54 BL00388B 31.38 3.864e-33 66-10 BL00388D 20.71 1.000e 21 153-184 BL00388C 18.79 8.147e-16 126- 148
264	BL00903	Cytidine and deoxycyticylate deaminases zinc-binding region s.	BL00903 12.93 5.821e- 09 91-101
267	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.529e
270	BL00226	Intermediate filaments proteins.	BL00226D 19.10 1.000e 37 362-409 BL00226B

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	NO.		RESULIS*
			23.86 8.043e-35 196-
ł			244 BL00226C 13.23 7.000e-20 261-292
			BL00226A 12.77 6.143e-
271	PD02952	KINACE COLNODO	15 96-111
	FD02332	KINASE TRANSFERASE CHOLINE PROTEIN	PD02952C 15.76 9.731e- 16 235-265 PD02952B
		MULTIGENE FAMI.	15.57 5.625e-09 215-
272	PD02929		229
1 2.2	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I	PD02929A 28.27 1.000e- 40 106-160 PD02929B
ł	-	33333333	18.36 8.800e-17 179-
274	BL01027		199
2/4	BEOTOS	Glycosyl hydrolases family 39 proteins.	BL01027B 15.34 3.486e-
275	PR00424	ADENOSINE RECEPTOR	09 213-250 PR00424D 14.32 6.451e-
		SIGNATURE	11 39-59
277	BL00052	Ribosomal protein S7	BL00052A 27.85 6.000e-
ĺ		proteins.	13 137-184 BL00052B 15.17 5.143e-12 208-
			235
279	BL00790	Receptor tyrosine kinase	BL00790N 13.25 5.659e-
280	PR00319	class V proteins. BETA G-PROTEIN	13 267-294 PR00319D 11.64 6.625e-
		(TRANSDUCIN) SIGNATURE	23 107-125 PR00319C
			13.41 1.000e-21 89-105
		1	PR00319A 15.27 8.364e- 21 51-68 PR00319B
			11.47 8.200e-19 70-85
281	PR00319	BETA G-PROTEIN	PR00319D 11.64 6.625e-
	İ	(TRANSDUCIN) SIGNATURE	23 94-112 PR00319C 13.41 1.000e-21 76-92
			PR00319A 15.27 8.364e-
-			21 38-55 PR00319B
287	PF00929	Exonuclease.	11.47 8.200e-19 57-72 PF00929D 16.17 7.366e-
291			09 149-163
291	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e- 09 93-127
292	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e-
294	PD00066	<u></u>	09 93-127
274	PD00006	PROTEIN ZINC-FINGER METAL-BINDI	PD00066 13.92 8.714e- 12 203-216
295	BL00028	Zinc finger, C2H2 type,	BL00028 16:07 5.500e-
		domain proteins.	15 322-339 BL00028
			16.07 9.471e-14 433-
			450 BL00028 16.07 4.600e-13 648-665
		1	BL00028 16.07 5.500e-
		1	13 760-777 BL00028
	}		16.07 9.550e-13 788- 805 BL00028 16.07
			3.348e-12 704-721
			BL00028 16.07 6.478e-
			12 461-478 BL00028 16.07 8.435e-12 844-
			861 BL00028 16.07
	j	i	1.692e-11 593-610
		. .	BL00028 16.07 2.038e- 11 211-228 BL00028
			16.07 5.154e-11 732-
			749 BL00028 16.07
			5.846e-11 377-394 BL00028 16.07 6.885e-
			11 816-833 BL00028
			16.07 7.231e-11 676-
			693 BL00028 16.07 9.654e-11 564-581
		·	J. VJ4C-11 304-581

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	NO.		BL00028 16.07 4.086e-
			09 517-534 BL00028
		1	16.07 7.429e-09 489-
			506
		Mitochondrial energy	BL00215A 15.82 8.333e-
96	BL00215	transfer proteins.	16 111-136 BL00215A
		transfer process.	15.82 2.723e-11 10-35
	i		BL00215B 10.44 9.526e-
	1	<u> </u>	11 152-165 BL00215B
	1		
		1	10.44 7.375e-10 59-72
		<u> </u>	BL00215A 15.82 9.824e-
	1		10 205-230
302	PF00953	Glycosyl transferase.	PF00953C 19.70 8.773e-
,02	1		34 236-269 PF00953A
	1		19.68 5.000e-25 102-
			129 PF00953B 6.17
		·	1.000e-13 182-194
		tRNA synthetases class	PF00152D 21.30 8.364e-
304	PF00152		28 422-461 PF00152C
	1	II.	28.03 9.250e-21 220-
	j .		28.03 9.250E-21 220- 257 PF00152B 15.67
)		
	1		2.658e-13 159-184
	1		PF00152A 19.68 5.714e-
			11 44-67
305	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 8.250e-
303	120200	ZINC-FINGER METAL-	35 37-76
		BINDING NU.	
	777777	PROTEIN NUCLEAR	PD02784B 26.46 5.840e-
305	PD02784	RIBONUCLEOPROTEIN.	09 92-135
		RIBUNUCLEOFROIDIN.	PR00454C 11.24 7.808e-
307	PR00454	ETS DOMAIN SIGNATURE	09 1167-1186
			PR00237E 13.03 5.091e-
308	PR00237	RHODOPSIN-LIKE GPCR	PR0023/E 13.03 3.031e-
		SUPERFAMILY SIGNATURE	13 188-212 PR00237G
	-		19.63 7.207e-13 268-
	!		295 PR00237A 11.48
	1		4.375e-11 24-49
	1	1	PR00237C 15.69 3.057e-
		·	10 101-124 PR00237D
			8.94 4.750e-10 137-159
	1	1	PR00237F 13.57 5.364e-
			10 230-255 PR00237B
			13.50 9.438e-10 57-79
		DNA polymerase family X	BL00522C 11.90 7.577e-
309	BL00522		24 315-339 BL00522F
	}	proteins.	14,90 1.310e-15 470-
		Į.	
			494 BL00522A 25.52
	}	1	1.265e-14 179-226
			BL00522E-19.63 8.615e-
	1	l	14 430-460 BL00522B
	1	!	27.30 9.625e-12 267-
	1	1	313
		Tropomyosins proteins.	BL00326D 8.76 5.235e-
310	BL00326	Tropomyosine processe.	10 856-897
·		1-1-1-1-1-1-1	BL00290A 20.89 4.706e-
312	BL00290	Immunoglobulins and	
	J	major histocompatibility	
	1	complex proteins.	13.17 9.000e-12 211-
			229
313	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e
		_	40 34-85 BL00345A
			13.95 9.217e-16 1-20
	DEOCCC:	BTB (also known as BR-	PF00651 15.00 5.091e-
315	PF00651	BIB (also known as BR	15 63-76
l		C/Ttk) domain proteins.	BL01020C 15.35 3.198e
317	BL01020	SAR1 family proteins.	
1	1		17 79-130
i		Sugar transport	BL00216B 27.64 4.696e
318	BL00216		
318	BP00519		11 164-214
318	PR00109	proteins. TYROSINE KINASE	11 164-214 PR00109B 12.27 4.814e

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321	PT COSOS	SIGNATURE	
	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.688e- 10 329-372
322	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 8.765e- 12 558-577
324	BL01241	Link domain proteins.	BL01241 35.81 8.313e- 30 183-236 BL01241 35.81 3.222c-13 282- 335
326	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 4.000e- 12 515-566 BL00412D 16.54 5.705e-11 516- 567 BL00412D 16.54 7.848e-10 518-569 BL00412D 16.54 1.827e- 09 514-565 BL00412D 16.54 1.918e-09 513- 564 BL00412D 16.54 2.102e-09 520-571
328	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 9.557e- 20 151-199 BL00232B 32.79 2.246e-18 41-89 BL00232B 32.79 5.985e- 18 370-418 BL00232B 32.79 5.500e-16 258- 306 BL00232B 32.79 9.384e-15 475-523 BL00232C 10.65 2.537e- 12 256-274 BL00232C 10.65 4.326e-11 368- 386 BL00232C 10.65 7.261e-11 473-491 BL00232C 10.65 7.457e-
330	PR00454	ETS DOMAIN SIGNATURE	11 39-57 PR00454C 11.24 7.808e-
331	BL00598	Chromo domain proteins.	09 1167-1186 BL00598 14.45 8.393e-
333	BL01016	Glycoprotease family proteins.	18 27-49 BL01016C 22.84 3.925e- 32 70-115 BL01016E 14.88 5.286e-19 149- 177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e- 11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e- 10 4-19 BL01016F 13.34 1.563e-09 200- 212 BL01016B 8.93 8.855e-09 38-50
339	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.500e- 11 17-61
340	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 1.231e- 33 10-49
341	BL01160	Kinesin light chain	PL01150B 19.54 5.042e-
342	PD01066	repeat proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	09 55-109 PD01066 19.43 2.400e- 30 16-55
343	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 1.000e-
346	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.764e- 11 135-154
347	PR00109	TYROSINE KINASE	PR00109B 12.27 4.764e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	NO.	CATALYTIC DOMAIN SIGNATURE	11 135-154
351	BL01187	Calcium-binding EGF-like domain proteins pattern	BL01187B 12.04 1.783e- 13 100-116 BL01187B
		proteins.	12.04 8.435e-13 276- 292 BL01187B 12.04 8.800e-11 13-29
			BL01187B 12.04 7.429e- 10 54-70 BL01187B
			12.04 5.725e-09 231- 247 BL01187A 9.98 7.000e-09 255-267
352	PD00078	REPEAT PROTEIN ANK	PD00078B 13.14 5.950e-
352	1000070	NUCLEAR ANKYR.	10 366-379 PD00078B 13.14 4.522e-09 168- 181
354	BL00380	Rhodanese proteins.	BL00380F 9.76 6.694e- 11 542-553
355	PF00628	PHD-finger.	PF00628 15.84 1.000e- 11 116-131
356	PR00587	SOMATOSTATIN RECEPTOR TYPE 1 SIGNATURE	PR00587A 8.06 9.700e- 09 17-37
359	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.462e- 15 261-274 PD00066
		PEIM-BINDI.	13.92 6.500e-13 233- 246 PD00066 13.92
			4.300e-09 289-302 PF00791B 28.49 9.604e-
361	PF00791	Domain present in ZO-1 and Unc5-like netrin	13 54-109 PF00791B
		receptors.	PF00791A 27.85 1.432e- 09 71-126 PF00791B 28.49 7.440e-09 184-
			239 PF00791B 28.49 2.273e-
362	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	11 279-334
363	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 5.080e- 10 73-95 PR00450C 12.22 3.278e-09 109- 131
364	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e- 09 22-68
365	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e- 09 22-68
366	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e- 09 1038-1092 PR00019B 11.36 1.360e-
367	PR.00019	LEUCINE-RICH REPEAT SIGNATURE	09 229-243 PR00019B 11.36 6.040e-09 91-105 PR00019A 11.19 8.667e- 09 370-384
368	PR00011	TYPE III EGF-LIKE SIGNATURE	PRO0011D 14.03 9.000e- 15 30-49 PRO0011A 14.06 9.830e-15 30-49
			PR00011B 13.08 4.500e- 14 30-49 PR00011C 24.25 5.143e-09 6-35
369	BL01032	Protein phosphatase 2C proteins.	BL01032H 11.25 4.150e- 09 417-430
372	BL00478	LIM domain proteins.	BL00478B 14.79 7.750e- 12 410-425
373	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.757e- 34 26-65
376	PR00170	SODIUM CHANNEL SIGNATURE	PR00170E 6.48 2.739e-
376	I TYOUT I		

SEQ ID 1	NO: ACCESSION NO.	DESCRIPTION	RESULTS*
			10 88-118
380	BL00107	Protein kinases ATP-	PL001075 10 70 - 000
		binding region proteins.	23 276-307 BL00107B
			13.31 1.692e-12 342-
20-			358
381	BL00455	Putative AMP-binding	BL00455 13.31 5.714e-
		domain proteins.	12 50-66
382	PR00624	HISTONE H5 SIGNATURE	PR00624G 4.08 4.900e-
			09 524-544
384	PD00078	REPEAT PROTEIN ANK	PD00078B 13.14 5.950e
		NUCLEAR ANKYR.	10 366-379 PD00078B
			13.14 4.522e-09 168-
385			281
303	PR00511	TEKTIN SIGNATURE	PR00511D 7.11 5.371e-
386			09 67-80
300	PD02870	RECEPTOR INTERLEUKIN-1	PD02870B 18.83 6.000e-
388		PRECURSOR.	10 97-130
200	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 5.000e-
389		METAL-BINDI.	13 516-529
303	BL00290	Immunoglobulins and	BL00290A 20.89 7.657e-
		major histocompatibility	09 151-174
390	BL00215	complex proteins.	1
	P000215	Mitochondrial energy	BL00215A 15.82 5.200e-
	1	transfer proteins.	15 221-246 BL00215A
	1		15.82 7.618e-14 20-45
			BL00215A 15.82 8.851e-
		}	11 123-148 BL00215B
	J		10.44 9.526e-11 69-82
			BL00215B 10.44 7.300e-
	ı	J	09 272-285 BL00215B
		Ì	10.44 8.500e-09 165-
394	BL00674	AAA-protein family	178
		proteins.	BL00674B 4.46 2.723e-
397	PR00048	C2H2-TYPE ZINC FINGER	16 299-321
		SIGNATURE	PR00048A 10.52 8.579e-
398	PR00761	BINDIN PRECURSOR	11 141-155
	!	SIGNATURE	PR00761B 9.93 6.764e-
399	BL00240	Receptor tyrosine kinase	BL00240B 24.70 7.907e-
		class III proteins.	10 118-142
101	PF00676	Dehydrogenase E1	PF00676B 24.71 8.071e-
	1	component.	18 331-369 PF00676D
		1	14.40 3.854e-15 486-
		1	506 PF00676C 16.88
02			9.182e-14 454-478
102	BL00514	Fibrinogen beta and	BL00514C 17.41 4.673e-
		gamma chains C-terminal	28 4432-4469 BL00514G
		domain proteins.	15.98 6.092e-14 4555-
	1		4585 BL00514D 15.35
			2.532e-12 4473-4486
			BL00514F 11.65 4.288e-
	•		10 4519-4534 BL00514H
	1		14.95 4.955e-10 4584-
03	PF00992		4609
	FF00992	Troponin.	FP00992A 16.67 5.974e-
04	PR00019	1 DUG 3-1-	09 105-140
-	-KOOOTA	LEUCINE-RICH REPEAT	PR00019B 11.36 1.450e-
	i	SIGNATURE	10 73-87 PROCO19A
	1	1	11.19 8.043e-10 76-90
	1	1	PR00019B 11.36 1.000e-
		1	09 50-64 PR00019B
)5	BL00232	0-3)	11.36 1.000e-09 96-110
	BE00232	Cadherins extracellular	BL00232B 32.79 9.557e-
	1	repeat proteins domain	20 139-187 BL00232B
]	proteins.	32.79 2.246e-18 29-77
	1		BL00232B 32.79 5.985e-
		1	18 358-406 BL00232B
			32.79 5.500e-16 246-

EQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	NO.	_	294 BL00232B 32.79
		1	9.384e-15 463-511
		†	BL00232C 10.65 2.537e-
			12 244-262 BL00232C
	1		10.65 4.326e-11 356-
			374 BL00232C 10.65
	Ì	1	7.261e-11 461-479
	1		BL00232C 10.65 7.457e-
		i	11 27-45
			PF00426S 15.67 5.634e-
07	PF00426	Outer Capsid protein VP4	09 902-940
. •		(Hemagglutinin).	
09	BL01160	Kinesin light chain	BL01160B 19.54 9.695e-
.05		repeat proteins.	09 126-180
110	BL00741	Guanine-nucleotide	BL00741B 14.27 2.731e-
110	B500741	dissociation stimulators	09 252-275
	ì	CDC24 family sign.	
	 	F-box domain proteins.	PF00646A 14.37 6.344e-
11	PF00646	F-DOX COMMAIN PROCESSES	09 86-100
	·		BL00603B 11.39 8.500e-
412	BL00603	Thymidine kinase	09 542-557
		cellular-type proteins.	BL00866B 36.29 3.571e-
415	BL00866	Carbamoyl-phosphate	
		synthase subdomain	31 245-291 BL00865C
		proteins.	23.26 9.000e-25 331-
		1	366
418	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239E 1.58 6.114e-
4.0	FROUZS	TERMINAL TAIL SIGNATURE	09 590-602
	PF00791	Domain present in 20-1	PF00791B 28.49 7.955e-
421	PF-00791	and Unc5-like netrin	14 23-78 PF00791B
			28.49 3.653e-12 273-
		receptors.	328 PF00791B 28.49
			4.273e-11 156-211
			pF00791B 28.49 7.818e-
		· '	
	ļ		11 89-144 PF00791B
		i	28.49 1.524e-10 56-111
		1	PF00791C 20.98 3.559e-
			09 37-76 PF00791C
			20.98 5.235e-09 170-
		Į.	209 PF00791C 20.98
			5.235e-09 381-420
	Ì		PF00791B 28.49 6.202e-
	1		09 189-244 PF00791B
	1		28.49 7.028e-09 435-
	ļ		. 490 PF00791B 28.49
	i	{	1 · · ·
			8.679e-09 367-422
424	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 7.207e-
767	2	1	28 1645-1679
405	PR00109	TYROSINE KINASE	PR00109D 17.04 5.881e-
425	PKOOTOS	CATALYTIC DOMAIN	10 228-251
		SIGNATURE	BL00518 12.23 4.600e-
429	BL00518	Zinc finger, C3HC4 type	
	.	(RING finger), proteins.	11 31-40
431	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 1.844e
		dependent helicases	34 490-536 BL00039A
)		proteins.	18.44 5.615e-19 205-
			244 BL00039B 19.19
	<u> </u>		8.920e-16 251-277
		Į.	BL00039C 15.63 5.781e
ļ			15 333-357
			PR00452B 11.65 7.652e
432	PR00452	SH3 DOMAIN SIGNATURE	12 169-185
1			
433	PR00828	FORMIN SIGNATURE	PR00828B 5.23 8.218e-
233			10 382-405
126	BL00415	Synapsins proteins.	BL00415N 4.29 8.643e-
436	פוניטטעם	Shireharma brocome.	11 195-239 BL00415N
			4.29 3.036e-09 809-85
1			PR00834F 10.91 6.040e
443	PR00834	HTRA/DEGQ PROTEASE	
I	ı	FAMILY SIGNATURE	11 221-234 PF01140D 15.54 9.663e
1		Matrix protein (MA),	

SEQ ID N	O: ACCESSION	DESCRIPTION	RESULTS*
		p15.	10 393 210 00011
			10 183-218 PF01140D 15.54 3.093e-09 246-
449	PR00568	DOPAMINE D3 RECEPTOR SIGNATURE	PRC0568G 13.95 5.551e- 09 39-53
451	PF00084	Sushi domain proteins	PF00084B 9.45 3.813e-
452	BL00790	(SCR repeat proteins. Receptor tyrosine kinase	10 47-59 BL00790I 20.01 2.821e-
		class V proteins.	09 618-649
456	PR00380	KINESIN HEAVY CHAIN	PR00380A 14.18 1.000e-
		SIGNATURE	25 77-99 PR00380D
			9.93 1.000e-21 281-303 PR00380C 13.18 8.286e-
			17 230-249 PR00380B
			12.64 4.724e-16 194- 212
457	PR00253	GAMMA-AMINOBUTYRIC ACID	PR00253A 9.15 9.143e-
		(GABA) RECEPTOR	24 246-267 PR00253B
		SIGNATURE	13.47 2.000e-23 272-
			294 PR00253C 13.85 7.000e-23 306-328
			PR00253D 16.68 5.950e-
467	PR00849	GLYCOSYL HYDROLASE	21 452-473
		PAMILY 58 SIGNATURE	PR00849D 9.77 9.236e- 09 910-937
471	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 8.200e-12
472	BL00226	proteins proteins. Intermediate filaments	33-44
450		proteins.	BL00226B 23.86 3.721e- 09 282-330
473	BL00344	GATA-type zinc finger	BL00344 17.99 7.000e-
474	BL00481	domain proteins. Thiol-activated	12 814-852 BL00481E 13.07 8.909e-
470		cytolysins proteins.	09 173-199
479	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 2.571e-
480	PD01066	PROTEIN ZINC FINGER	09 393-408 PD01066 19.43 1.900e-
		ZINC-FINGER METAL-	38 8-47
481	PR00405	BINDING NU. HIV REV INTERACTING	
		PROTEIN SIGNATURE	PR00405C 19.41 1.000e- 19 451-473 PR00405B
			11.83 4.333e-18 430-
			448 PR00405A 17.71 4.971e-18 411-431
482	PR00049	WILM'S TUMOUR PROTEIN	PR00049D 0.00 9.285e-
	ļ	SIGNATURE	10 959-974 PR00049D
			0.00 9.857e-10 958-973 PR00049D 0.00 1.305e-
		1	09 937-952 PR00049D
486	PR00007	COMPLEMENT C1Q DOMAIN	0.00 8.322e-09 939-954
		SIGNATURE	PR00007B 14.16 8.615e- 23 653-673 PR00007A
			19.33 6.192e-22 626-
			653 PR00007C 15.60
		,	5.846e-19 698-720 PR00007D 9.64 3.647e-
487	7700569		13 732-743
-07	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567B 18.23 2.853e-
488	PR00988	URIDINE KINASE SIGNATURE	09 200-214 PR0098BA 6.39 4.569e-
189	PD01066		12 3-21
	EDOTORR	PROTEIN ZINC FINGER ZINC-FINGER METAL-	PD01066 19.43 4.882e-
		BINDING NU.	27 30-69 PD01066 19.43 3.430e-10 71-110
190	PR00049	WILM'S TUMOUR PROTEIN	PR00049D 0.00 7.864e-
192	BL01128	SIGNATURE Shikimata kinasa	09 663-678
		Shikimate kinase proteins.	BL01128A 18.84 6.464e- 17 58-92
97	PF00429	ENV polyprotein (coat	PF00429 31.08 7.171e-

EQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.	polyprotein).	15 21-71
		Lipases, serine	BL00120B 11.37 7.923e-
98	BL00120	proteins.	09 185-200
	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 7.353e-
00	BT00020	region RNP-1 proteins.	11 299-318
01	BL01159	WW/rsp5/WWP domain	BL01159 13.85 8.579e-
901	BEOTISS	proteins.	12 131-146
05	BL00021	Kringle domain proteins.	BL00021B 13.33 3.739e-
,03	1 2200022	_	17 492-510
508	PR00120	H+TRANSPORTING ATPASE	PR00120C 9.90 5.800e-
,00		(PROTON PUMP) SIGNATURE	19 705-722
509	DM01417	6 kw INDUCING X2MC2	DM01417E 20.62 2.938e-
	•	MUSHROOM SPAC22G7.04.	16 362-395 DM01417D
	İ)	11.08 3.800e-13 322-
	1		338 PF00534B 14.47 6.625e-
510	PF00534	Glycosyl transferases	1
	}	group 1.	09 346-370 PF00534B 14.47 6.625e-
511	PF00534	Glycosyl transferases	
	1	group 1.	09 293-317 PF00534B 14.47 6.625e-
512	PF00534	Glycosyl transferases	09 366-390
		group 1.	PD01841A 21.71 1.000e-
513	PD01841	PHOSPHORYLASE KINASE	40 110-160 PD01841B
	i	ALPHA MUSCL.	14.35 1.000e-40 181-
			222 PD01841D 17.87
			1.000e-40 243-295
		1	PD01841F 13.36 1.000e-
			40 333-382 PD01841G
			24.26 1.000e-40 386-
	1		440 PD01841L 18.42
			1.000e-40 968-1010
		1	PD01841I 23.00 4.545e-
		•	37 762-804 PD01841E
			18.60 3.750e-36 295-
	İ		333 PD01841J 14.94
	.		6.023e-35 851-888
	ļ		PD01841H 21.30 2.909e-
	1		33 490-527 PD01841K 14.81 7.088e-33 924-
		}	954 PD01841C 13.78
	1	1	9.386e-23 222-243
	1		PD01841M 10.82 8.594e-
			21 1054-1073 PD01841I
	,	į.	23.00 2.667e-13 549-
			591
	P200353	CYCLOPHILIN PEPTIDYL-	PR00153C 11.01 7.188e-
514	PR00153	PROLYL CIS-TRANS	13 95-111 PR00153E
		ISOMERASE SIGNATURE	9.10 4.150e-12 122-138
E3.5	BL00740	MAM domain proteins.	BL00740A 13.87 7.188e-
515	2500140		12 410-423
516	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 6.087e-
210	200032		12 1018-1052
517	BL00242	Integrins alpha chain	BL00242C 16.86 8.320e-
J.,	22000	proteins.	09 12-42
523	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e-
		1	39 20-68 DM00031B
	1		15.41 1.000e-25 84-118
525	BL00319	Amyloidogenic	BL00319C 17.12 8.375e
		glycoprotein	10 61-95
ļ	1	extracellular domain	1
	1	proteins.	
526	PF00789	Domain present in	PF00789B 19.70 3.308e
1		ubiquitin-regulatory	12 322-343 PF00789C
!		proteins.	20.98 5.269e-09 367-
i	l l	1-	392
528	BL01162	Quinone oxidoreductase /	BL01162C 22.80 1.500e
}	1	zeta-crystallin	16 120-164
		proteins.	

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529	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 3.893e-
532	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.000e 17 11-36 BL00215A 15.82 8.660e-11 123-
533	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.000e- 17 11-36 BL00215A
534	BL00098	Thiolases acyl-enzyme intermediate proteins.	15.82 8.660e-11 97-122 BL00098C 21.65 2.800e- 38 181-227 BL00098B
			32.59 5.345e-38 86-141 BL00098D 26.30 8.364e- 35 245-288 BL00098E 22.12 1.000e-34 314- 352 BL00098F 10.18 4.971e-22 365-386 BL00098A 10.60 6.455e-
535	PR00370	FLAVIN-CONTAINING MONOOXYGENASE (FMO) SIGNATURE	11 38-50 PR00370E 11.96 7.429e- 22 321-340 PR00370D 16.33 6.143e-21 185- 204 PR00370F 17.75 6.559e-21 376-396 PR00370B 10.91 9.591e- 21 27-46 PR00370C 12.72 3.500e-20 140-
536	BL00028	Zinc finger, C2H2 type, domain proteins.	157 PR00370A 3.35 6.442e-17 4-20 BL00028 16.07 7.429e- 16 285-302 BL00028
537			16.07 6.294e-14 341- 358 BL00028 16.07 1.346e-11 369-386 BL00028 16.07 1.692e- 11 397-414 BL00028 16.07 4.462e-11 453- 470 BL00028 16.07 7.231e-11 425-442 BL00028 16.07 4.300e- 10 313-330
538	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e- 15 844-881
539	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e- 15 819-856
540	PR00985	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e- 15 822-859
341		LEUCYL-TRNA SYNTHETASE SIGNATURE	PR00985A 12.10 9.000e- 10 357-375
	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	PD02102A 16.74 1.000e- 40 3-47 PD02102B 18.28 4.375e-34 57-100 PD02102D 21.69 1.923e- 30 179-218 PD02102C 26.34 8.929e-26 100- 146
43	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e- 10 49-65 BL00026 16.07 6.400e-10 193- 210 BL00028 16.07 1.000e-09 343-360 BL00028 16.07 6.914e- 09 78-95
45	BL00250	TGF-beta family proteins.	BL00250A 21.24 8.000e- 31 293-329 BL00250B 27.37 5.286e-24 354-
47	PR00319	BETA G-PROTEIN	390 PR00319B 11.47 2.714e-

TRANSDUCIN SIGNATURE 09 186-201 PR00319A 12-77 -3446-09 210-227 12-77 -3446-09 210-227 12-77 -3446-09 210-227 12-77 -3446-09 210-227 12-77 -3464-09 210-227 12-77 -3464-09 210-221 12-77 -3464-09 210-221 12-77 -3464-09 210-221 12-77 -3464-09 210-221 12-77 -321 12-77 -3466-10 12-77 -321 12-77 -3466-10 12-77 -321 12-77 -3466-10 12-77 -321 12-77 -321 12-77 -3466-10 12-77 -321 12-	SEQ ID NO:	ACCESSION NO.	DESCRIPTION ·	RESULTS*
December December		NO.		227
### PROTEIN PAMILY SIGNATURE 15 255-276 ####################################	548	BL01204		40 8-56 BL01204D 16.42 1.000e-40 177- 221 BL01204E 13.83 7.652e-30 225-250 BL01204C 13.93 8.714e- 22 141-160 BL01204B 15.41 4.333e-16 102- 116
### Transferase 23 1569-1601 PP006325 18.45 3.700e-21 1515-1543 18.45 3.700e-21 1515-1543 18.45 3.700e-21 1515-1543 18.45 3.700e-21 1515-1543 18.602908 18.45 3.700e-21 1515-1543 18.602908 18.17 1.600e-1515 18.600e-1515 18.600e-1515 18.600e-1515 18.600e-1515 18.600e-1515 18.600e-1515 18.600e-1515 18.600e-1515 18.600e-1515 18.600e-1515 18.600e-1515 18.600e-1515 18.600e-1515 18.600e-1516 18.60	549	PR00326	PROTEIN FAMILY SIGNATURE	15 255-276
Major histocompatibility 14 187-205 BL00290A 20.89 2.059e-14 130-153 20.89 2.059 2.059e-14 130-153 20.89 2.059e-14 130-153 20.89 2.059e-14 130-153 20.89 2.059e-14 130-153 20.89 2.059e-14 130-153 20.89 2.059e-14 130-153 20.89 2.059e-14 130-153 20.89 2.059e-14 130-153 20.89 2.059e-14 130-153 20.89 2.059e-14 130-153 20.89 2.059e-14 130-153 20.89 2.059e-14 130-153 20.89 2.059e-14 130-153 20.89 2.059e-14 130-153 20.89 2.059e-14 130-153 20.89 2.059e-14 130-153 20.89 2.059e-14 130-153 20.89 2.059 2.059e-14 130-153 20.89 2	551	PF00632	transferase).	23 1569-1601 PF00632B 18 45 3.700e-21 1515- 1543
1	554	BL00290	major histocompatibility complex proteins.	14 187-205 BL00290A 20.89 2.059e-14 130- 153
TRANSFORMING 61K PDF1	557	DM00215		09 846-879
Protein, unique domain 32 118-155 proteins. 32 118-155 proteins. 32 118-155 32 118-155 34 470-499 32 118-155 34 470-499 32 118-155 34 470-499 32 118-155 34 470-499 32 118-155 37 5 13 5 13 75 32 118-155 37 5 13 5 13 75 32 118-15	559	DM01111	TRANSFORMING 61K PDF1.	09 7-35
### aspartyl proteases proteins. ### proteins	562	PF00658	protein, unique domain proteins.	32 118-155
Solution	564	BL00141	aspartyl proteases	10 472-488
ZINC-FINGER METAL-BINDING NU. 13 229-268	566	PF00855		15 272-289
binding region proteins. 19 118-149 BL00107B 13.31 5.500e-15 183-199 Protein kinases ATP- BL00107A 18.39 7.000e 19 118-149 BL00107B 13.31 5.500e-15 183-199 PRO0193 MYOSIN HEAVY CHAIN PRO0193D 14.36 1.857e 34 454-483 PR00193C 12.60 2.636e-31 223-251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e 22 115-135 PR00193B 19.47 6.559e-19 508-537 PRO0193 MYOSIN HEAVY CHAIN PR00193D 14.36 1.857e 34 470-499 PR00193C 12.60 2.636e-31 239-267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e 22 115-135 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e 22 115-135 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e 22 115-135 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e 22 115-135 PR00193B 19.47 6.559e-19 524-553 BL00752 XPA protein. BL00752B 19.17 9.703e 19.47 6.559e-19 524-553 Eukaryotic RNA-binding R00030A 14.39 7.000e 09 276-295	567	PD01066	ZINC-FINGER METAL- BINDING NU.	13 229-268
binding region proteins. 19 118-149 BL00107B 13.31 5.500e-15 183-199 572 PR00193 MYOSIN HEAVY CHAIN PR00193D 14.36 1.857e 34 454-483 PR00193C 12.60 2.636e-31 223-251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e 22 115-135 PR00193E 19.47 6.559e-19 508-537 573 PR00193 MYOSIN HEAVY CHAIN PR00193D 14.36 1.857e 34 470-499 PR00193C 12.60 2.636e-31 239-267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e 22 115-135 PR00193E 19.47 6.559e-19 524-553 575 BL00752 XPA protein. BL00752B 19.17 9.703e 10 885-929 576 BL00030 Eukaryotic RNA-binding PL00030A 14.39 7.000e 7 region RNP-1 proteins. 09 276-295	569	BL00107	binding region proteins.	19 118-149 BL00107B 13.31 5.500e-15 183-
SIGNATURE SIGNATURE 34 454-483 PR00193C 12.60 2.636e-31 223- 251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e 22 115-135 PR00193E 19.47 6.559e-19 508- 537 PR00193 MYOSIN HEAVY CHAIN SIGNATURE PR00193D 14.36 1.857e 34 470-499 PR00193C 12.60 2.636e-31 239- 267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e 22 115-135 PR00193E 19.47 6.559e-19 524- 553 S75 BL00752 XPA protein. BL00752B 19.17 9.703e 10 885-929 Eukaryotic RNA-binding region RNP-1 proteins. BL00030A 14.39 7.000e	570	BL00107	Protein kinases ATP- binding region proteins.	19 118-149 BL00107B 13.31 5.500e-15 183- 199
SIGNATURE 34 470-499 PR00193C 12.60 2.636e-31 239- 267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.5886 22 115-135 PR00193E 19.47 6.559e-19 524- 553 SPA protein. BL00752 Eukaryotic RNA-binding region RNP-1 proteins. BL00030 BL00030A 14.39 7.0006 09 276-295	572	PR00193		34 454-483 PR00193C 12.60 2.636e-31 223- 251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 508- 537
576 BL00030 Eukaryotic RNA-binding BL00030A 14.39 7.000e region RNP-1 proteins. 09 276-295	573	PR00193	SIGNATURE	34 470-499 PR00193C 12.60 2.636e-31 239- 267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 524- 553
region RNP-1 proteins. 09 276-295		·	1	10 885-929
577 BL00116 DNA polymerase family B BL00116A 12.81 5.7376	L		region RNP-1 proteins. DNA polymerase family B	

SEQ ID	NO: ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins.	13 864-877 BL00116B 11.82 1.529e-12 952-
578	BL00195	Glutaredoxin proteins.	965 BL00195B 15.31 7.158e- 09 121-141
579	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PRO0019B 11.36 9.000e- 11 217-231 PR00019B 11.36 1.360e-09 386- 400 PR00019A 11.19 3.333e-09 389-403 PR00019B 11.36 8.920e-
580	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	09 363-377 PR00253A 9.15 2.125e- 25 275-296 PR00253B 13.47 7.923e-24 301- 323 PR00253D 16.68 5.846e-23 444-465 PR00253C 13.85 2.241e-
583	PR00343	SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	20 335-357 PR00343C 16.85 2.286e- 11 1233-1252 PR00343C 16.85 5.500e-11 333- 352 PR00343C 16.85 5.500e-11 783-802 PR00343C 16.85 4.246e- 10 1491-1510 PR00343C 16.85 8.230e-10 1686- 1705
584	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.	DM01537B 21.63 1.878e- 37 79-126 DM01537B 21.63 9.491e-30 916- 963 DM01537A 15.14
586	PFC0013	KH domain proteins family of RNA binding proteins.	3.186e-11 784-804 PF00013 5.78 1.450e-09 124-136
587	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 4.409e- 13 262-296
589	BL00478	LIM domain proteins.	BL00478B 14.79 1.643e- 13 261-276 BL00478B 14.79 7.709e-09 321-
590	PF00855	PWWP domain proteins.	9F00855 13.75 8.000e-
591	PF00855	PWWP domain proteins.	15 931-948 PF00855 13.75 8.000e- 15 1062-1079
593	PF00628	PHD-finger.	PF00628 15.84 3.455e- 12 424-439
594	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 2.241e- 16 558-576 PR00205A 14.73 9.308e-13 542- 558 PR00205C 13.65 5.304e-12 594-609 PR00205B 11.39 4.273e-
596	BL00107	Protein kinases ATP-	10 336-354 BL00107A 18.39 4.789e-
598	PD01675	binding region proteins. GLYCOPROTEIN MAJOR ENVELOPE PROBABLE U3.	18 307-338 PD01675C 19.89 2.330e-
500	BL00242	Integrins alpha chain proteins.	10 55-89 BL00242E 9.03 9.591e- 27 985-1014 BL00242C 16.86 4.115e-26 286- 316 BL00242D 13.57 4.150e-25 357-382 BL00242B 8.13 7.353e- 12 189-199 BL00242D 13.57 3.455e-11 421- 446 BL00242A 13.80

EQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	140.		5.000e-11 61-73 BL00242D 13.57 4.986e- 10 291-316
			PRO0320A 16.74 5.610e-
01	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	09 198-213
02	PR00278	PANCREATIC HORMONE SIGNATURE	PRO0278A 12.43 4.569e- 10 331-348
	BL00479	Phorbol esters /	BL00479C 12.01 3.250e-
03	BEOOGIS	diacylglycerol binding domain proteins.	12 170-183
04	BL00315	Dehydrins proteins.	BL00315A 9.35 1.672e- 09 424-452
505	BL00415	Synapsins proteins.	BL00415N 4.29 9.794e- 10 295-339
506	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926F 17.75 1.000e- 13 335-358
	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-
508		PWWP domain proteins.	15 265-282 PF00855 13.75 5.167e-
509	PF00855	}	15 211-228 DM01206B 10.69 7.411e-
612	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	10 877-897 DM01206B 10.69 8.027e-10 861- 881 DM01206B 10.69
			9.137e-10 873-893 DM01206B 10:69 1.456e- 09 859-879 DM01206B 10.69 1.797e-09 879-
			899 DM01206B 10.69 4.076e-09 865-885 DM01206B 10.69 7.038e-
			09 898-918 DM01206B 10.69 7.949e-09 871- 891 DM01206B 10.69
		The second secon	8.291e-09 767-787 PD02699A 8.91 2.023e-
615	PD02699	PROTEIN DNA-BINDING BINDING DNA	28 129-158 PD02699C 24.84 1.000e-27 317- 364 PD02699B 18.28
	1		1.000e-17 158-182
616	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PRO0380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e-
			16 410-428 PR00380C 13.18 2.976e-13 436-
617	PR00380	KINESIN HEAVY CHAIN	PR00380A 14.18 4.086e- 22 288-310 PR00380D
		SIGNATURE	9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436-
618	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 5.143e-
919	D.101200	PROTEIN.	12 531-551 DM012068 10.69 2.603e-10 535-
621	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 3.160e- 21 561-582
622	BL00239	Receptor tyrosine kinase class II proteins.	BL00239F 28.15 3.222e- 10 647-692 BL00239C 18.75 8.304e-10 543- 566
623	PR00407	EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE	1 09 326-339
624	BL00641	Respiratory-chain NADH	BL00641C 21.10 1.000e-
1 323	220031	dehydrogenase 75 Kd	40 157-202 BL00641E

SEQ ID	NO: ACCESSION NO	DESCRIPTION	RESULTS*
		subunit proteins.	24.37 1.000e-40 255-
			308 BL00641F 33.12
			1.000e-40 571-623 BL00641A 17.15 1.818e-
1			37 48-80 BL00641B
1			12.62 5.846e-34 113-
			139 BL00641D 13.23
627	PR00103	CAMP-DEPENDENT PROTEIN	9.308e-29 216-240 PR00103E 17.80 2.500e-
1		KINASE SIGNATURE	18 367-380 PR00103B
			13.39 2.080e-14 297-
			312 PR00103A 9.59 2.957e-14 282-297
	İ		PR00103D 10.83 3.077e-
			12 346-358 PR00103C
			15.68 1.000e-11 334-
			344 PR00103B 13.39
		1	1.450e-11 175-190 PR00103A 9.59 1.720e-
630	220000		10 160-175
	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY	PR00081A 10.53 6.211e-
		SIGNATURE	16 4-22
631	PF00651	BTB (also known as BR-	PF00651 15.00 8.500e-
632	DM01206	C/Ttk) domain proteins.	14 37-50
	20.101208	CORONAVIRUS NUCLEOCAPSID PROTEIN	DM01206B 10.69 2.233e-
			10 1324-1344 DM01206B 10.69 4.822e-10 1276-
			1296 DM01206B 10.69
			7.658e-10 1328-1348
			DM01206B 10.69 8.274e- 10 1280-1300 DM01206B
			10.69 4.532e-09 1320-
			1340 DM01206B 10.69
635	BL00107	Protein kinascs ATP-	7.266e-09 1326-1346
		binding region proteins.	BL00107A 18.39 7.600e- 23 145-176 BL00107B
			13.31 2.636e-13 211-
636	BL00657	Fork head domain	227
		proteins.	BL00657A 19.39 1.545e- 30 101-143 BL00657B
		1	22.27 7.750e-26 149-
637	BL00107	Protect - International	192
	_	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.000e- 10 607-623
643	BL00018	EF-hand calcium-binding	BL00018 7.41 4.913e-09
647	PF00628	domain proteins.	199-212
	2500628	PHD-finger.	PF00628 15.84 2.350e-
	j ']	13 385-400 PF00628 15.84 3.455e-12 464-
648			479
040	BL01129	Hypothetical	BL01129E 13.25 4.000e-
		yab0/yceC/sfhB family proteins.	25 332-357 BL01129C
		proceins.	25.56 8.200e-23 236- 279 BL01129B 12.51
649			6.118e-13 191-212
047	BL01228	Hypothetical cof family	BL01228D 17.44 3.908e-
650	BL00027	'Homeobox' domain	10 455-480
C.C.	·	proteins.	BL00027 26.43 6.684e- 13 771-814
651	BL50002	Src homology 3 (SH3)	BL50002A 14.19 1.750e-
653	PR00253	domain proteins profile	12 1026-1045
_	1.00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR	PRO0253A 9.15 4.000e-
		SIGNATURE	24 253-274 PR00253C 13.85 8.800e-24 313-
	1		335 PR00253B 13.47
	1		3.143e-22 279-301
		i i	PR00253D 16.68 7.652e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	+		20 422-443
554	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 4.452e- 11 969-997 PD01719A 12.89 3.961e-10 128- 156 PD01719A 12.89 7.395e-10 1276-1304 PD01719A 12.89 1.222e-
		HMG-I and HMG-Y DNA-	09 1220-1248 BL00354C 6.61 8.397e-
657	BL00354	binding domain proteins (Ahook).	09 563-578
658	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook)	BL00354C 6.61 8.397e- 09 580-595 DM00215 19.43 2.174e-
659	DM0 0215	PROLINE-RICH PROTEIN 3.	13 539-572 DM00215 19.43 4.750e-12 549- 582 DM00215 19.43 9.824e-11 551-584 DM00215 19.43 2.929e- 10 548-581 DM00215 19.43 4.054e-1C 550- 583 DM00215 19.43 5.339e-10 552-585 DM00215 19.43 7.107e- 10 544-577
660	PR00688	XYLOSE ISOMERASE SIGNATURE	PR00688I 13.78 9.518e- 09 224-236 BL00027 26.43 5.950e-
661	ВЬ00027	'Homeobox' domain proteins.	23 249-292 PR00360B 13.61 7.158e-
662	PR00360	C2 DOMAIN SIGNATURE	10 596-610 PR00360B 13.61 7.158e-
663	PR00360	C2 DOMAIN SIGNATURE	10 596-610 PR00360B 13.61 7.158e-
664	PR00360	C2 DOMAIN SIGNATURE	10 596-610 PR00819B 10.83 8.988e-
666	PR00819	CEXX/CFQX SUPERFAMILY SIGNATURE	10 704-720 BL50040C 22.62 2.143e-
667	BL50040	Elongation factor 1 gamma chain profile.	16 135-178 PR00019B 11.36 1.360e-
668	PR00019	LEUCINE-RICH REPEAT SIGNATURE	09 139-153 PR00019A 11.19 1.667e-09 94-108 PR00019B 11.36 4.600e- 09 163-177
670	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 3.250e-10 681-694 BL00018 7.41 6.400e-10 717-730
672	PD00131	ATP-BINDING TRANSPORT TRANSMEMBR.	PD00131B 34.97 1.000e- 34 356-410 PD00131C 19.59 1.346e-26 504- 542 PR00667G 15.33 7.557e-
673	PR00667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE	10 106-123 PR00320A 16.74 4.857e-
674	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	13 593-608 PR00320B 12.19 4.115e-12 635- 650 PR00320C 13.01 8.435e-11 717-732 PR00320C 13.01 2.800e- 10 635-650 PR00320C 13.01 6.400e-10 593- 608 PR00320B 12.19 3.250e-09 593-608
675	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e- 13 572-587 PR00320B 12.19 4.115e-12 614-

SEQ ID NO	: ACCESSION	DESCRIPTION	RESULTS*
	NO.		
ļ			629 PR00320C 13.01
			8.435e-11 696-711
			PR00320C 13.01 2.800e-
			10 614-629 PR00320C
l			13.01 6.400e-10 572-
Ì			587 PR00320B 12.19
676	PR00019	LEUCINE-RICH REPEAT	3.250e-09 572-587
		SIGNATURE	PR00019A 11.19 9.667e- 09 249-263
679	PF00642	Zinc finger C-x8-C-x5-C-	PF00642 11.59 3.700e-
		x3-H type (and similar).	16 225-236 PF00642
			11.59 7.900e-12 187-
680			198
880	PR00308	TYPE I ANTIFREEZE	PR00308C 3.83 8.754e-
681	BL00019	PROTEIN SIGNATURE	10 286-296
001	PEOOLIA	Actinin-type actin-	BL00019D 15.33 4.200e-
682	PR00700	binding domain proteins. PROTEIN TYROSINE	19 227-257
	1200700	PHOSPHATASE SIGNATURE	PR00700D 12.47 4.000e-
687	PR00049	WILM'S TUMOUR PROTEIN	09 99-118
		SIGNATURE	PR00049D 0.00 8.500e-
689	BL01024	Protein phosphatase 2A	BL01024A 10.26 1.000e-
	-	regulatory subunit PR55	40 22-69 BL01024B
		proteins.	8.91 1.000e-40 86-127
	İ		BL01024C 7.80 1.000e-
			40 146-185 BL01024D
			13.22 1.000e-40 185-
			222 BL01024E 11.96
		1	1.000e-40 222-266
			BL01024F 9.42 1.000e-
			40 266-317 BL01024G 11.09 1.000e-40 317-
		1	349 BL01024H 13.88
			1.000e-40 389-442
691	BL00027	'Homeobox' domain	BL00027 26.43 8.071e-
692	BL00211	proteins. ABC transporters family	31 152-195
		proteins.	BL00211A 12.23 5.050e- 09 45-57
693	BL00211	ABC transporters family	BL00211A 12.23 5.050e-
		proteins.	09 45-57
694	BL00211	ABC transporters family	BL00211A 12.23 5.050e-
696		proteins.	09 58-70
696	BL00680	Methionine	BL00680 14.37 5.304e-
		aminopeptidase subfamily	17 173-195
697	BL00741	1 proteins.	
	2500/41	Guanine-nucleotide	BL00741B 14.27 3.418e-
		dissociation stimulators CDC24 family sign.	11 242-265
698	DM01930	2 kw FINGER SMCX SMCY	DM07.0307.45
		YDRO96W.	DM01930E 15.41 1.367e- 37 170-215 DM01930F
			14.16 B.232e-28 267-
			303 DM01930B 19.86
			9.163e-10 37-71
700	PR00869	DNA-POLYMERASE FAMILY X	PR00869A 12.80 1.281e-
701	7700010	SIGNATURE	16 245-263
.01	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 2.174e-
		SIGNATURE	10 77-91 PR00048A
	i	į	10.52 6.870e-10 133-
	1		147 PR00048A 10.52
			8.826e-10 105-119
	į		PR00048A 10.52 5.320e-
			09 161-175
702	BL00523	Sulfatases profeine	BI-00523E 10 27 2 222
702	BL00523	Sulfatases proteins.	BL00523E 19.27 2.565e-
702	BL00523	Sulfatases proteins.	25 326-356 BL00523A
702	BL00523	Sulfatases proteins.	25 326-356 BL00523A 13.36 5.050e-16 38-55
702	BL00523	Sulfatases proteins.	25 326-356 BL00523A

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		148 BL00523D 9.89
	ļ		1.844e-11 290-302
			BL00523G 9.46 5.500e-
			10 513-523 BL00523F
			10.85 6.351e-09 413-
	1	<u> </u>	424
703	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 8.412e-
703	1.1.00040	SIGNATURE	12 376-390 PR00048B
	1		6.02 1.000e-10 334-344
			PR00048B 6.02 1.474e-
			09 364-374
707	PD00787	SYNTHASE BIOSYNTHESIS	PD00787A 14.84 8.941e-
		TRANSFERASE.	14 66-82
708	PR00761	BINDIN PRECURSOR	PR00761E 14.32 8.500e-
		SIGNATURE	10 822-841
712	DM01354	kw TRANSCRIPTASE REVERSE	DM01354Y 10.69 4.977e-
	1	II ORF2.	38 425-465 DM01354X
		ļ.	13.86 7.300e-34 376-
	1		415 DM01354V 12.97
			4.923e-17 311-358
		!	DM01354W 12.64 5.596e-
			10 356-376
713	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 7.545e-
ł		dependent helicases	27 450-496 BL00039A
)		proteins.	18.44 2.537e-18 147-
•			186 BL00039C 15.63 2.216e-14 280-304
			BL00039B 19.19 1.947e-
1	1		•
			13 194-220 BL00383E 10.35 4.981e-
715	BL00383	Tyrosine specific	10 150-161
		protein phosphatases	10 130-161
		proteins. Sialyltransferase	PF00777C 18.60 4.035e-
717	PF00777	family.	21 106-161
718	DM00031	TMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e-
/10	DM00031	1	39 20-68 DM00031B
Į.		į	15.41 2.688e-28 84-118
ì		i	DM00031C 12.79 1.300e-
]	12 131-142
719	BL00243	Integrins beta chain	BL00243B 17.54 1.000e-
		cysteine-rich domain	40 131-172 BL00243C
	ł	proteins.	16.42 1.000e-40 172-
	Į	-	208 BL00243D 24.07
ł			1.000e-40 222-274
			BL00243F 22.63 1.000e-
Į.			40 314-358 BL00243I
1			31.77 6.571e-39 607-
			650 BL00243E 16.70
			3.077e-35 274-304.
1			BL00243G 21.38 3.625e-
	1		34 358-400 BL00243H
j	ì	•	17.53 5.235e-29 567-
	}	!	593 BL00243A 17.61
	1		3.250e-21 63-84
1	1		BL00243H 17.53 7.167e-
		1	16 477-503 BL30243H
ł	}	1	17.53 2.304e-11 524-
	- [1	550 BL00243H 17.53
1	1	\	5.304e-11 606-632
Ī	1	1	BL00243I 31.77 1.380e-
L			09 610-653
720	PR00217	43 KD POSTSYNAPTIC	PR00217C 10.91 8.022e-
		PROTEIN SIGNATURE	09 20-36
722	PR00704	CALPAIN CYSTEINE	PR00704D 11.05 5.909e-
1	1	PROTEASE (C2) FAMILY	34 135-161 PR00704F
1		SIGNATURE	13.61 7.000e-26 190-
1			218 PR00704E 12.55
1	1	}	8.071e-26 165-189

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.	DESCRIPTION	RESULTS*
			PR00704B 17.94 2.241e-
		1	23 75-98 PR00704A
İ			14.68 4.094e-19 30-54
	į	1	PR00704C 11.88 1.871e-
775	-		18 99-116
725	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e-
726	DD00104		09 169-187
120	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e-
727	PR00320	0.0000000000000000000000000000000000000	09 169-187
121	FR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 2.125e-
		REPEAT SIGNATURE	13 277-292 PR00320A
	ļ		16.74 1.310e-11 277-
			292 PR00320C 13.01
			4.522e-11 323-338 PR00320A 16.74 6.586e-
			11 323-338 PR00320B
			12.19 4.343e-10 323-
			338 PR00320B 12.19
	1		6.914e-10 277-292
731	PR00195	DYNAMIN SIGNATURE	PR00195A 11.94 8.627e-
	1		16 288-307 PR00195E
	}		9.82 3.912e-11 457-474
733	PF00642	Zinc finger C-x8-C-x5-C-	PF00642 11.59 9.082e-
		x3-H type (and similar).	10 787-798
738	BL00039	DEAD-box subfamily ATP-	BL00039A 18.44 2.565e-
		dependent helicases	28 26-65 BL00039D
		proteins.	21.67 2.105e-20 338-
			384 BL00039C 15.63
			9.100e-13 160-184
		1	BL00039B 19.19 9.617e-
739	BL01289	TSC-22 / dip / bun	11 73-99
	-202205	family proteins.	BL01289A 12.18 8.909e-
		process.	31 326-353 BL01289B 10.45 9.571e-17 353-
			383
742	BL01019	ADP-ribosylation factors	BL01019A 13.20 7.078e-
		family proteins.	12 41-81
743	BL00965	Phosphomannose isomerase	BL00965C 23.78 1.000e-
		type I proteins.	40 256-305 BL00965B
		ſ	17.77 1.600e-25 126-
		1	153 BL00965A 10.57
747	BL00021	V-J-1	6.400e-19 94-113
	DD00021	Kringle domain proteins.	BL00021D 24.56 4.563e-
		•	25 231-273 BL00021B
748	BL00612	Osteonectin domain	13.33 5.345e-21 60-78
		proteins.	BL00612B 11.35 2.034e- 11 93-126
749	PR00450	RECOVERIN FAMILY	PR00450C 12.22 6.880e-
		SIGNATURE	10 135-157
752	BL00795	Involucrin proteins.	BL00795C 17.06 6.000e-
			11 384-429 BL00795C
		1	17.06 9.444e-11 370-
		1	415
754	BL00051	Ribosomal protein L39e	BL00051 20.92 1.935e-
555		proteins.	16 4-50
755			
	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 7.723e-
760		0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.723e- 09 171-184
760	DM01970 BL01020	0 kw ZK632.12 YDR313C	DM01970B 8.60 7.723e- 09 171-184 BT-01020C 15.35 9.020e-
	BL01020	0 kw ZK632.12 YDR313C ENDOSOMAL III. SAR1 family proteins.	DM01970B 8.60 7.723e- 09 171-184 BM01020C 15.35 9.020e- 12 99-150
760 762		0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.723e- 09 171-184 BM01020C 15.35 9.020e- 12 99-150 BL00046 12.95 1.000e-
762	BL01020 BL00046	0 kw ZK632.12 YDR313C ENDOSOMAL III. SAR1 family proteins. Histone H2A proteins.	DM01970B 8.60 7.723e- 09 171-184 BI.01020C 15.35 9.020e- 12 99-150 BL00046 12.95 1.000e- 40 33-88
	BL01020	0 kw ZK632.12 YDR313C ENDOSOMAL III. SAR1 family proteins. Histone H2A proteins.	DM01970B 8.60 7.723e- 09 171-184 BL01020C 15.35 9.020e- 12 99-150 BL00046 12.95 1.000e- 40 33-88 PD02411 21.89 9.137e-
762	BL01020 BL00046 PD02411	0 kw ZK632.12 YDR313C ENDOSOMAL III. SAR1 family proteins. Histone H2A proteins. PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	DM01970B 8.60 7.723e- 09 171-184 BI.01020C 15.35 9.020e- 12 99-150 BL00046 12.95 1.000e- 40 33-88 PD02411 21.89 9.137e- 10 206-240
762 763	BL01020 BL00046	0 kw ZK632.12 YDR313C ENDOSOMAL III. SAR1 family proteins. Histone H2A proteins. PROTEIN TRANSCRIPTION REGULATION NUCLEAR. 'Homeobox' domain	DM01970B 8.60 7.723e- 09 171-184 BI.01020C 15.35 9.020e- 12 99-150 BL00046 12.95 1.000e- 40 33-88 PD02411 21.89 9.137e- 10 206-240 BL00027 26.43 8.800e-
762 763 764	BL01020 BL00046 PD02411 BL00027	0 kw ZK632.12 YDR313C ENDOSOMAL III. SAR1 family proteins. Histone H2A proteins. PROTEIN TRANSCRIPTION REGULATION NUCLEAR. 'Homeobox' domain proteins.	DM01970B 8.60 7.723e- 09 171-184 BI.01020C 15.35 9.020e- 12 99-150 BL00046 12.95 1.000e- 40 33-88 PD02411 21.89 9.137e- 10 206-240 BL00027 26.43 8.800e- 29 417-460
762 763 764	BL01020 BL00046 PD02411	0 kw ZK632.12 YDR313C ENDOSOMAL III. SAR1 family proteins. Histone H2A proteins. PROTEIN TRANSCRIPTION REGULATION NUCLEAR. 'Homeobox' domain	DM01970B 8.60 7.723e- 09 171-184 BL01020C 15.35 9.020e- 12 99-150 BL00046 12.95 1.000e- 40 33-88 PD0241 21.89 9.137e- 10 206-240 BL00027 26.43 8.800e- 29 417-460 BL01208B 15.83 6.063e-
762 763 764	BL01020 BL00046 PD02411 BL00027	0 kw ZK632.12 YDR313C ENDOSOMAL III. SAR1 family proteins. Histone H2A proteins. PROTEIN TRANSCRIPTION REGULATION NUCLEAR. 'Homeobox' domain proteins.	DM01970B 8.60 7.723e- 09 171-184 BI.01020C 15.35 9.020e- 12 99-150 BL00046 12.95 1.000e- 40 33-88 PD02411 21.89 9.137e- 10 206-240 BL00027 26.43 8.800e- 29 417-460

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
SEQ ID NO.	NO.		
			180 BL01208B 15.83 4.162e-09 85-100
770	BL00031	Nuclear hormones	BL00031A 19.55 9.571e-
,,,	2200032	receptors DNA-binding	32 ·208-241 BL00031B
		region proteins.	22.25 5.500e-27 242-
772	PRO0449	TRANSFORMING PROTEIN P21	274 PR00449A 13.20 1.450e-
1,72	PROUTTS	RAS SIGNATURE	18 4-26 PR00449E
			13.50 3.520e-14 142-
	ł		165 PR00449C 17.27 3.032e-13 44-67
			PR00449D 10.79 8.579e-
			13 107-121 PR00449B
773	BL00523	Sulfatases proteins.	14.34 3.455e-11 27-44 BL00523E 19.27 9.333e-
//3	BL00523	Saliacases processes.	23 299-329 BL00523A
			13.36 2.200e-13 47-64
			BL00523B 8.64 2.607e- 13 91-103 BL00523D
ļ			9.89 7.923e-12 224-236
}		}	BLC0523C 12.64 4.512e-
:			10 141-152 BL00523F 10.85 5.821e-10 373-
į.			384
775	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e- 09 568-585
776	BL00028	domain proteins. Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
	2200020	domain proteins.	09 621-638
777	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
778	BL00030	domain proteins. Eukaryotic RNA-binding	BL00030A 14.39 8.412e-
'''	1220000	region RNP-1 proteins.	11 322-341 BL00030A
	}		14.39 7.000e-10 220- 239
779	PR00079	GLUCOSE-6-PHCSPHATE	PR00079B 12.98 2.929e-
		DEHYDROGENASE SIGNATURE	26 193-222 PR00079E
	1		16.65 4.150e-23 348- 375 PR00079C 8.68
1	}		6.351e-16 246-264
			PR00079D 13.51 7.070e- 16 264-281 PR00079A
			16.12 6.769e-13 169-
			183
781	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 9.250e- 17 10-35 BL00215A
		cranster procerns.	15.82 6.000e-16 221-
,			246 BL00215A 15.82
1			7.857e-12 108-133 BL00215B 10.44 9.526e-
	-		11 168-181
783	PD00239	PROTEIN SH3 DOMAIN	PD00289 9.97 6.276e-09
785	BL00690	REPEAT PRESYNA. DRAH-box subfamily ATP-	159-173 BL00690B 13.38 1.000e-
1		dependent helicases	12 147-165 BL00690A
		proteins.	6.87 5.320e-10 114-124 BL00690C 7.51 3.189e-
	1		09 218-228
786	PR00449	TRANSFORMING PROTEIN P21	PR00449C 17.27 8.500e-
1	1	RAS SIGNATURE	16 50-73 PR00449A 13.20 5.235e-14 8-30
			PR00449E 13.50 2.853e-
	1		11 150-173 PR00449D
			10.79 1.545e-09 111- 125
788	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 8.767e-
		PROTEIN.	10 1-21
790	BL00915	Phosphatidylinositol 3-	BL00915C 22.43 9.182e- 39 725-764 BL00915B
1	i	and 4-kinases proteins.	73 143-104 BHAA3T3B

SEQ ID	NO: ACCESSION	DESCRIPTION	RESULTS*
<u> </u>	NO.		
			22.78 5.050e-33 633-
			671 BL0091SD 27.02 1.529e-21 795-831
	İ	1	BL00915A 10.09 1.000e-
791	PR00208		13 395-407
,,,,	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	
		SOFERFAMILI SIGNATURE	10 120-138 PR0020BA
			12.59 6.294e-10 121- 139 PR00208A 12.59
		1	6.294e-10 122-140
			PR00208A 12.59 6.294e-
			10 123-141 PR00208A
			12.59 6.294e-10 124- 142 PR00208A 12.59
			6.294e-10 125-143
		•	PR00208A 12.59 6.294e-
		1	10 126-144 PR00208A
		İ	12.59 6.294e-10 127- 145 PR00208A 12.59
			6.294e-10 128-146
	İ		PR00208A 12.59 6.294e-
		,	10 129-147 PR00208A
		'	12.59 7.411e-09 130- 148 PR00208A 12.59
•			7.658e-09 131-149
		ĺ	PR00208A 12.59 7.904e-
			09 132-150 PR00208A
		ĺ	12.59 8.274e-09 118- 136 PR00208A 12.59
			8.274e-09 119-137
795	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 5.034e-
			16 302-320 PR00205A
	1		14.73 1.257e-11 284- 300 PR00205C 13.65
~~~			1.333e-11 337-352
796	BL00412	Neuromodulin (GAP-43)	BL00412D 16.54 4.000c
		proteins.	12 196-247 BL00412D
			16.54 5.705e-11 197- 248 BL00412D 16.54
			7.848e-10 199-250
			BL00412D 16.54 1.827e-
		1	09 195-246 BL00412D
			16.54 1.918e-09 194- 245 BL00412D 16.54
		<b>1</b> .	2.102e-09 201-252
797	BL00021	Kringle domain proteins.	BL00021B 13.33 6.339e-
799	BL01052	(0)	13 40-58
	2401032	Calponin family repeat proteins.	BL01052C 18.51 1.000e-
			40 87-127 BL01052A 16.12 1.529e-32 3-35
		•	BL01052B 15.31 1.257e-
			25 52-78 BL01052D
			10.26 5.737e-25 174-
300	BL00348	p53 tumor antigen	194 BL00348F 23.19 3.714e-
		proteins.	09 197-240
301	BF0030a	Vertebrate galactoside-	BL00309C 18.65 1.621e-
902	PR00245	binding lectin proteins.	09 62-87
	FR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245D 10.47 5.224e-
04	PF00774	Dihydropyridine	09 187-199
		sensitive L-type calcium	PF00774A 16.47 8.457e- 10 110-156
00		channel (Beta subuni.	220 250
08	PR00667	RETINAL PIGMENT	PR00667C 11.71 9.875e-
		EPITHELIUM-RETINAL GPCR	09 12-28
10	PD02346	PHOTOSYSTEM II PROTEIN	PD02346B 40 00 - 2-2
		PRECURSOR	PD02346F 12.89 4.340e- 09 317-354
			U- 31/-334

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	<del> </del>	PHOTOSYNTHESIS.	
811	BL00685	CBF-A/NF-YB subunit	BL00685B 14.41 6.779e-
		proteins.	14 54-95 BL00685A 11.22 4.798e-13 5-54
812	PROCOBO	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE	PRO0080A 9.32 9.419e-
813	BL00357	Histone H2B proteins.	BL00357 7.74 1.988e-17
815	PD00056	PROTEIN ZINC-FINGER	PD00066 13.92 7.923e-
013	PDOVOSO	METAL-BINDI.	15 158-171 PD00066
			13.92 5.200e-14 46-59
		1	PD00066 13.92 7.000e-
		Į.	·14 18-31 PD00066
			13.92 7.000e-13 130- 143 PD00066 13.92
			7.500e-13 214-227
		· ·	PD00066 13.92 9.000e-
			13 102-115 PD00066
	1		13.92 4.429e-12 186-
			199 PD00066 13.92
			1.783e-11 74-87
816	BL01195	Peptidyl-tRNA hydrolase	BL01195C 20.12 3.348e-
		proteins.	20 100-139 BL00520A 6.21 6.471e-
820	BLC0520	Interleukin-10 family	09 1-14
		proteins. Ubiquitin carboxyl-	BL00972A 11.93 8.113e-
822	BL00972	terminal hydrolases	09 224-242
		family 2 proteins.	
825	PR00876	NEMATODE METALLOTHIONEIN	PR00876B 7.66 2.268e-
025	(Moos)	SIGNATURE	10 101-115
829	PD02855	FLAVOPROTEIN PROTEIN	PD02855A 18.37 4.732c-
	1	DNA/PANTOTHEN.	28 88-124 PD02855B
			8.36 6.478e-09 132-142 PR00405B 11.83 7.000e-
830	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	21 44-62 PR00405C
		PROIEIN SIGNATORE	19.41 1.000e-13 65-87
		1	PR00405A 17.71 7.283e-
			13 25-45
831	2R00019	LEUCINE-RICH REPEAT	PR00019A 11.19 1.000e-
		SIGNATURE	09 47-61 PR00019B
			150 PRO0019B 11.36
			3.880e-09 44-58
832	PR00011	TYPE III EGF-LIKE	PR00011B 13.08 3.438e-
032	PROODEE	SIGNATURE	16 164-183 PR00011D
			14.03 6.850e-16 164-
	į		183 PRO0011A 14.06
	1		8.364e-14 164-183 PR00011C 24.25 5.415e-
	<b>j</b>		12 231-260 PR00011D
	1		14.03 9.852e-11 212-
			231
834	PD00306	PROTEIN GLYCOPROTEIN	PD00306A 10.26 7.000e-
33.2	1.2.3.00	PRECURSOR RE.	12 232-246
835	PD00306	PROTEIN GLYCOPROTEIN	PD00306A 10.26 4.000e-
	<b>,</b>	PRECURSOR RE.	10 290-304
836	PD00306	PROTEIN GLYCOPROTEIN	PD00306A 10.26 7.000e-
		PRECURSOR RE.	12 216-230
837	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.898e- 09 78-111
		PROPERTY MICH CATA	PD02784B 26.46 8.302e-
839	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	09 73-116
840	PR00700	PROTEIN TYROSINE	PR00700B 16.80 5.091e-
040	2800700	PHOSPHATASE SIGNATURE	22 369-390 PR00700D
]			12.47 5.765e-21 491-
1	1	1	510 PR00700C 13.17
1			4.750e-14 449-467
1	1		PR00700F 11.18 8.500e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			11 538-549 PR00700E 17.57 3.100e-10 522- 538
841	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 5.404e- 13 134-153
844	PD02785	PROTEIN RIBOSOMAL 60S L22 RNA-BINDING HEP.	PD02785B 14.43 1.000e- 40 58-112 PD02785A 15.23 1.915e-28 8-57
845	BLC0826	MARCKS family proteins.	BL00826C 7.63 6.738e- 09 203-230
846	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.429e- 10 15-24
849	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.000e- 08 340-349
850	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 6.506e-
851	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 7.000e- 16 246-280
852	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 1.000e- 40 723-778 BL00420B 22.67 1.321e-38 933- 988 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e- 27 587-642 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 830-885 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 808- 819 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e- 11 141-152 BL00420C 11.90 5.119e-11 1018- 1029 BL00420C 11.90 7.955e-10 567-578
-	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 1.000e- 40 756-811 BL00420B 22.67 1.321e-38 966- 1021 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e- 27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 863-918 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 841- 852 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e- 11 141-152 BL00420C 11.90 5.119e-11 1051- 1062 BL00420C 11.90

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		7.955e-10 567-578
	PR00388	3',5'-CYCLIC NUCLEOTIDE	PR00388A 10.45 2.778e-
357	PR00388	CLASS II	09 64-83
		PHOSPHODIESTERASE	
	Į.	SIGNATURE	
359	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 2.929e-
		region RNP-1 proteins.	13 37-56 BL00030B
			7.03 1.900e-11 167-177
			BL00030A 14.39 2.000e-
			10 128-147
861	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.250e- 17 23-41 PR00988C
		Ì	13.64 8.714e-16 107-
		ļ	123 PR00988F 12.23
			7.828e-15 198-212
			PR00988E B.27 9.769e-
	)	į	12 176-188 PR00988D
		1	5.95 8.250e-11 163-174
		i	PR00988B 11.60 4.512e-
	İ		10 60-72
863	BL00215	Mitochondrial energy	BL00215B 10.44 8.071e-
		transfer proteins.	12 41-54
864	PR00775	90 KD HEAT SHOCK PROTEIN	PR00775E 8.06 1.000e-
		SIGNATURE	24 198-221 PR00775B
	1	1	3.52 1.837e-23 107-130
			PR00775D 8.91 4.484e-
			17 171-189 PR00775A 9.90 8.342e-17 86-107
			PR00775C 10.68 9.379e-
	ì	Í	17 153-171 PR00775G
	1		10.64 6.850e-15 267-
			286 PR00775F 12.76
			6.769e-14 249-267
866	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 9.460e-
850	Briozood		09 89-121
867	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 5.596e-
	-	ZINC-FINGER METAL-	29 14-53
		BINDING NU.	BL01287A 17.95 2.688e-
868	BL01287	RNA 3'-terminal	26 16-48
		phosphate cyclase	26 16-48
		proteins.  PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.464e-
869	DM00215	PROLINE-RICH PROTEIN 3.	10 304-337
		Histone H2A proteins.	BL00046 12.95 1.000e-
872	BL00046	nistone nza proceins.	40 30-85
874	BL00188	Biotin-requiring enzymes	BL00188 30.29 9.036e-
8/4	DITOATOR	attachment site	32 665-711
1		proteins.	_
876	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
1		domain proteins.	09 298-315
877	PD02102	SUBUNIT E V-ATPASE	PD02102A 16.74 4.176e-
1	1	VACUOLAR ATP SYNTHASE	10 97-141
1	•	HYDROL.	
879	BL01189	Ribosomal protein S12e	BL01189A 14.27 1.000e-
1	1	proteins.	40 35-71 BL01189B 13.49 1.000e-40 71-125
L			BL00284C 28.56 6.400e-
882	BL00284	Serpins proteins.	25 62-104 BL00284B
1			17.99 6.182e-12 35-56
			BL00216B 27.64 4.375e-
889	BL00216	Sugar transport	21 35-85
		proteins.	PR00391E 12.50 7.785e-
896	PR00391	PHOSPHATIDYLINOSITOL TRANSFER PROTEIN	15 211-231 PR00391B
F		SIGNATURE	8.39 1.000e-13 83-104
	1	3. GRALOKE	PR00391D 12.21 9.328e-
1			13 191-207 PR00391A
1	1		7.83 5.390e-11 16-36
I			PR00327C 6.37 5.247e-

SEQ ID NO:	ACCESSION	DESCRIPTION	
	NO.		RESULTS*
898		SIGNATURE	09 313-328
898	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 7.800e-
		dependent helicases	26 386-432 BL00039A
	1	proteins.	18.44 6.674e-16 113-
1			152 BL00039B 19.19
İ	1	1	1.947e-13 153-179
		1	BL00039C 15.63 9.460e-
-			11 236-260
901	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 8.200e-
ļ	1	METAL-BINDI.	16 254-267 PD00066
	i	İ	13.92 8.200e-16 282-
			295 PD00066 13.92
	1		8.200e-16 310-323
•			PD00066 13.92 8.200e-
	)	,	16 366-379 PD00066
	1		13.92 8.200e-16 394-
			407 PD00066 13.92
			8.200e-14 338-351
902	BI-01115	GTP-binding nuclear	BL01115A 10.22 9.321e-
	1	protein ran proteins.	11 6-50
903	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 9.160e-
			09 97-111
904	PR00381	KINESIN LIGHT CHAIN	PR00381E 8.75 6.586e-
		SIGNATURE	25 335-356 PR00381B
			18.17 2.667e-24 204-
			224 PR00381A 9.55
			2.800e-24 107-125
	1	1	PR00381C 12.48 4.522e-
			24 226-245 PR00381D
			13.94 1.084e-22 291-
	1		309 PR00381F 9.13
			3.288e-22 370-392
			PR00381F 9.13 7.181e-
			13 286-308 PR00381E
			8.75 4.066e-11 251-272
			PR00381E 8.75 7.033e-
			11 293-314 PR00381E
			8.75 8.364e-10 377-398
			PR00381D 13.94 5.230e-
		·	09 333-351 PR00381C
	1		12.48 7.120e-09 310-
555			329
906	PR00345	STATHMIN FAMILY	PR00345C 4.54 8.557e-
000		SIGNATURE	09 525-549
907	PR00345	STATHMIN FAMILY	PR00345C 4.54 8.557e-
000		SIGNATURE	09 513-537
908	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 9.308e-11
A		proteins proteins.	144-155
910	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 2.800e-
		ZINC-FINGER METAL-	30 48-87
		BINDING NU.	1
912	BL01104	Ribosomal protein L13e	BL01104C 15.14 6.000e-
		proteins.	09 364-392
922	3L00678	Trp-Asp (WD) repeat	BL00678 9.67 3.842e-09
		proteins proteins.	500-511
923	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 2.500e-
;		REPEAT SIGNATURE	09 323-338 PR00320C
1			13.01 5.500e-09 187-
			202
924	PD02181	PROTOCHLOROPHYLLIDE	PD02181D 12.85 8.609e-
		REDUCTASE PHOTOSYNT.	09 36-54
26	BL00019	Actinin-type actin-	BL00019C 14.66 7.453e-
		binding domain proteins.	
		voluatii proceins.	25 108-144 BL00019B
l		I	13.34 6.510c-11 61-84
			BL00019D 15.33 9.338e-
1		1	11 205-235 BL00019A
28	BL00678	Trp-Asp (WD) repeat	12.56 2.373e-10 34-45
		1 5 vob (un) Lehear	BL00678 9.67 9.308e-11

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	1	proteins proteins.	273-284 BL00678 9.67
			1.600e-10 314-325 BL00678 9.67 7.600e-10
			360-371 BL00678 9.67
1			8.579e-09 206-217
929	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 1.857e- 10 137-146
930	BL01085	(RING finger), proteins. Ribulose-phosphate 3-	BL01085D 16.55 4.600e-
930	PROTOGS	epimerase family	24 134-165 BL01085B
		proteins.	10.15 5.680e-22 30-52
		1	BL01085E 18.87 8.676e- 20 172-202 BL01085C
	İ		21.81 2.038e-14 66-97
931	BL01085	Ribulose-phosphate 3-	BLC1085D 16.55 4.600e-
		epimerase family	24 152-183 BL01085B 10.15 5.680e-22 30-52
		proteins.	BL01085E 18.87 8.676e-
			20 190-220 BL01085C
			21.81 2.038e-14 66-97
933	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301A 10.24 6.400e- 09 160-171
936	PF00168	C2 domain proteins.	PF00168C 27.49 4.000e-
			12 336-362
937	BL00415	Synapsins proteins.	BL00415N 4.29 9.519e-
940	PR00862	PROLYL OLIGOPEPTIDASE	PRO0862D 16.17 4.086e-
		SERINE PROTEASE (S9A)	09 63-84
		SIGNATURE RNA methyltransferase	BL01230B 11.62 2.373e-
945	BL01230	trmA family proteins.	09 407-420
948	BL00479	Phorbol esters /	BL00479B 12.57 7.429e-
		diacylglycerol binding	18 52-68 BL00479A 19.86 2.200e-13 26-49
949	BL00678	domain proteins.  Trp-Asp (WD) repeat	BL00678 9.67 1.474e-09
	22000.0	proteins proteins.	100-111
954	PD01311	PROTEIN OXIDOREDUCTASE	PD01311A 30.23 5.909e-
955	PF00651	NAD INTERGENIC RE. BTB (also known as BR-	PF00651 15.00 3.250e-
555		C/Ttk) domain proteins.	12 47-60
956	PF00651	BTB (also known as BR-	PF00651 15.00 3.250e-
957	BL00379	C/Ttk) domain proteins.	12 47-60 BL00379 24.64 1.610e-
737	BE00379	phosphatidyltransferases	15 111-148
		proteins.	
959	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 1.884e-
960	BL01115	GTP-binding nuclear	BL01115A 10.22 3.438e-
		protein ran proteins.	14 110-154
962	BL00061	Short-chain	BL00061B 25.79 6.586e-
		dehydrogenases/reductase s family proteins.	13 130-230
963	PR00502	MUTT DOMAIN SIGNATURE	PR00502A 15.06 8.200e-
			11 210-225 PR00308A 5.90 7.035e-
966	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	09 55-70
967	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 1.286e-
1	l l	PROTEIN.	12 104-124 DM01206B
		1	10.69 5.299e-11 23-43 DM01206B 10.69 8.274e-
			10 73-93 DM01206B
		•	10.69 3.962e-09 108-
]	Į		128 DM01206B 10.69 5.671e-09 38-58
969	PF01008	Initiation factor 2	PF01008B 25.59 4.724e-
	1202000	subunit.	31 417-460 PF01008C
			12.25 5.333e-18 506-
1			526 PF01008A 20.14 5.875e-15 369-390
L			10.0736 20 305-374

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970	BL01277	Ribonuclease PH proteins.	BL01277C 10.18 7.648e- 10 112-143 BL01277A
975	BL01159	WW/rsp5/WWP domain proteins.	17.39 9.806e-10 40-78  BL01159 13.85 3.605e- 12 130-145 BL01159 13.85 4.122e-10 171- 186
977	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791C 20.98 2.235e- 09 55-94
978	BL01167	Ribosomal protein L17 proteins.	BL01167B 20.66 8.258e- 19 88-127
979	BL00478	LIM domain proteins.	BL00478B 14.79 9.357e- 13 33-48 BL00478B 14.79 7.250e-12 98-113
980	PR00312	CALSEQUESTRIN SIGNATURE	PR00312E 8.32 3.423e- 36 169-199 PR00312I 15.78 5.286e-35 332- 361 PR00312F 15.06 5.865e-35 199-229 PR00312H 13.31 8.313e- 35 263-291 PR00312J 13.73 5.688e-34 363- 392 PR00312D 9.43 2.636e-33 128-158 PR00312C 15.14 8.839e- 33 92-122 PR00312B 15.08 8.941e-33 62-92 PR00312G 11.11 6.657e- 32 230-258 PR00312A 11.70 6.914e-27 35-59
981	PF00992	Troponin.	PF00992A 16.67 8.816e-
982	PR00299	ALPHA CRYSTALLIN SIGNATURE	PR00299F 13.20 2.367e- 09 127-149
983	BL01150	Respiratory-chain NADH dehydrogenase 20 Kd subunit proteins.	BL01150B 17.16 1.000e- 40 156-202 BL01150A 14.10 8.200e-39 100-
986	BL00795	Involucrin proteins.	BL00795C 17.06 7.211e- 14 4-49 BL00795C 17.06 1.778e-11 1-46 BL00795C 17.06 3.407e- 10 14-59 BL00795C 17.06 7.802e-10 2-47 BL00795C 17.06 8.640e- 10 19-64 BL00795C 17.06 7.400e-09 11-56 BL00795C 17.06 7.800e- 09 3-48
987	BL00939	Ribosomal protein Lle proteins.	BL00939F 17.27 5.393e- 09 810-840
988	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e- 11 525-541
989	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e- 11 497-513
994	BL00027	'Homeobox' domain proteins.	BL00027 26.43 2.500e- 25 146-189
997	BL01304	ubiH/COQ6 monooxygenase family proteins.	BL01304A 8.05 3.893e-
998	DM01767	5 TRANSMITTER DOMAIN.	DM01767B 10.07 7.868e-
1000	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926C 16.07 1.750e- 24 73-94 PR00926D 10.53 3.250e-23 126- 145 PR00926F 17.75 6.211e-23 217-240 PR00926E 11.70 6.625e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
SEQ ID NO.	NO.		
, , , , , , , , , , , , , , , , , , , ,			20 174-193 PR00926B 16.07 2.125e-18 24-39 PR00926A 10.41 1.00Ce- 15 11-25 PR00926F 17.75 5.565e-09 120-
			143
1005	BL00406	Actins proteins.	BL00406B 5.47 1.000e- 40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406D 12.58 3.700e- 40 270-325 BL00406E 8.44 7.375e-38 327-377 BL00406A 9.95 3.348e- 29 11-46
1006	BL00406	Actins proteins.	BL00406B 5.47 1.000e- 40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406E 8.44 1.000e- 35 248-298 BL00406A 9.95 3.348e-29 11-46
1007	PR00304	TAILLESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE	PR00304D 11.04 8.714e- 22 384-407 PR00304C 8.69 4.667e-20 98-118 PR00304B 11.60 7.577e- 19 68-87 PR00304A 9.20 3.382e-16 46-63 PR00304E 7.79 6.870e- 13 418-431
1009	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.929e- 32 9-48
1011	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2,929e- 32 68-107
1012	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.143e- 10 64-73
1016	PD01168	SYNTHETASE LIGASE PROTEIN ALANYL.	PD01168H 12.08 1.000e- 11 174-194
1018	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 1.391e- 32 261-302 PD00930A 25.62 9.550e-22 157- 183
1022	BL00175	Phosphoglycerate mutase family phosphohistidine proteins.	BL00175A 15.42 5.179e- 12 6-26 BL00175C 23.75 8.062e-10 79-111
1025	PR00305	14-3-3 PROTEIN ZETA SIGNATURE	PR00305D 16.34 1.439e- 10 158-185
1026	BL00353	HMG1/2 proteins.	BL00353B 11.47 2.436e- 18 238-288 BL00353C 14.83 8.844e-11 288- 335
1028	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.310e- 33 43-91
1033	PF00580	UvrD/REP helicase.	PF00580A 13.37 4.720e- 09 111-133
1034	PR00413	HALOACID DEHALOGENASE/EPOXIDE HYDROLASE FAMILY SIGNATURE	PR00413E 15.78 3.429e- 09 154-171
1037	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.657e- 09 5-44
1038	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	PD01796 15.01 4.259e- 11 55-82
1039	BL00299	Ubiquitin domain proteins.	BL00299 28.84 9.036e- 09 17-69
1040	PR00970	ARGININE ADP- RIBOSYLTRANSFERASE	PR00970A 17.73 6.143e- 20 56-78 PR00970D

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		SIGNATURE	9.96 2.154e-18 154-171 PR00970F 12.30 1.000e- 16 224-241 PR00970G 9.97 9.229e-15 242-258 PR00970B 16.37 1.290e- 13 86-105 PR00970C 11.05 1.643e-11 115- 130 PR00970E 11.23
1042	BL00678	Trp-Asp (WD) repeat	9.820e-11 202-218 BL00678 9.67 2.200e-10
		proteins proteins.	243-254
1043	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.786e- 13 114-128 PR00048A 10.52 1.000e-09 172- 186
1045	BL00615	C-type lectin domain proteins.	BL00615A 16.68 1.720e- 11 218-236 BL00615B 12.25 1.857e-10 317- 331
1046	BL01092	Adenylate cyclases class-I proteins.	BL01092N 13.54 8.924e- 10 3-40
1047	BL01216	ATP-citrate lyase / succinyl-CoA ligases family proteins.	BL01216D 21.75 4.316e- 28 314-344 BL01216A 13.91 1.000e-10 97-112
1049	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 7.618e-
1050	BL01073	Ribosomal protein L24e proteins.	BL01073 24.30 1.000e- 40 12-62
1054	BL00571	Amidases proteins.	BL00571 25.69 5.875e- 31 160-212
1055	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 5.235e- 11 98-117 BL00030B 7.03 4.316e-09 137-147
1058	BL00223	Annexins repeat proteins domain proteins.	BL00223C 24.79 8.754e- 23 262-317 BL00223A 15.59 9.478e-14 46-80 BL00223A 15.59 5.557e-
1060	BL00027	'Homeobox' domain proteins.	11 118-152 BL00027 26.43 3.455e- 35 158-201
1064	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 6.211e- 13 280-296
1065	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101
1066	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PRO0326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236
1071	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 8.518e- 11 164-197
1072	PF00856	SET domain proteins.	PF00856A 26.14 5.976e- 09 350-387
1075	BL01009	Extracellular proteins SCF/Tpx-1/Ag5/FR-1/Sc7 proteins.	BL01009D 14.19 4.300e- 20 127-148 BL01009A 13.75 6.586e-13 57-75 BL01009E 13.50 1.439e- 11 159-175
1077	PR00724	CARBOXYPEPTIDASE C SERINE PROTEASE (S10) FAMILY SIGNATURE	PR00724A 10.91 1.000e- 08 366-379
1078	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 1.000e- 12 170-195 BL00215A 15.82 7.529e-10 79-104
1079	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 4.316e-09

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	- NO.	proteins proteins.	298-309
1081 .	BL00326	Tropomyosins proteins.	BL00326A 14.01 7.398e- 10 23-57
1094	B1.00460	Glutathione peroxidases selenocysteine proteins.	BL00460A 28.67 3.204e- 18 57-92 BL00460B 9.73 6.400e-13 100-118 BL00460D 16.89 9.143e- 12 162-182 BL00460C 14.35 5.500e-09 133- 156
1095	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e- 22 67-105 PD02811B 17.07 2.263e-21 118- 151 PD02811C 13.25 5.696e-13 154-167
1096	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e- 22 60-98 PD02811B 17.07 2.263e-21 111- 144 PD02811C 13.25 5.696e-13 147-160
1097	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.143e- 09 200-216
1105	PF00881	Nitroreductase family.	PF00881A 27.15 9 229e- 13 111-147
1109	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 3.077e- 10 15-37 PR00449E 13.50 1.857e-09 185- 208 PR00449D 10.79 8.364e-09 131-145
1115	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 5.737e- 20 42-60 PR00405A 17.71 2.703e-17 23-43 PR00405C 19.41 6.902e- 10 53-85
1116	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1117	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1120	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 4.857e- 10 290-306
1123	PR00412	EPOXIDE HYDROLASE SIGNATURE	PR00412F 18.76 9.526e- 12 301-324
1125	PR00186	HEMERYTHRIN SIGNATURE	PR00186A 13.62 2.800e- 09 87-101
1129	BL00170	Cyclophilin-type peptidyl-prolyl cis- trans isomerase signatur.	BL00170C 18.49 3.077e- 33 84-129 BL00170B 20.97 6.838e-25 37-77 BL00170A 17.08 3.455e- 15 10-37
1131	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80
1132	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09 29-40
1133	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09 29-40
1136	BL00990	Clathrin adaptor complexes medium chain proteins.	BL00990C 18.78 4.176e- 38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e- 27 157-187 BL00990D 16.13 5.320e-18 403- 422
1137	PR00314	CLATHRIN COAT ASSEMBLY PROTEIN SIGNATURE	PR00314B 15.68 8.000e- 34 100-128 PR00314D 9.66 3.531e-33 233-261 PR00314C 16.05 8.909e-

SEQ ID N		DESCRIPTION	RESULTS*
	NO.		122 150 100
			32 159-188 PR00314A 14.53 1.281e-22 13-34
1139	BL01115	GTP-binding nuclear	BL01115A 10.22 6.364e-
1141	BL00107	protein ran proteins.  Protein kinases ATP-	13 13-57
		binding region proteins.	BL00107A 18.39 4.00Ge- 19 451-482 BL00107B
	1		13.31 3.077e-12 519-
1148	PR00685	MONIOCO TO TO TO TO TO TO TO TO TO TO TO TO TO	535
	1200000	TRANSCRIPTION INITIATION FACTOR IIB SIGNATURE	PR00685A 13.62 4.676e- 09 21-42
1155	PD01652	RECEPTOR CELL NK	PD01652B 8.50 9.396e-
		GLYCOPROTEIN IMMUNOGLOB.	10 522-574 PD01652B
1157	PD02894	HYDROLASE N4- PRECURSOR	8.50 9.463e-10 740-792
		PROTEIN SIGNAL BE.	PD02894A 21.96 7.873e- 28 81-127 PD02894B
			13.93 1.188e-27 178-
1159	BL00623		211
1139	BE00653	GMC oxidoreductases proteins.	BL00623E 15.00 3.531e-
		proceins.	20 391-414 BL00623C 10.86 4.240e-20 155-
43.63			176
1161	PD01937	DNA PROTEIN POLYMERASE ENDONUCLEASE DNA	PD01937A 6.68 3.475e-
1162	PD01937	DNA PROTEIN POLYMERASE	09 330-341 PD01937A 6.68 3.475e-
		ENDONUCLEASE DNA	09 221-232
1163	PR00624	HISTONE H5 SIGNATURE	PR00624D 11.94 7.455e-
			10 214-239 PR00624D
			11.94 1.961e-09 312-
1167	BL00226	Intermediate filaments	BL00226B 23.86 7.384e-
1177	BL01032	proteins.	09 302-350
	BEOLOSE	Protein phosphatase 2C proteins.	BL01032G 8.33 1.422e- 10 34-48
1178	PR00320	G-PROTEIN BETA WD-40	PR00320A 16.74 1.794e-
		REPEAT SIGNATURE	10 205-220 PR00320C
			13.91 7.840e-10 205- 220 PR00320B 12.19
			8.457e-10 35-50
			PR00320A 16.74 7.146e-
			09 35-50 PR00320B
1180	PR00454	ETS DOMAIN SIGNATURE	12.19 9.100e-09 79-94 PR00454D 10.89 4.150e-
1181		ſ	19 765-784
1191	BL00291	Prion protein.	BL00291A 4.49 8.962e-
1184	BL00720	Guanine-nucleotide	11 152-187 BL00720B 16.57 4.103e-
		dissociation stimulators	18 1089-1113
1185	BL00215	CDC25 family sign.	1
1103	BT00512	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.553e-
		cramater proteins.	13 204-229 BL00215A 15.82 1.429e-12 11-36
			BL00215A 15.82 9.809e-
1187	BL00983	1	11 104-129
	5000303	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 2.761e- 10 77-93
1188	BL00878	Orn/DAP/Arg	BL00878B 10.95 6.000e-
	[	decarboxylases family 2	16 189-204 BL00878C
	ļ	pyridoxal-P attachment	17.74 8.435e-15 225-
	1	si.	245 BL00878F 19.67 3.625e-13 379-402
			BL00878D 16.56 1.621e-
1191	- DD00000		09 270-289
-+2T	PD02939	PROTEIN GLUTATHIONE	PD02939B 10.10 2.723e-
		SYNTHETASE SY.	12 203-220 PD02939C
			20.01 1.000e-11 224- 252
193	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			8.54 7.652e-28 149-174 PR00345C 4.54 9.100e- 28 101-125 PR00345D 10.97 1.964e-24 125- 149 PR00345A 13.46 5.645e-16 43-62
1194	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800e- 28 108-137 PR00345E 8.54 7.652e-28 185-210 PR00345C 4.54 9.100e- 28 137-161 PR00345D 10.97 1.964e-24 161- 185 PR00345A 13.46 5.645e-16 79-98
1195	PF00995	Secl family.	PF00995B 17.37 1.120e- 13 224-264
1196	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 6.738e- 11 15-47
1197	BL01298	Dihydrodipicolinate reductase proteins.	BL01298A 13.90 5.959c- 09 51-73
1203	BL00061	Short-chain dehydrogenases/reductase s family proteins.	BL00061B 25.79 1.000e- 14 152-190
1204	PR00118	BETA-LACTAMASE CLASS A SIGNATURE	PRO0118F 16.42 9.386e- 09 213-229
1206	BL01183	ubiE/COQ5 methyltransferase family proteins.	BL01183B 21.31 1.429e- 37 184-229 BL01183D 27.71 8.535e-27 264- 307 BL01183A 13.25 3.250e-23 51-73 BL01183C 10.77 5.295e- 09 246-258
1208	BL00979	G-protein coupled receptors family 3 proteins.	BL00979L 20.63 2.485e- 09 105-146
1209	PFC0023	Ank repeat proteins.	PF00023A 16.03 4.857e- 11 49-65 PF00023B 14.20 1.818e-09 45-55
1212	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.750e- 14 227-241 PR00048A 10.52 4.316e-11 199- 213
1213	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 1.720e- 10 20-42 PR00450C 12.22 3.506e-09 56-78 PR00450D 16.58 6.769e- 09 44-64
1216	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.598e- 10 179-230
1219	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 5.348e- 11 249-264
1222	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.231e- 15 295-308 PD00066 13.92 7.231e-15 406- 419 PD00066 13.92 2.286e-12 378-391 PD00066 13.92 7.857e- 12 434-447 PD00066 13.92 3.348e-11 350- 363
1223	BL50058	G-protein gamma subunit profile.	BL50058 27.23 1.000e- 40 13-61
1226	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 8.439e- 09 279-330
1227	BL00437	Catalase proximal heme- ligand proteins.	BL00437A 18.82 1.000e- 40 49-101 BL00437B 16.28 1.000e-40 114- 168 BL00437C 21.86

BL00437: 40 248- 23.95 1 379	40 190-239 D 25.72 1.000e-
BL00437: 40 248- 23.95 1 379	D 25.72 1.000e-
40 248- 23.95 1 379	
23.95 1 379	
379	301 BL00437E
	.000e-40 327-
1230 BL01160 Kinesin light chain BL01160	B 19.54 8.297e-
repeat proteins. 10 5-60	
	A 11.19 6.857e-
FAMILY 8 SIGNATURE 09 391-	405
	A 6.92 5.553e-
FACTOR P40 SIGNATURE 10 158-	
PRO0497	A 6.92 5.553e-
FACTOR P40 SIGNATURE 10 158-: 1235 BL00866 Carbamovl-phosphate BL008661	
Edibamoyi phosphace Bhooses	B 36.29 2.776e-
synthase subdomain 09 75-12 proteins.	41
1008	26.43 1.818e-
proteins. 21 36-79	
1040	B 12.19 1.184e-
11 10-25	5
	L 9.47 2.837e-
	6 PD01168L
	490e-10 174-189
PD011681	L 9.47 7.612e-
1046	7.41 2.800e-10
domain proteins. 183-196	
1054	28.97 2.440e-
enzymes proteins. 36 96-14	
1255 BL01115 GTP-binding nuclear BL011157	A 10.22 5.670e-
protein ran proteins. 11 8-52 1256 BL00373 Phosphoribosylglygipamid BL003736	
Thospholibosylgiyelilanid Bh003/30	C 10.35 3.348e-
e formyltransferase 12 143-1 proteins.	156
1050	3 13.08 3.217e-
SIGNATURE 10 174-1	
1259 BL00518 Zinc finger, C3HC4 type BL00518	12.23 8.286e-
(RING finger), proteins. 10 31-40	)
DINIDROPOMATE REDUCTASE   PRO00/00	11.63 1.000e-
	127 PR00070C
	.500e-15 51-63 A 12.92 5.500e-
12 16-27	
10.00	20.89 6.438e-
glutamyltranspeptidase   24 140-1	83 BL00462B
proteins. 17.88 5.	500e-20 230-
	10462C 27.41
1262	1 292-347
Myc.typc, 'helix-loop- BL00038B helix' dimerization 11 62-83	16.97 9.455e-
domain proteins.	
1064	10.22 5.670e-
protein ran proteins. 11 17-61	_
1266 PR00837 ALLERGEN V5/TPX-1 FAMILY PR00837C	17.21 2.714e-
SIGNATURE 18 165-1	82 PR00837A
	512e-12 86-105
	11.12 7.577e-
12 201-2: 1269 PR00449 TRANSFORMING PROTEIN P21 PR00449C	
TRANSFORMING PROTEIN P21 PRO0449C	17.27 9.308e- PR00449E
,	000e-16 137-
	0449D 10.79
	1 102-116
	8.87 1.500e-
1270   000000	
1270 BL00276 Channel forming colicins BL00276A proteins. 09 17-29	
1270 BL00276 Channel forming colicins BL00276A proteins. 09 17-29 1275 PD02327 GLYCOPROTEIN ANTIGEN PD02327C	15.47 9.769e-
1270 BL00276 Channel forming colicins BL00276A proteins. 09 17-29 1275 PD02327 GLYCOPROTEIN ANTIGEN PD02327C PRECURSOR IMMUNOGLO. 09 228-24	15.47 9.769e-

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SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESOLIS
	NO.	SIGNATURE	12 119-135 PR00412C
		SIGNATURE	11.30 1.857e-11 165-
	Ì		179 PR00412A 13.23
			3.400e-11 100-119
1277	PF00756	Putative esterase.	PF00756C 14.12 9.53Be-
		<u>'</u>	10 127-157
1279	BL00134	Serine proteases,	BL00134A 11.96 9.325e-
		trypsin family,	13 128-145
	<u> </u>	histidine proteins.	
1280	BL01220	Phosphatidylethanolamine	BL01220C 14.75 9.348e- 15 248-276
		-binding protein family	15 246-276
	BL00518	proteins. Zinc finger, C3HC4 type	BL00518 12.23 2.286e-
1285	BLOOSIS	(RING finger), proteins.	10 33-42
1287	PF00791	Domain present in ZO-1	PF00791B 28.49 7.182e-
1207	1100/31	and Unc5-like netrin	11 288-343
		receptors.	
1292	PR00802	SERUM ALBUMIN FAMILY	PR00802B 16.51 1.610e-
= -		SIGNATURE	10 81-105
1297	PR00716	M-PHASE INDUCER	PR00716C 17.65 5.696e-
		PHOSPHATASE SIGNATURE	09 23-44
1298	BL00478	LIM domain proteins.	BL00478B 14.79 6.478e-
			14 268-283 BL00127C 31.49 3.571e-
1301	BL00127	Pancreatic ribonuclease family proteins.	28 82-126 BL00127B
		ramity proteins.	26.57 8.800e-28 23-68
1302	PR00637	TYPE 3 BOMBESIN RECEPTOR	PR00637E 11.27 4.250e-
1302	PROUGS	SIGNATURE	09 290-306
1307	BL00215	Mitochondrial energy	BL00215A 15.82 5.500e-
1307		transfer proteins.	17 13-38 BL00215A
		-	15.82 1.000e-16 226-
			251 BL00215A 15.82
			2.658e-13 107-132
1308	PRC0898	VASOPRESSIN V2 RECEPTOR	PR00898H 11.34 4.682e- 09 552-572
	7500301	SIGNATURE PROTEIN REPEAT MUSCLE	PD00301B 5.49 2.731e-
1309	PD00301	CALCIUM-BI.	09 390-401
1310	BL00983	Ly-6 / u-PAR domain	BL00983C 12.69 9.654e-
1310	DECOSOS	proteins.	13 73-89 BL00983B
	1		8.19 3.132e-09 12-22
1313	BL00194	Thioredoxin family	BL00194 12.16 1.900e-
		proteins.	11 15-28
1314	BL00594	Aromatic amino acids	BL00594A 16.75 8.969e-
		permeases proteins.	10 53-97
1316	BL00134	Serine proteases,	BL00134A 11.96 9.325e- 13 128-145
	1	trypsin family, histidine proteins.	13 120-143
1320	BL00783	Ribosomal protein L13	BL00783C 22.43 6.559e-
1 1320	5500783	proteins.	24 87-117 BL00783A
1	1		14.55 1.600e-19 8-33
			BL00783B 12.76 3.500e-
I		1	12 74-86
1327	PF00514	Armadillo/beta-catenin-	PF00514A 31.30 7.268e-
L		like repeat proteins.	11 82-120
1329	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 6.294e-
		region RNP-1 proteins.	11 129-148 BL00030B 7.03 4.789e-09 168-178
L	1 220010	NOVEMBROANTI OVERGEOT	PR00497A 6.92 7.239e-
1331	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	09 25-43
1332	PR00161	NICKEL-DEPENDENT	PR00161C 9.51 4.930e-
1334	FKOOTET	HYDROGENASE/B-TYPE	09 317-337
Į.		CYTOCHROME SIGNATURE	
1333	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 6.769e-
1 2333	120200	ZINC-FINGER METAL-	33 10-49
		BINDING NU.	
1336	PR00700	PROTEIN TYROSINE	PR00700D 12.47 2.200e-
		PHOSPHATASE SIGNATURE	09 262-281
1337	PR00700	PROTEIN TYROSINE	PR00700D 12.47 2.200e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		KESOB15-
1340	DD00000	PHOSPHATASE SIGNATURE	09 211-230
1340	PR00860	VERTEBRATE METALLOTHIONEIN SIGNATURE	PR00860A 5.46 5.034e- 13 5-18
1341	BL00893	mutT domain proteins.	BL00893 18.99 6.750e-
1343	BL01282	BIR repeat proteins.	BL01282E 30.49 5.974e- 21 383-422
1344	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 8.313e- 09 417-427
1345	BL00923	Aspartate and glutamate racemases proteins.	BL00923B 11.41 5.935e- 10 135-146
1348	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 7.231e- 13 44-57
1350	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 3.571e- 32 416-445 PR00193C 12.60 6.318e-31 179- 207 PR00193B 11.69 3.571e-24 133-159 PR00193E 19.47 9.069e- 22 470-499 PR00193A
1352	PR00447	NATURAL RESISTANCE- ASSOCIATED MACROPHAGE PROTEIN SIGNATURE	15.41 1.783e-20 77-97 PR00447E 9.73 1.554e- 15 299-319 PR00447D 13.54 3.408e-15 200- 224 PR00447A 12.73 6.357e-11 97-124 PR00447G 6.69 9.877e-
1353	BL00303	S-100/ICaBP type calcium	10 353-373 BL00303A 21.77 6.667e-
<i>:</i>		binding protein.	26 45-82 BL00303B 26.15 1.000e-24 93-130
1355	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 5.950e- 29 375-421 BL00039A 18.44 7.136e-29 99-138 BL00039C 15.63 4.000e- 18 225-249 BL00039B 19.19 3.182e-14 141- 167
1357	PF00615	Regulator of G protein signalling domain proteins.	PF00615B 16.25 2.216e- 12 84-101 PF00615C 10.06 8.412e-12 162-
1360	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	176 PD01066 19.43 9.234e- 29 10-49
1361	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE	PR00925A 5.47 5.091e- 18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D
1362	BL01272	Glucokinase regulatory protein family proteins.	6.56 1.857e-10 76-87 BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117
1363	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e- 30 113-148 BL01272C 11.68 3.314e-25 226- 251 BL01272A 6.49 1.231e-18 76-94
1364	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.304e- 09 167-177
1368	PR00169	POTASSIUM CHANNEL	PR00169A 16.77 1.592e-
í		SIGNATURE	09 76-96

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
<u> </u>	NO.		10 1-19
	BL00242	Integrins alpha chain	BL00242B 8.13 8.615e-
1371	BLUUZ4Z	proteins.	09 469-479
222	PR00625	DNAJ PROTEIN FAMILY	PR00625B 13.48 7.353e-
1372	PROUBZS	SIGNATURE	19 46-67 PR00625A
			12.84 1.39le-16 14-34
1373	BL00434	HSF-type DNA-binding	BL00434C 23.85 3.778e-
1373	2200.31	domain proteins.	09 90-130
1374	PR00962	LETHAL (2) GIANT LARVAE	PR00952C 8.00 6.337e-
		PROTEIN SIGNATURE	09 505-526
1375	PD02475	MUCIN EPITHELIAL TUMOR-	PD02475A 23.18 8.552e-
		ASSOCIATE.	10 1111-1150 PD01066 19.43 9.571e-
1376	PD01066	PROTEIN ZINC FINGER	
	1	ZINC-FINGER METAL-	32 24-63
	1	BINDING NU.	BL00194 12.16 8.333e-
1380	BL00194	Thioredoxin family	12 48-61
		proteins.	DM01970B 8.60 1.458e-
1381	DM01970	0 kw ZK632.12 YDR313C	15 1123-1136
		ENDOSOMAL III.	BL00678 9.67 7.600e-10
1383	BL00678	Trp-Asp (WD) repeat	243-254
		proteins proteins.  Trp-Asp (WD) repeat	BL00678 9.67 7.600e-10
1384	BL00678	proteins proteins.	271-282
		S-100/ICaBP type calcium	BL00303B 26.15 6.203e-
1385	BL00303	binding protein.	10 95-132
	BI-01160	Kinesin light chain	BL01160B 19.54 5.042e-
1386	Brotten	repeat proteins.	09 1574-1628
1302	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 1.000e-
1387	ВТООЭТО	(RING finger), proteins.	11 52-61
1389	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 3.600e-
1363	PDULUUU	ZINC-FINGER METAL-	30 10-49
	ļ	BINDING NU.	
1390	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 3.512e-
1330		ZINC-FINGER METAL-	31 32-71
		BINDING NU.	PR00308C 3.83 9.723e-
1392	PR00308	TYPE I ANTIFREEZE	10 127-137
	l	PROTEIN SIGNATURE	PR00380A 14.18 9.625e-
1393	PR00380	KINESIN HEAVY CHAIN SIGNATURE	25 88-110 PR00380D
	İ	SIGNATURE	9.93 2.406e-20 304-326
		į.	PR00380B 12.64 4.414e-
	,		16 208-226 PR00380C
	1		13:18 6.538e-16 243-
		]	262
1394	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 3.400e-
}		METAL-BINDI.	14 462-475 PD00066
1	1	1	13.92 8.800e-14 348-
İ		· ·	361 PD00066 13.92
1	1	}	9.571e-12 405-418 · PD00066 13.92 6.087e-
i	ì	1	11 490-503 PD00066
			13.92 8.043e-11 320-
İ			333
		THE PLANT STATES	PD01066 19.43 6.786c-
1398	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	32 10-49
1		BINDING NU.	
	10002220	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 7.038e-
1400	DM01206	PROTEIN.	09 270-290
3400	PD00930	PROTEIN GTPASE DOMAIN	PD00930A 25.62 7.324e-
1406	עככטטעי	ACTIVATION.	15 363-389
3407	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 7.500e-
1407	BB00030	region RNP-1 proteins.	10 457-476
1408	PR00019	LEUCINE-RICH REPEAT	PR00019A 11.19 9.550e-
1,400	FKOOOLS	SIGNATURE	11 179-193 PR00019A
1	1		11.19 8.826e-10 228-
ŀ	1		242 PR00019B 11.36
Į.	1		1.360e-09 199-213 PR00019B 11.36 4.960e-
i			

SEQ ID	NO: ACCESSION NO.	DESCRIPTION	RESULTS*
	NO.		
1409	PR00510	NEBULIN SIGNATURE	09 176-190
ĺ	1 -100510	NEBOLIN SIGNATURE	PR00510A 9.09 4.150e-
1	1		12 182-202 PR00510B
1		ļ	12.96 8.767e-12 210-
l			230 PR00510F 9.88
	ļ		8.172e-10 58-75
			PR00510D 9.21 2.367e-
1410	PD00078	DEDEAM PRO	09 251-267
	-200078	REPEAT PROTEIN ANK	PD00078B 13.14 5.696e
1412	BL00358	NUCLEAR ANKYR.	09 31-44
	2200336	Ribosomal protein L5	BL00358B 22.76 1.00Ce-
		proteins.	40 57-103 BL00358C
		İ	13.75 6.087e-14 122-
		<b> </b>	136 BL00358D 14.26
		l l	5.500e-13 143-158
		}	BL00358A 13.06 1.931e-
1414	BL00282		11 33-44
7777	PP00585	Kazal serine protease	BL00282 16.88 7.338e-
		inhibitors family	10 511-534
1415	DY 0000	proteins.	
1410	BL00023	Type II fibronectin	BL00023 24.31 4.300e-
		collagen-binding domain	29 40-77
1417		proteins.	1
T#1/	PR00681	RIBOSOMAL PROTEIN S1	PR00681G 12.54 2.149e-
1418		SIGNATURE	09 38-60
1418	DM00973	3 kw RESISTANCE BENOMYL	DM00973A 21.17 1.462e-
1419		APPOS8M CACPOHEXIMIDE	09 171-208
1419	PR00319	BETA G-PROTEIN	PR00319B 11.47 1.571e-
1400		(TRANSDUCIN) SIGNATURE	09 428-443
1420	PD01941	TRANSMEMBRANE	PD01941A 14.81 1.000e-
		COTRANSPORTER SYMP.	40 142-196 PD01941B
	ļ		15.02 7.049e-30 400-
	Į		447 PD01941E 15.92
	ĺ		2.475e-20 817-864
			PD01941C 19.96 3.118e~
			19 488-543 PD01941D
			27.18 9.614e-18 641-
	1	İ	690 PD01941F 28.52
		į.	5.382e-15 1038-1093
1422	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 8.043e-
			12 199-217
1423	PR00209	ALPHA/BETA GLIADIN	PR00209B 4.88 6.318e-
		FAMILY SIGNATURE	
1424		I PARTURE	17 :000 1000
	BL50002	Src homology 3 (SH3)	11 1009-1028
	BL50002	Src homology 3 (SH3)	11 1009-1028 BL50002A 14.19 8.200e-
	BL50002	Src homology 3 (SH3) domain proteins profile.	11 1009-1028 BL50002A 14 19 8.200e- 14 367-386 BL50002A
	BL50002	Src homology 3 (SH3)	11 1009-1028 BL50002A 14 19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298-
	BL50002	Src homology 3 (SH3)	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19
	BL50002	Src homology 3 (SH3)	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227
	BL50002	Src homology 3 (SH3)	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e-
425		Src homology 3 (5H3) domain proteins profile.	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258
425	BL50002	Src homology 3 (SH3)	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e-
425 426	PF00628	Src homology 3 (5H3) domain proteins profile.  PHD-finger.	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345
		Src homology 3 (5H3) domain proteins profile.	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345
426	PF00628	Src homology 3 (5H3) domain proteins profile.  PHD-finger.  PHD-finger.	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392
	PF00628	Src homology 3 (SH3) domain proteins profile.  PHD-finger.  PHD-finger.  HIV REV INTERACTING	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e-
426	PF00628	Src homology 3 (5H3) domain proteins profile.  PHD-finger.  PHD-finger.	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e-
426	PF00628	Src homology 3 (SH3) domain proteins profile.  PHD-finger.  PHD-finger.  HIV REV INTERACTING	11 1009-1028  BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258  PF00628 15.84 3.045e- 12 330-345  PF00628 15.84 3.045e- 12 377-392  PR00405B 11.83 5.114e- 16 281-299 PR00405A
426	PF00628 PF00628 PR00405	Src homology 3 (SH3) domain proteins profile.  PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e-
426	PF00628	Src homology 3 (SH3) domain proteins profile.  PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE  DEAD-box subfamily ATP-	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 282
426	PF00628 PF00628 PR00405	Src homology 3 (SH3) domain proteins profile.  PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE  DEAD-box subfamily ATP- dependent helicases	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 262 BL00039D 21.67 5.219e-
426	PF00628 PF00628 PR00405 BL00039	Src homology 3 (SH3) domain proteins profile.  PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE  DEAD-box subfamily ATP- dependent helicases proteins.	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 282
426	PF00628 PF00628 PR00405	Src homology 3 (SH3) domain proteins profile.  PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE  DEAD-box subfamily ATP- dependent helicases proteins. G-PROTEIN BETA WD-40	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 262 BL00039D 21.67 5.219e- 34 147-193
426	PF00628 PF00628 PR00405 BL00039 PR00320	Src homology 3 (SH3) domain proteins profile.  PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE  DEAD-box subfamily ATP- dependent helicases proteins. G-PROTEIN BETA WD-40 REPEAT SIGNATURE	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 262 BL00039D 21.67 5.219e- 34 147-193 PR00320C 13.01 8.920e-
426	PF00628 PF00628 PR00405 BL00039	Src homology 3 (SH3) domain proteins profile.  PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE  DEAD-box subfamily ATP- dependent helicases proteins. G-PROTEIN BETA WD-40 REPEAT SIGNATURE	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 262 BL00039D 21.67 5.219e- 34 147-193 PR00320C 13.01 8.920e- 10 577-592
426	PF00628 PF00628 PR00405 BL00039 PR00320	Src homology 3 (SH3) domain proteins profile.  PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE  DEAD-box subfamily ATP- dependent helicases proteins. G-PROTEIN BETA WD-40 REPEAT SIGNATURE  INOSITOL PHOSPHATASE	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 262 BL00039D 21.67 5.219e- 34 147-193 PR00320C 13.01 8.920e- 10 577-592 PR00378D 16.86 7.563e-
426	PF00628 PF00628 PR00405 BL00039 PR00320	Src homology 3 (SH3) domain proteins profile.  PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE  DEAD-box subfamily ATP- dependent helicases proteins. G-PROTEIN BETA WD-40 REPEAT SIGNATURE	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 262 BL00039D 21.67 5.219e- 34 147-193  PR00320C 13.01 8.920e- 10 577-592 PR00378D 16.86 7.563e- 12 295-314 PR00378B
426	PF00628 PF00628 PR00405 BL00039 PR00320	Src homology 3 (SH3) domain proteins profile.  PHD-finger.  PHD-finger.  HIV REV INTERACTING PROTEIN SIGNATURE  DEAD-box subfamily ATP- dependent helicases proteins. G-PROTEIN BETA WD-40 REPEAT SIGNATURE  INOSITOL PHOSPHATASE	11 1009-1028 BL50002A 14.19 8.200e- 14 367-386 BL50002A 14.19 9.250e-12 298- 317 BL50002A 14.19 4.462e-11 208-227 BL50002B 15.18 1.000e- 09 244-258 PF00628 15.84 3.045e- 12 330-345 PF00628 15.84 3.045e- 12 377-392 PR00405B 11.83 5.114e- 16 281-299 PR00405A 17.71 4.306e-14 262- 262 BL00039D 21.67 5.219e- 34 147-193 PR00320C 13.01 8.920e- 10 577-592 PR00378D 16.86 7.563e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.	DOMONIA GEORGE	10.103.134
		PROTEIN SIGNATURE	10 103-124
1433	BL01113	Clq domain proteins.	BL01113B 18.26 7.049e- 15 14-50 BL01113C
			13.18 7.000e-12 82-102
1424	PR00319	BETA G-PROTEIN	PR00319B 11.47 7.983e-
1434	PROUSTS	(TRANSDUCIN) SIGNATURE	10 135-150
1436	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 1.000e-
1436	BE00030	region RNP-1 proteins.	12 84-103
1438	BL00290	Immunoglobulins and	BL00290B 13.17 2.500e-
1420	BE00290	major histocompatibility	09 250-268 BL00290A
		complex proteins.	20.89 4.000e-09 188-
		- Partie	211
1440	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-
			09 38-52
1441	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-
			09 88-102
1444	BL00422	Granins proteins.	BL00422D 19.48 1.000e-
			08 114-138
1445	PD01841	PHOSPHORYLASE KINASE	PD01841A 21.71 1.000e-
		ALPHA MUSCL.	40 73-123 PD01841B
		ì	14.35 1.000e-40 144-
			185 PD01841D 17.87
	]		1.000e-40 206-258
		1	PD01841F 13.36 1.000e-
		•	40 296-345 PD01841G
			24.26 1.000e-40 349- 403 PD01841I 23.00
			1.000e-40 494-536
			PD01841J 14.94 1.000e-
			40 895-932 PD01841L
			18.42 1.000e-40 1083-
			1125 PD01841E 18.60
			9.719e-38 258-296
	<b>\</b>		PD01841K 14.81 1.000e-
			35 1041-1071 PD01841H
			21.30 3.189e-31 435-
	•	İ	472 PD01841C 13.78
			1.000e-25 185-206
	1		PD01841M 10.82 1.250e-
			20 1175-1194
1446	PF00816	H-NS histone family.	PF00816B 13.84 8.875e-
			09 190-220
1447	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 2.080e-
	i	SIGNATURE	09 402-416
1448	DM00315	072 RIBONUCLEASE	DM00315D 18.40 7.393e-
		INHIBITOR.	09 23-67
1451	BL00030	Eukaryotic RNA-binding	BL00030B 7.03 2.800e-
		region RNP-1 proteins.	10 94-104
1454	DM01688	2 POLY-IG RECEPTOR.	DM01688D 13.44 7.146e-
			09 382-405
1455	PF00777	Sialyltransferase	PF00777C 18.60 2.929e-
		family.	22 4-59
1457	ВЬ00927	Trehalase proteins.	BL00927C 10.83 8.085e-
1.50	<u> </u>	27.20	BL00545C 11.28 7.353e-
1460	BL00545	Aldose 1-epimerase	17 169-182 BL00545A
		proteins.	10.20 2.071e-15 73-89
			BL00545B 13.10 3.942e-
			09 140-153
1466	PR00097	ANTHRANILATE SYNTHASE	PR00097C 9.42 9.069e-
T#00	PRUUUSI	COMPONENT II SIGNATURE	09 233-245
1473	PT 01120	Hypothetical	BL01129E 13.25 5.250e-
1472	BL01129	yabO/yceC/sfhB family	22 170-195 BL01129C
		proteins.	25.56 9.526e-18 63-106
1472	BL00790	Receptor tyrosine kinase	BL007901 20.01 2.821e-
1473	BT00130	class V proteins.	09 2114-2145
	PF00686	Starch binding domain	PF00686A 13.45 9.100e-
		· staren minding demain	, eruupoom 13.40 7.1VVC-
1475	1200000	proteins.	09 267-277

SEQ ID NO:		DESCRIPTION	RESULTS*
1477	NO. PF00566	D-ob-bl	
14//	PF00566	Probable rabGAP domain proteins.	PF00566A 12.64 7.333e- 10 466-476
1478	BL00030	Eukaryotic RNA-binding	BL00030B 7.03 9.400e-
		region RNP-1 proteins.	10 43-53
1479	DM00406	GLIADIN.	DM00406 7.73 8.541e-10 292-305
1480	BL00290	Immunoglobulins and	BL00290B 13.17 2.385e-
		major histocompatibility	15 69-87 BL00290A
1481	PR00150	PHOSPHOENOLPYRUVATE	20.89 5.091e-11 12-35
	PROOF	CARBOXYLASE SIGNATURE	PR00150F 10.45 9.039e- 09 21-51
1482	PF00780	Domain found in NIK1-	PF00780I 14.69 4.825e-
		like kinases, mouse	09 107-137
1483	77.004.50	citron and yeast ROM.	
1403	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 1.153e-
1485	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 5.909e-
		ZINC-FINGER METAL-	25 17-56
		BINDING NU.	
1486	BL00107	Protein kinases ATP-	BL00107B 13.31 1.529e-
1488	BL00039	binding region proteins.  DEAD-box subfamily ATP-	09 34-50 BL00039D 21.67 9.586e-
	1 220000	dependent helicases	10 116-162
		proteins.	100
1490	BL00166	Enoyl-CoA	BL00166D 22.87 2.607e-
		hydratase/isomerase proteins.	24 190-226 BL00166C
		proceins.	18.93 5.500e-14 140- 167 BL00166B 16.92
			9.357e-11 93-115
1491	BL00452	Guanylate cyclases	BL00452D 28.59 3.700e-
		proteins.	31 63-106 BL00452E
			11.92 3.045e-13 115- 131
1492	PR00019	LEUCINE-RICH REPEAT	PR00019A 11.19 3.667e-
		SIGNATURE	09 532-546
1497	BL00107	Protein kinases ATP-	BL00107B 13.31 1.000e-
		binding region proteins.	11 384-400 BL00107A 18.39 5.345e-11 322-
			353
1500	PF00876	Ogre family.	PF00876E 7.99 1.947e-
1500			10 107-117
1502	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.789e-
1503	BL00027	'Homeobox' domain	24 112-155 BL00027 26.43 4.789e-
		proteins.	24 112-155
1505	BL01177	Anaphylatoxin domain	BL01177E 20.64 5.800e-
	ľ	proteins.	24 448-475 BL01177C
		1	17.39 5.333e-19 402-
	1	ļ	7.840e-16 155-171
	Ī		BL01177D 17.50 1.900e-
1506	BY 00000		15 427-445
1300	BL00972	Ubiquitin carboxyl- terminal hydrolases	BL00972D 22.55 5.500e- 14 311-336 BL00972A
	1	family 2 proteins.	11.93 7.429e-14 48-66
	1		BL00972E 20.72 8.759e-
1510			10 341-363
1512	BL00523	Sulfatases proteins.	BL00523R 19.27 4.536e-
			22 76-106 BL00523D 9.89 1.563e-11 40-52
			BL00523F 10.85 4.162e-
			09 159-170 BL00523G
1516			9.46 5.333e-09 256-266
1516	BL00914	Syntaxin / epimorphin	BL00914 24.91 7.045e-
1518	BL00600	family proteins. Aminotransferases class-	14 168-218 BL00600A 17.98 6.143e-
		III pyridoxal-phosphate	19 98-122 BL00600E
		attachment si.	16.43 1.771e-17 302-

Q ID NO:	ACCESSION	DESCRIPTION	ESULTS*
•	NO.	3	31 BL006COG 12.43
		1	625e-17 377-396
	Ì	1	NL00600B 19.60 5.091e-
	Į.	1	15 160-186 BL00600C
	1	1	6.18 6.040e-12 190-
			206 BL006COF 8.77
			1.000e-11 343-356
	1	1:	BL00600D 8.71 1.000e-
			10 281-295 PD00930B 33.72 9.600e-
	PD00930		
523	PDOGAZO	1	18 41-82
	<u> </u>	40	PR00320B 12.19 4.774e-
528	PR00320		11 192-207 PR00320B
	1	1	12.19 8.839e-11 272-
			287 PR00320B 12.19
	1	l l	9.743e-10 106-121
	l .	1	PRO0320A 16.74 1.878e-
	1	1	09 192-207 PR00320A
		1	16.74 2.317e-09 106-
	1	1.	121 PR00320A 16.74
		1	121 PKUJ32UA 10./4
		1	8.683e-09 272-287
		}	PR00320C 13.01 8.800e-
		1	09 106-121
_		0 kw ZK632.12 YDR313C	DM01970B 8.60 4.508e-
L538	DM01970	ENDOSOMAL III.	15 171-184
		Diacylglycerol kinase	PF00781D 11.11 7.593e-
1539	PF00781	Diacylglycerol Kinase	10 103-127
	ł	catalytic domain	10 112
	'	proteins (presumed).	PR00965H 10.73 1.231e-
1540	PR00965	OCULAR ALBINISM TYPE 1	29 312-334 PR00965E
T240		PROTEIN SIGNATURE	12.93 5.846e-29 172-
		1	12.93 5.8466-25 172 195 PR00965F 5.98
			195 PROUSES 5.30
		}	1.123e-28 209-231
		1	PR00965C 15.04 1.000e-
	1		27 131-151 PR00965D
			5.84 1.000e-27 150-170
		1	PR00965G 8.52 2.440e-
	1		27 258-279 PR00965B
		<b>\</b>	4.80 8.650e-26 88-109
			PR00965A 12.52 1.000e-
			25 35-55 PR00965I
	1		3.91 6.442e-25 385-406
			BL01013D 26.81 9.719e-
	BL01013	Oxysterol-binding	
1541	BHOTOTA	protein family proteins.	17 163-207
		PROTEIN DNA-BINDING	PD02699C 24.84 1.000e-
1543	PD02699	BINDING DNA.	40 599-646 PD02699A
		BINDING DAY.	R 91 2 286e-34 219-248
	1		PD02699B 18.28 6.143e-
			21 485-509
			PRODUCED 0.00 7.857e-
1544	PR00049	WILM'S TUMOUR PROTEIN	10 182-197 PR00049D
1344	1	SIGNATURE	0.00 7.102e-09 67-82
<b> </b>	1		0.00 7.1026-09 67-62
		ER lumen protein	BL00951C 19.35 1.000e
1547	BL00951	retaining receptor	40 93-142 BL00951D
1	1	recarning receptor	13.94 B.714e-40 142-
1		proteins.	177 BL00951A 15.10
1	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	1	1 000e-38 2-38 ·
1	l l		BL00951B 14.23 6.250e
1	1	\ 	
1	1		33 38-69
	77.00536	Ubiquitin-activating	BL00536F 13.65 8.920e
1548	BL00536	enzyme proteins.	30 279-318 BL00536D
1	1	enzyme Procerus.	1 22 91 5.737e-24 21-65
l .	ł		BL00536E 16.94 4.6966
1	1		18 248-279
1	Ţ	<u></u>	
L	PR00139	ASPARAGINASE/GLUTAMINAS	
	EKOOTSS	FAMILY SIGNATURE	
1549			
1549	PR00049	WILM'S TUMOUR PROTEIN	PR00049D 0.00 5.119e-

SEQ ID No	O: ACCESSION NO.	DESCRIPTION	RESULTS*
1556	BL00061	Short-chain	
		dehydrogenases/reductase	BL00061B 25.79 6.276e
1557	BL01228	s family proteins.  Hypothetical cof family	BL01228D 17.44 8.105e
1558	BL01228	proteins. Hypothetical cof family	12 107-132
1559	BL01228	proteins.	BL01228D 17.44 8.105e 12 107-132
		Hypothetical cof family proteins.	BL01228D 17.44 8.105e
1562	BL00522	DNA polymerase family X	BL00522C 11.90 6.600e
		proteins.	18 412-436 BL00522B
		•	27.30 1.738e-16 364- 410 BL00522A 25.52
			6.000e-16 279-326
		1	BL00522E 19.63 6.123e- 14 502-532 BL00522F
			14.90 2.385e-13 551-
1563	PF00651	BTB (also known as BR-	PF00651 15.00 1.947e-
1564	BL00299	C/Ttk) domain proteins	11 46-59
	_	Ubiquitin domain proteins.	BL00299 28.84 2.823e-
1566	BL01013	Oxysterol-binding	10 324-376 RL01013D 26.81 8.594e-
		protein family proteins.	17 184-228 BL01013C
1567	BL00678	Trp-Asp (WD) repeat	9.97 4.906e-12 14-24 BL00678 9.67 3.400e-10
	-	proteins proteins.	378-389 BL00678 9.67
		}	5.800e-10 418-429
1570	BL00479		BL00678 9.67 8.800e-10 295-306
	2200475	Phorbol esters / diacylglycerol binding	BL00479B 12.57 5.235e-
		domain proteins.	17 297-313 BL00479A 19.86 6.625e-15 271-
			294 BL00479A 19.86
			2.667e-14 147-170 BL00479B 12.57 6.294e-
576	PR00665	OXYTOCIN RECEPTOR	12 173-189
		SIGNATURE	PR00665G 12.36 4.673e- 24 364-384 PR00665D
			9.93 1.200e-22 138-155
			PR00665F 11.73 4.000e- 22 337-354 PR00665C
	1	1	5.89 1.000e-20 65-80
	j		PR00665B 5.29 4.337e- 19 24-39 PR00665E
		!	5.60 2.929e-15 246-260
577	<u> </u>		PR00665A 5.99 5.622e-
<i>311</i>	DM00099	4 kw A55R REDUCTASE TERMINAL	DM00099B 14.73 9.308e-
579		DIHYDROPTERIDINE.	10 127-137
,,,	BL00524	Somatomedin B domain	BL00524A 9.65 6.776e-
80	PD02894 .	Processes.	14 52-73
			PD02894B 13.93 6.959e- 16 182-215 PD02894A
81	BL00411	77	21.96 2.125e-10 57-103
		I	BL00411C 15.04 5.292e- 12 32-54 BL00411H
		•	15.66 4.441e-11 245-
82	PR00604	CLASS IA AND IB	276 PR00604A 11.13 2.440e-
84	PF00651	CYTOCHROME C SIGNATURE	09 79-87
		BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 1.000e-
85	DM01551	kw OSTEOINDUCTIVE YOPM	10 225-238 DM01551C 14.62 9.455e-
36	DM01354	MEMBRANE OUTER.	11 125-145
,	-	AMMOUNTAINE REVERSE IT	M01354S 11.61 7.750e-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		PR00072B 13.77 7.955e-
1587	PR00072	MALIC ENZYME SIGNATURE	33 180-210 PR00072A 12.75 6.040e-25 120- 145 PR00072C 11.42 2.286e-24 216-239 PR00072D 10.77 3.400e-
	BL00191	Cytochrome b5 family,	22 276-295 PR00072E 10.54 1.360e-19 301- 318 PR00072G 10.45 5.304e-19 433-450 PR00072F 8.87 5.935e- 15 332-349 BL00191H 15.64 1.537e-
1589	BP00131	heme-binding domain proteins.	22 61-113 BL00191K 17.38 9.027e-12 398- 442
1590	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.716e- 13 211-224 DM01970B 8.60 2.157e-12 94-107
1591	DM00517	5 kw NUCLEAR 60.7 NUP1 CHROMOSOME.	DM00517B 10.96 6.625e- 16 1175-1193 DM00517A 8.21 1.000e-11 1015- 1026
1592	BL00037	Myb DNA-binding domain proteins repeat proteins proteins.	BL00037B 15.92 3.250e- 27 116-142 BL00037A 16.68 2.500e-24 83-107 BL00037A 16.68 3.250e- 12 31-55 BL00037B 15.92 3.526e-11 64-90 BL00037C 16.86 9.654e- 10 146-164
1595	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.514e- 09 110-127
1598	PF00628	PHD-finger.	PF00628 15.84 3.250e- 11 1667-1682
1599	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014D 12.04 5.500e- 09 980-995
1600	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.571e- 10 30-39
1602	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.402e- 10 136-187
1605	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 3.571e- 10 44-57
1607	BL00252	Interferon alpha, beta and delta family proteins.	BL00252A 18.49 6.657e- 23 20-57 BL00252B 19.78 9.125e-16 58-109
1610	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.000e- 08 61-94
1611	BL00904	Protein prenyltransferases alpha subunit repeat proteins proteins.	BL00904C 8.98 7.353e- 10 91-125 BL00904D 1.47 6.018e-09 127-168
1612	PF00168	C2 domain proteins.	PF00168C 27.49 3.250e- 09 365-391
1613	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 6.051e- 09 932-983 BL00412D 16.54 7.153e-09 933- 984
1614	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.	BL00559I 13.63 3.531e- 25 54-83 BL00559K 13.17 2.957e-18 197- 224 BL00559J 19.63 6.870e-16 124-176 BL00559L 13.60 9.000e- 16 266-284
1615	PD01427	TRANSFERASE METHYLTRANSFERASE BI.	PD01427B 22.45 3.025e- 22 500-541 PD01427A 19.94 8.773e-18 439-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
			472
1616	BL00115	Eukaryotic RNA	BL00115Z 3.12 7.485e-
		polymerase II heptapeptide repeat	09 152-201 BL00115Z 3.12 9.603e-09 145-194
		proteins.	3.12 9.8030-09 145-194
1617	BL00303	S-100/ICaBP type calcium	BL00303B 26.15 7.750e-
		binding protein.	32 51-88 BL00303A
		_	21.77 1.947e-31 4-41
1618	BL01254	Fetuin family proteins.	BL01254F 10.02 8.754e-
1619	PD01888	PEPTIDE REDUCTASE	09 137-147 PD01888B 25.10 1.000e-
1013	1,001,000	PROTEIN METHI.	40 47-97 PD01888C
			21.56 7.000e-30 125-
			155 PD01888A 12.84
			8.800e-15 7-23
1621	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239E 1.58 3.455e-
		TERMINAL TAIL SIGNATURE	09 692-704 PR00239E
			1.58 4.580e-09 697-709 PR00239E 1.58 4.580e-
			09 702-714 PR00239E
			1.58 5.193e-09 703-715
1622	PR00860	VERTEBRATE	PR00860B 7.04 1.900e-
:		METALLOTHIONEIN SIGNATURE	18 27-41 PR00860C 9.61 1.474e-14 41-51
	1	SIGNATURE	PR00860A 5.46 1.720e-
			14 5-18
1624	PR00784	MITOCHONDRIAL BROWN FAT	PR00784D 15.86 8.027e-
		UNCOUPLING PROTEIN	11 77-95
1626	BL00325	SIGNATURE Actin-depolymerizing	BL00325B 21.66 1.000e-
1020	D200323	proteins.	40 93-139 BL00325A
	1		24.83 6.786e-23 61-93
1631	BL00064	L-lactate dehydrogenase	BL00064B 23.57 1.000e-
		proteins.	40 82-130 BL00064C
			17.28 1.000e-40 137- 182 BL00064E 27.20
			1.000e-40 223-275
			BL00064F 25.14 7.882e-
			36 286-331 BL00064A
			21.16 1.000e-33 22-60
		ł	BL00064D 14.19 6.500e-
1632	PR00063	RIBOSOMAL PROTEIN L27	PR00063B 15.24 9.700e-
	ļ	SIGNATURE	11 59-84 PR00063A
			11.71 1.614e-09 34-59
1634	PR00239	MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE	PR00239D 0.00 1.105e-
		IEMITAL TAIL SIGNATURE	11 36-49 PR00239C 3.51 2.538e-09 37-45
1636	BL01210	Caveolins proteins.	BL01210B 13.92 9.531e-
	1	_	10 133-183
1637	BL00982	Bacterial-type phytoene	BL00982A 18.41 5.388e-
1639	BL01183	dehydrogenase proteins.	11 11-43
2035	PRATTOS	methyltransferase family	BL01183B 21.31 8.144e- 12 132-177
		proteins.	
1640	PR00015	GRAM-POSITIVE COCCUS	PR00015B 9.84 8.468e-
		SURFACE PROTEIN ANCHOR	10 128-149
1641	PR00320	SIGNATURE	2200
TOAT	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320B 12.19 5.935e-
	1	ADEBAT SIGNATURE	11 364-379 PRO0320A 16.74 7.828e-11 364-
	}	·	379 PR00320C 13.01
			2.800e-10 279-294
	1		PR00320C 13.01 2.800e-
			10 364-379 PR00320B
	Į.		12.19 5.114e-10 279- 294 PR00320A 16.74
	1	]	1.659e-09 279-294

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PR00320A 16.74 2.098e- 09 229-244
1642	PF00023	Ank repeat proteins.	PF00023A 16.03 6.464e- 09 114-130
1643	PR00169	POTASSIUM CHANNEL SIGNATURE	PRO0169A 16.77 1.806e- 11 74-94
1644	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 2.200e-10 109-120 BL00678 9.67 5.737e-09 528-539
1645	BL01108	Ribosomal protein L24 proteins.	BL01108A 20.33 7.366e- 17 56-89
1646	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PRO0380A 14.18 9.270e- 21 103-125 PR00380D 9.93 6.308e-18 386-408 PR00380C 13.18 7.923e- 16 332-351 PR00380B 12.64 6.657e-15 292- 310
1647	DM01242	3 THREONINETRNA LIGASE.	DM01242C 17.15 9.791e- 37 340-381 DM01242E 23.00 5.071e-31 463- 505 DM01242D 23.29 3.925e-30 420-463 DM01242B 23.57 8.054e- 18 265-314 DM01242F 10.61 7.618e-14 526- 540
1649	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 5.500e- 10 13-34
1651	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.720e- 11 431-485
1652	BL00933	FGGY family of carbohydrate kinases proteins.	BL00933A 17.50 4.673e- 12 11-35 BL00933E 13.80 9.217e-09 456- 472
1653	BL00795	Involucrin proteins.	BL00795C 17.06 2.988e- 10 70-115
1654	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 302-334
1655	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 282-314
1656	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 1.391e- 16 607-630
1657	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 7.938e- 11 114-136
1658	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.889e- 10 442-455
1659	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 4.140e- 12 376-401 BL00972E 20.72 5.629e-09 446- 468
1660	BL00406	Actins proteins.	BL00406D 12.58 8.767e- 15 188-243
1661	PR00105	CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE	PR00105A 10.36 4.900e- 13 1140-1157 PR00105B 12.32 2.800e-12 1259- 1274 PR00105C 10.86 1.000e-10 1305-1319
1662	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.	BL00280 24.61 3.172e- 33 3119-3163
1663	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 5.714e-20 89-105 PR00319A 15.27 5.286e- 19 51-68 PR00319B 11.47 8.200e-19 70-85

1664   BL00018   EF-hand calcium-binding domain proteins ad 99-503   2100-7100   2100-7100   2100-7100   2100-7100   2100-7100   2100-7100   2100-7100   2100-7100   2100-7100   2100-7100   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-710   2100-71	SEQ ID N	O: ACCESSION NO.	DESCRIPTION	RESULTS*
1667   PD01066   PROPEIN ZINC FINGER   PD01066   19.43 8.500e   ZINC-FINGER METAL   BINDING NU.	1664			
ZINC-FINGER METAL-BINDING NU.	1667		domain proteins.	
BL01153   NOLL/NOP2/sun family   EL01153D 19.69   1   Record   17   15-14   Bl011515   13.67 8.9778-15.66-80   10.13.37 8.9778-15.66-80   10.13.37 8.9778-15.66-80   10.13.37 8.9778-15.66-80   10.13.37 8.9778-15.66-80   10.13.37 8.9778-15.66-80   10.13.37 8.9778-15.66-80   10.13.37 8.9778-15.66-80   10.13.37 8.9778-15.66-80   10.13.37 8.9778-15.66-80   10.13.37 8.9778-15.66-80   10.13.37 8.9778-15.66-80   10.13.37 8.9778-15.66-80   10.13.37 8.9778-15.66-80   10.13.37 8.9788-15.80   10.13.37 8.9788-15.80   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1169   10.146-1	1667	PD01066	ZINC-FINGER METAL-	
Proteins	1669	BL01153	1	PL01153D 10 60 1 100-
13.67 8.97%-15 66-80     1013-37     1013-37     1013-37     1013-37     1013-37     1013-37     1013-37     1013-37     1013-37     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     10146-1169     1027-149     1027-149     1027-149     1027-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-149     1028-14				
BL01153B 20.52 1.885e-10 13-37	1			
1671   PR00678   PI3 XINASE PS   REGULATORY SUBURIT   10 1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-1169   1146-11				
REQUIATORY SUBUNIT SIGNATURE  1672  BL00598  Chromo domain proteins.  BL00598 14.45 8.500e- 20 27-49  PRO0326  GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE  1674  PR00049  WILLY SIGNATURE  1676  FR00747  GLYCOSYL NYDROLASE FAMILY 47 SIGNATURE  19 427-448  PR007471 12.76 8.636e- 13 39 PR00747C 12.06  7.500e-18 112-131  PR00747A 14.05 4.600e- 13 28-8-17 163- 183 PR00747E 15.13  8.244e-15 254-272  PR00747A 7.65 5.355e- 13 75-90 PR00747  GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE  19 309-330 PR00747C 12.06  7.500e-18 112-131  PR00747A 14.05 4.600e- 13 28-8  13 75-90 PR00747  FR00747 FR00747 FR00747B  14.50 2.286e-18 250- 275 PR00747C 12.06  7.500e-18 112-131  PR00747A 14.05 4.600e- 19 309-330 PR00747G  14.50 2.286e-18 250- 275 PR00747F 13.56 8.714e-10 311- 328  FR00747A 14.05 4.600e- 17 42-63 PR00747B  7.65 5.355e-13 75-90 PR00747F 13.56 8.714e- 10 193-2210  1680  BL00678  FRD0326  FRD0326  FRD0326  FRD0326  FRD0326  FRD0326  FRD0326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR00326  FR0032				10 13-37
SIGNATURE	1671	PR00678		
1672   BL00598   Chromo domain proteins   BL00598 14.45 8.500e-   20 27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49   27-49	<u> </u>		•	10 1146-1169
1673   PR00326   GTP1/OBG GTP-BINDING   PR00326A B.75 B.329e-PR07TSIN FAMILY SIGNATURE   PR00326A B.75 B.329e-PR07TSIN FAMILY SIGNATURE   PR00049D 0.00 7.580e-SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   SIGNATURE   S	1672	RT.00598	I	77.005.0
1673   PRO0326   CTP1/OBG GTP-BINDING   PRO03268 8.75 8.329e   PROTEIN FAMILY SIGNATURE   PRO0049   WILM'S TUMOUR PROTEIN   11 343-358   PRO00490   O.00 7.580e-11 343-358   PRO00490   O.00 7.580e-11 343-358   PRO00490   PRO07471   PRO07471   PRO07471   PRO07471   PRO07471   PRO07471   PRO07471   PRO07471   PRO07472   PRO07471   PRO07474   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476   PRO07476		2200350	Chromo domain proceins.	1
PROTEIN FAMILY SIGNATURE   09 686-707     WILM'S TUMOUR PROTEIN   PROTEIN   PROTEIN   1343-358   PROTEIN   1343-358   PROTEIN   1343-358   PROTEIN   1343-358   PROTEIN   1343-358   PROTEIN   1343-358   PROTEIN   1343-358   PROTEIN   14,50   2,266-18   342-348   14,50   2,266-18   366-393   PROTA'R   12,76   8,6366-19   427-448   PROTA'R   12,106   7,5006-18   112-131   PROTA'R   12,106   7,5006-18   112-131   PROTA'R   12,106   7,5006-18   112-131   PROTA'R   12,106   7,5006-18   122-131   13,56   8,7146-10   311-390   PROTA'R   13,56   8,7146-10   311-390   PROTA'R   13,56   8,7146-10   311-390   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   8,6366-18   250-275   PROTA'R   12,76   PROTA'R   12,76   PROTA'R   12,76   PROTA'R   12,76   PROTA'R   12,76   PROTA'R   12,76   PROTA'R   12,76   PROTA'R   12,76   PROTA'R   12,76   PROTA'R   12,76   PROTA'R   12,76   PROTA'R   12,76   PROTA'R   12,76   PROTA'R   12,76   PROTA'R   12,76   PROTA'R	1673	PR00326	GTP1/OBG GTP-RINDING	
1674   PR00049   MILM'S TUMOUR PROTEIN   11 343-358 PR30049D   0.00 1.286c-10 342-357   0.00 1.286c-10 342-357   0.00 1.286c-10 342-357   PR00747H 12.76 8.636c-10 342-357   PR00747H 12.76 8.636c-10 342-357   14.50 2.286c-18 363 393 PR00747C 12.06 7.500c-18 112-131 PR00747A 14.05 4.600c-17 42-63 PR00747F 15.23 8.759c-17 163-183 PR00747F 15.13 8.244c-15 254-272 PR00747F 15.23 8.759c-17 163-183 PR00747F 15.13 8.244c-15 254-272 PR00747F 13.56 8.714c-10 311-328   PR00747F 13.56 8.714c-10 311-328   PR00747F 13.56 8.714c-10 311-328   PR00747F 13.56 8.714c-10 311-328   PR00747C 12.06 7.500c-18 112-131   PR00747B 14.05 4.600c-18 112-131   PR00747F 13.56 8.714c-10 313-320   PR00747F 13.56 8.714c-10 313-320   PR00747F 13.56 8.714c-10 313-320   PR00747F 13.56 8.714c-10 313-320   PR00747B 7.55 5.355c-13 75-90 PR00747F 13.56 8.714c-10 313-320   PR00747B 7.55 5.355c-13 75-90 PR00747F 13.56 8.714c-10 193-210   PR00747B 7.55 5.355c-13 75-90 PR00747F 13.56 8.714c-10 193-210   PR00747B 7.55 5.355c-13 75-90 PR00747F 13.56 8.714c-10 193-210   PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.55 5.355c-13 75-90 PR00747B 7.50 6.684c-09 320-331   PR00747B 7.55 6.845c-09 320-331   PR00747B 7.55 6.845c-09 320-331   PR00747B 7.55 6.845c-09 320-331   PR00747B 7.55 6.845c-09 320-331   PR00747B 7.55 6.845c-09 320-331   PR00747B 7.55 6.845c-09 320-331   PR00747B 7.55 6.845c-09 320-331   PR00747B 7.55 6.845c-09 320-331   PR00747B 7.55 6.845c-09 320-331   PR00747B 7.55 6.845c-09 320-331   PR00747B 7.55 6.845c-09 320-331   PR00747B 7.55 6.845c-09 320-331   PR00747B 7.55 6.845c-09				
SIGNATURE	1674	PR00049		
1676   PR00747   GLYCOSYL HYDROLASE   PR00747R   12.75 8.636-19 427-448   PR00747G   14.50 2.286e-18 368-393   PR00747C 12.06 7.500e-18 112-131   PR00747A 14.05 4.600e-17 42-63   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.13   PR00747E 15.			SIGNATURE	11 343-358 PR00049D
FAMILY 47 SIGNATURE    PAMILY 47 SIGNATURE   PARO7476   14.50 2.286e-18 368-39   PR007477   12.06   7.500e-18   112-131   PRR007477   15.23 8.759e-17   163-183   PR007477   15.23 8.759e-17   163-183   PR007477   15.23 8.759e-17   163-183   PR007478   15.24 8.759e-17   163-183   PR007478   15.24 8.759e-17   163-183   PR007478   15.254-272   PRR007478   13.56 8.714e-10 311-328   PR007478   13.56 8.714e-10 311-328   PR007478   12.76 8.636e-18 250-275   PR007478   14.50 2.286e-18 250-275   PR007478   14.50 2.286e-18 250-275   PR007478   14.50 2.286e-18 250-275   PR007478   14.50 2.286e-18 250-275   PR007478   13.56 8.714e-10   17.65 5.355e-13 75-90   PR007478   13.56 8.714e-10   17.65 5.355e-13 75-90   PR007478   13.56 8.714e-10   17.65 5.355e-13 75-90   PR007478   13.56 8.714e-10   17.65 5.355e-13 75-90   PR007478   13.56 8.714e-10   17.65 5.355e-13 75-90   PR007478   13.56 8.714e-10   17.65 5.355e-13 75-90   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.3-210   PR007478   13.56 8.714e-10   13.56 8.714e-10   13.56 8.714e-10   13.56 8.714e-10   13.56 8.714e-10   13.56 8.714e-10   13.56 8.714e-10   13.56 8.714e-10   13.56 8.714e-10   13.56 8.714e-10   13.56 8.714e-10   13.56 8.714e-10   13.56 8.714e-10   13.56 8.714e-10   13.56 8.714e-10   13.56 8.714e-10   13.56 8.714e-10   13.56 8.7	1676			<u> </u>
14.50 2.286e-18 368-393 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-17 42-63 PR00747D 15.23 8.759e-17 163-183 PR00747B 15.23 8.759e-17 163-183 PR00747E 15.13 8.244e-15 254-272 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-10 311-328  1677 PR00747 GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE 19 309-330 PR00747B 14.50 2.286e-18 250-275 PR00747T 12.16 8.636e-19 309-330 PR00747G 14.50 2.286e-18 250-275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-10 742-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-10 193-220 1680 BL00678 Trp-Asp (WD) repeat BL00678 9.67 4.600e-10 406-417 BL00678 9.67 6.684e-09 320-331 1681 BL00678 Trp-Asp (WD) repeat BL00678 9.67 4.600e-10 Proteins proteins. 329-340 BL00678 9.67 6.684e-09 243-254 1683 PR00326 GTP1/OBG GTP-BINDING PR00326A 8.75 1.346e-13 189-410 1685 PR00326 GTP1/OBG GTP-BINDING PR00326A 8.75 1.346e-13 189-410 1689 BL01160 Kinesin light chain repeat proteins. 9755-771 1690 BL01160 Kinesin light chain PR00326A 8.75 1.346e-13 189-410 1691 PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e-10 418-432 PR00456E 3.06 7.281e-10 418-432 PR00456E 3.06 7.281e-10 418-432 PR00456E 3.06 7.281e-10 418-432 PR00456E 3.06 7.281e-10 418-432 PR00456E 3.06 7.281e-10 418-432 PR00456E 3.06 7.281e-10 418-432 PR00456E 3.06 7.281e-10 418-432 PR00456E 3.06 7.281e-10 418-432 PR00456E 3.06 7.281e-10 418-432 PR00456E 3.06 7.281e-10 418-432 PR00456E 3.06 7.281e-10 418-432 PR00456E 3.06 7.281e-10 418-432 PR00456E 3.06 7.281e-10 418-432 PR00456E 3.06 7.281e-10 418-432 PR00456E 3.06 7.281e-10 418-503 PR00456E 3.06 7.281e-10 418-503 PR00456E 3.06 7.281e-10 418-503 PR00456E 3.06 7.281e-10 418-503 PR00456E 3.06 7.281e-10 418-503 PR00456E 3.06 7.281e-10 418-503 PR00456E 3.06 7.281e-10 418-503 PR00456E 3.06 7.281e-10 418-503 PR00456E 3.06 7.281e-10 418-503 PR00456E 3.06 7.281e-10 418-503 PR00456E 3.06 7.281e-10 418-503 PR00456E 3.06 7.281e-10 418-503 PR00456E 3.06 7.281e-10 418-503 PR00456E 3.06 7.281e-10 418-503 PR00456E 3.06 7.281e-10 418-503 PR00456E 3.06 7.281e-10 418-503 PR00456E 3.06	TO 10	PR00747		
393 PR00747C 12.06   7.500e-18 112-131   PR00747A 14.05 4.600e-10 17 42-63 PR00747B 15.23 8.759e-17 163-183 PR00747B 15.23 8.759e-17 163-183 PR00747B 7.65 5.355e-13 75-90 PR00747F 15.13   8.244e-15 254-272 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.156 8.714e-10 311-328     1677   FR00747   GLYCOSYL HYDROLASE PR00747H 12.76 8.636e-1 9309-330 PR00747G 12.06 7.500e-18 112-131     PR00747A 12.76 8.636e-1 9309-330 PR00747G 12.06 7.500e-18 112-131     PR00747A 14.05 4.600e-1 17 42-63 PR00747C 12.06 7.500e-18 112-131     PR00747A 14.05 4.600e-1 17 42-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-10 193-210     1680   BL00678   Trp-Asp (WD) repeat   BL00678 9.67 4.600e-10 406-417 BL00678 9.67 6.684e-09 320-331     FR00646   Trp-Asp (WD) repeat   BL00678 9.67 4.600e-10 406-417 BL00678 9.67 6.684e-09 243-254     1681   BL00678   Trp-Asp (WD) repeat   BL00678 9.67 6.684e-09 243-254     1682   FR00456   GTP1/OBG GTP-BINDING PR0078 9.67 6.684e-09 243-254     FR00456   RDC1 ORPHAN RECEPTOR PR006466 6.32 4.188e-09 243-254     FR00456   RDC1 ORPHAN RECEPTOR PR006466 6.32 4.188e-09 755-771     1690   BL0160   Kinesin light chain repeat proteins.   D406466 6.32 4.188e-09 755-771     1691   FR00456   RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e-10 419-434     PR00456E 3.06 8.125e-10 420-435     1692   PR00456   RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e-10 419-434     PR00456E 3.06 8.125e-10 420-435     10 487-502 PR00456E 3.06 7.281e-10 498-503     PR00456E 3.06 8.125e-10 489-503     PR00456E 3.06 8.125e-10 489-503     PR00456E 3.06 8.125e-10 489-504     1693   BL00674   AAA-protein family   BL006742 2.60 8.043e-1			FAMILY 27 SIGNATURE	
7.500e-18 112-131 PRO0747A 14.05 4.600e-17 42-63 PRO0747D 15.23 8.759e-17 163-183 PRO0747E 15.13 8.244e-15 254-272 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-10 311-328  1677 PR00747 GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE PR00747H 12.76 8.636e-18 250-275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-10 14.50 2.286e-18 250-275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-10 17.42-65 PR00747B 1680 BL00678 Trp-Asp (WD) repeat PR00747F 13.56 8.714e-10 193-210 BL00678 Trp-Asp (WD) repeat PR00747F 13.56 8.714e-10 193-210 BL00678 PR00747F 13.56 8.714e-10 193-210 BL00678 PR00326 GR064B PR00328 PR00328 PR00326 PR00328 PR00326 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 PR00328 P				
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15.23 8.759e.17 163- 183 PR00747E 15.13 8.244e-15 254-272 PR00747B 7.65 5.355e- 13.75-90 PR00747F 13.56 8.714e-10 311- 328   1677   PR00747   GLYCOSYL HYDROLASE   FR00747H 12.76 8.636e- FAMILY 47 SIGNATURE   19 309-330 PR00747G 14.50 2.286e-18 250- 275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e- 17 42-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e- 10 193-210   PR00747F 13.56 8.714e- 10 193-210   PR00747F 13.56 8.714e- 10 193-210   PR00747F 13.56 8.714e- 10 193-210   PR00747F 13.56 8.714e- 10 193-210   PR00747F 13.56 8.714e- 10 193-210   PR00747F 13.56 8.714e- 10 193-210   PR00747F 13.56 8.714e- 10 193-210   PR00747F 13.56 8.714e- 10 193-210   PR00678 9.67 4.600e-10   406-417 BL00678 9.67 6.684e-09 320-331   PR00326   GTP-ASP (WD) repeat   BL00678 9.67 6.684e-09 320-331   PR00326   GTP-BINDING   PR00326A 8.75 1.346e- 1683   PR00326   GTP-BINDING   PR00326A 8.75 1.346e- 1685   PR00646   RDC1 ORPHAN RECEPTOR   PR00646H 6.32 4.188e- 1690   BL01160   Kinesin light chain   repeat proteins.   PR00456H 6.32 4.188e- 1691   PR00456   RIBOSOMAL PROTEIN P2   PR00456E 3.06 7.281e- 10 418-432   PR00456E 3.06 8.125e- 10 420-435   PR00456E 3.06 8.125e- 10 487-502   PR00456E 3.06 8.125e- 10 487-502   PR00456E 3.06 8.125e- 10 488-503   PR00456E 3.06 8.125e- 10 489-504		!		I
183 PR00747E 15.13   8.244e-15 254-272   PR00747B 7.65 5.355e-13 75-90 PR00747F   13.56 8.714e-10 311-328   PR00747H 12.76 8.636e-13 75-90 PR00747E   13.56 8.714e-10 311-328   PR00747H 12.76 8.636e-13 75-90 PR00747C 12.06   7.500e-18 112-131   PR00747A 14.05 4.600e-17 42-63 PR00747E 12.06   7.500e-18 112-131   PR00747A 14.05 4.600e-17 42-63 PR00747B   7.65 5.355e-13 75-90   PR00747F 13.56 8.714e-10 193-210   PR00747F 13.56 8.714e-10 193-210   PR00747F 13.56 8.714e-10 193-210   PR00747F 13.56 8.714e-10 193-210   PR00747F 13.56 8.714e-10 193-210   PR00747F 13.56 8.714e-10 193-210   PR00747F 13.56 8.714e-10 193-210   PR00747F 13.56 8.714e-10 193-210   PR00747F 13.56 8.714e-10 193-210   PR00747F 13.56 8.714e-10 193-210   PR00747F 13.56 8.714e-10 193-210   PR00747F 13.56 8.714e-10 193-210   PR00678 9.67 4.600e-10 406-417 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 329-340 BL00678 9.67 4.600e-10 409-434 PR004568 3.06 7.281e-10 497-504 BL00678 9.67 4.600e-10 497-504 BL00678 9.67 4.600e-10 497-504 BL00678 9.67 4.600e-10 497-504 BL00678 9.67 4.600e-10 497-504 BL00678 9.67 4.600e-10 497-504 BL0067				1
B. 244e-15 254-272   PR00747F 1.355e-13 75-90 PR00747F 1.3.56 8.714e-10 311-328   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR00747   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074   PR0074				
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13 75-90 PR00747F 13.56 8.714e-10 311-328  PR00747 GLYCOSYL HYDROLASE PR00747H 12.76 8.635e-19 309-330 PR00747C 14.50 2.286e-18 250-275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-17 42-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-10 193-210  BL00678 Trp-Asp (WD) repeat BL00678 9.67 4.600e-10 406-417 BL00678 9.67 6.684e-09 320-331  1681 BL00678 Trp-Asp (WD) repeat BL00678 9.67 4.600e-10 406-417 BL00678 9.67 6.684e-09 320-331  1683 PR00326 GTP1/OBG GTP-BINDING PR00366B 9.67 4.600e-10 329-340 BL00678 9.67 6.684e-09 243-254  PR00546 RDCI ORPHAN RECEPTOR PR0036AB 6.32 4.188e-31690 BL01160 Kinesin light chain BL0160B 19.54 6.644e-19 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 8.125e-10 4420-435  PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e-10 449-504  PR00456E 3.06 8.125e-10 448-503 PR00456E 3.06 7.281e-10 448-503 PR00456E 3.06 7.281e-10 448-503 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.125e-10 448-504 PR00456E 3.06 8.043e-10 448-504 PR00456E 3.06 8.043e-10 448-504 PR00456E 3.06 8.043e-10 448-504 PR00456E 3.06				
13.56 8.714e-10 311- 328  PR00747				
1677   PR00747   GLYCOSYL HYDROLASE   PR00747H 12.76 8.636e-  FAMILY 47 SIGNATURE   19 309-330 PR00747G 14.50 2.286e-18 250-  275 PR00747C 12.06 7.500e-18 112-131   PR00747A 14.05 4.600e-  17 42-63 PR00747B 13.56 8.714e-  10 193-210   PR00747F 13.56 8.714e-  10 193-210   PR00747F 13.56 8.714e-  10 193-210   PR00747F 13.56 8.714e-  10 193-210   PR00747F 13.56 8.714e-  10 193-210   PR00747F 13.56 8.714e-  10 193-210   PR00747F 13.56 8.714e-  10 193-210   PR00747F 13.56 8.714e-  10 193-210   PR00747F 13.56 8.714e-  10 193-210   PR00747F 13.56 8.714e-  10 193-210   PR00747F 13.56 8.714e-  10 193-210   PR00747F 13.56 8.714e-  10 193-210   PR00747F 13.56 8.714e-  10 193-210   PR00747F 13.56 8.714e-  10 193-210   PR00747F 13.56 8.714e-  10 193-210   PR00747F 13.56 8.714e-  10 193-210   PR00747F 13.56 8.714e-  13 329-340 BL00678 9.67 6.684e-09 320-331   PR00326A 8.75 1.346e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00747F 13.746e-  PR00				
FAMILY 47 SIGNATURE  FAMILY 47 SIGNATURE  19 309-330 PR00747G 14.50 2.286e-18 250- 275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e-1 17 42-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e-1 10 193-210  BL00678  Trp-Asp (WD) repeat Proteins proteins.  406-417 BL00678 9.67 6.684e-09 320-331  BL00678 9.67 4.600e-10 Proteins proteins.  1681  BL00678  FR00326  GTP1/OBG GTP-BINDING PR00326A 8.75 1.346e-1 13 389-410  FR00326  FR00164  RDC1 ORPHAN RECEPTOR FR00546B 6.32 4.188e-09 755-771  BL01160B 19.54 6.644e-1 1690  BL01160  Kinesin light chain repeat proteins.  1691  PR00456  RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e-1 10 420-435  PR00456E 3.06 8.125e-1 10 487-502 PR00456E 3.06 7.281e-10 448-503 PR00456E 3.06 8.125e-1 10 489-504  AAA-protein family BL00674C 22.60 8.043e-				5
14.50 2.286e-18 250- 275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e- 17 42-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e- 10 193-210  BL00678 Trp-Asp (WD) repeat DE00678 9.67 4.600e-10 proteins proteins. 406-417 BL00678 9.67 6.684e-09 320-331  1681 BL00678 Trp-Asp (WD) repeat DE00678 9.67 4.600e-10 proteins proteins. 229-340 BL00678 9.67 6.684e-09 243-254  FR00326 GTP1/OBG GTP-BINDING PR00326A 8.75 1.346e- PROTEIN FAMILY SIGNATURE 13 389-410  1685 PR00646 RDC1 ORPHAN RECEPTOR PR00646H 6.32 4.188e- SIGNATURE 09 755-771  1690 BL01160 Kinesin light chain PR00646H 6.32 4.188e- 1691 PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e- 10 418-432 PR00456E SIGNATURE 10 418-432 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 8.125e- 10 420-435  PR00456E 3.06 8.125e- 10 487-502 PR00456E 3.06 7.281e-10 488-503 PR00456E 3.06 8.125e- 10 489-504 BL00674 AAA-protein family BL00674C 22.60 8.043e-	1677	PR00747		
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7.500e-18 112-131 PR00747A 14.05 4.600e- 17 42-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e- 10 193-210  BL00678 Trp-Asp (WD) repeat BL00678 9.67 4.600e-10 Proteins proteins. 406-417 BL00678 9.67 6.684e-09 320-331  BL00678 Trp-Asp (WD) repeat BL00678 9.67 4.600e-10 Proteins proteins. 329-340 BL00678 9.67 6.684e-09 243-254  PR00326 GTP1/OBG GTP-BINDING PR00326A 8.75 1.346e- 1685 PR00646 RDC1 ORPHAN RECEPTOR PR00646H 6.32 4.188e- SIGNATURE 09 755-771  1690 BL01160 Kinesin light chain BL01160B 19.54 6.644e- repeat proteins. 09 75-129  RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e- 10 418-413 PR00456E SIGNATURE 10 449-434 PR00456E 3.06 8.125e- 10 420-435 SIGNATURE 10 488-503 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e-10 488-503 PR00456E 3.06 8.125e- 10 489-504  BL00674 AAA-protein family BL00674C 22.60 8.043e-				
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BL00678   Trp-Asp (WD) repeat			1	
Proteins proteins.   406-417 BL00678 9.67	1680	BL00678	Trn-Asp (WD) reneat	
BL00678   Trp-Asp (WD) repeat   BL00678 9.67 4.600e-10   29-340 BL00678 9.67   6.684e-09 243-254   6.684e-09 243-254   6.684e-09 243-254   6.684e-09 243-254   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-10   78.00326A 8.75 1.346e-			proteins proteins.	
PRO0326   GTP1/OBG GTP-BINDING   PRO0326A 8.75 1.346e-   13 389-410   PRO0546   RDC1 ORPHAN RECEPTOR   SIGNATURE   13 389-410   PRO0546H 6.32 4.188e-   1690   BL01160   Kinesin light chain   BL01160B 19.54 6.644e-   1691   PRO0456   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 7.281e-   10 418-423   PRO0456E   3.06 7.281e-   10 420-435   PRO0456E 3.06 7.281e-   10 487-502   PRO0456E 3.06 7.281e-   10 487-502   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   RIBOSOMAL PROTEIN P2   PRO0456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   RIBOSOMAL PROTEIN P2   RIBOSOMAL PROTEIN P2   RIBOSOMAL PROTEIN P2   RIBOSOMAL PROTEIN P2   RIBOSOMAL PROT				
1683   PR00326   GTP1/OBG GTP-BINDING   PR00326A 8.75 1.346e-   13 389-410   1685   PR00646   RDCI ORPHAN RECEPTOR   PR00646H 6.32 4.188e-   13 389-410   1690   BL01160   Kinesin light chain   RDL0160B 19.54 6.644e-   1691   PR00456   RIBOSOMAL PROTEIN P2   PR00456E 3.06 7.281e-   10 418-423 PR00456E 3.06 7.281e-   10 420-435   PR00456   RIBOSOMAL PROTEIN P2   PR00456E 3.06 8.125e-   10 420-435   PR00456E 3.06 7.281e-   10 487-502 PR00456E 3.06 7.281e-   10 487-502 PR00456E 3.06 7.281e-   10 487-502 PR00456E 3.06 7.281e-   10 487-502 PR00456E 3.06 7.281e-   10 487-502 PR00456E 3.06 7.281e-   10 487-502 PR00456E 3.06 7.281e-   10 487-502 PR00456E 3.06 7.281e-   10 487-504 PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-504   PR00456E 3.06 8.125e-   10 489-5	1681	BL00678		BL00678 9.67 4.600e-10
PR00326   GTP1/OBG GTP-BINDING   PR00326A 8.75 1.346e-   13 389-410   1685   PR00646   RDCI ORPHAN RECEPTOR   PR00646H 6.32 4.188e-   09 755-771   1690   BL01160   Kinesin light chain   RDC1160B 19.54 6.644e-   09 75-129   PR00456E 3.06 7.281e-   10 418-423   PR00456E 3.06 7.281e-   10 418-423   PR00456E 3.06 8.125e-   10 420-435   PR00456E 3.06 7.281e-   10 420-435   PR00456E 3.06 7.281e-   10 487-502   PR00456E 3.06 7.281e-   10 487-502   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P2   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   RIBOSOMAL PROTEIN P3   PR00456E 3.06 8.125e-   10 489-504   RIBOSOMAL PROTEIN P3   RIBOSOMAL PROTEIN P3   RIBOSOMAL PROTEIN P3   RIBOSOMAL PROTEIN P3   RIBOSOMAL PROTEIN P3   RIBOSOMAL PROTEIN P3   RIBOSOMAL PROTEIN P3   RIBOSOMAL PROTEIN P3   RIBOSOMAL PROTEIN P3   RIBOSOMAL PROTEIN P3   RIBOSOMAL PROTEIN P3   RIBOSOMAL PROTEIN P3   RIBOSOMAL PROTEIN P3   RIBOSOMAL PROTEIN P3   RIBOSOMAL PROTEIN			proteins proteins.	
PROTEIN FAMILY SIGNATURE  13 389-410  1695  PRO0646  RDC1 ORPHAN RECEPTOR SIGNATURE  09 755-771  1690  BL01160  Kinesin light chain repeat proteins.  09 75-129  PRO0456  RIBOSOMAL PROTEIN P2 SIGNATURE  10 418-433 PRO0456E 3.06 7.281e-10 419-434 PRO0456E 3.06 8.125e- 10 420-435  PRO0456  RIBOSOMAL PROTEIN P2 SIGNATURE  10 487-502 PRO0456E 3.06 7.281e-10 488-503 PRO0456E 3.06 8.125e- 10 489-504  BL00674  AAA-protein family  BL00674C 22.60 8.043e-	1683	PROUZZE	GTD1 /ORC CON DESCRIPTION	
PR00646   RDC1 ORPHAN RECEPTOR   SIGNATURE   O9 755-771		200320	,	1
SIGNATURE 09 755-771  1690 BL01160 Kinesin light chain repeat proteins. 09 75-129  1691 PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e-10 418-423 PR00456E 3.06 7.281e-10 418-434 PR00456E 3.06 8.125e-10 420-435  1692 PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e-10 420-435  SIGNATURE PR00456E 3.06 7.281e-10 487-502 PR00456B 3.06 7.281e-10 487-502 PR00456B 3.06 7.281e-10 488-503 PR00456E 3.06 8.125e-10 489-504  BL00674 AAA-protein family BL00674C 22.60 8.043e-	1685	PR00646		
BL01160   Kinesin light chain repeat proteins.   BL01160B 19.54 6.644e- 09 75-129			1	
repeat proteins. 09 75-129  PRO0456 RIBOSOMAL PROTEIN P2 PRO0456E 3.06 7.281e- 10 418-433 PR00456E 3.06 7.281e- 10 418-433 PR00456E 3.06 8.125e- 10 420-435  PRO0456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e- SIGNATURE 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e-	1690	BL01160	Kinesin light chain	
SIGNATURE SIGNATURE 10 418-433 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 8.125e-10 420-435  PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e-10 487-502 PR00456E 3.06 7.281e-10 487-502 PR00456E 3.06 7.281e-10 489-503 PR00456E 3.06 8.125e-10 489-504  BL00674 AAA-protein family BL00674C 22.60 8.043e-	7.607		<del></del>	09 75-129
3.06 7.281e-10 419-434 PR00456E 3.06 8.125e- 10 420-435  PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e- SIGNATURE 10 487-502 PR00456E 3.06 7.281e-10 488-503 PR00456E 3.06 8.125e- 10 489-504  BL00674 AAA-protein family BL00674C 22.60 8.043e-	TOAT	PR00456		
PR00456E 3.06 8.125e- 10 420-435  PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e- SIGNATURE 10 487-502 PR00456E 3.06 7.281e-10 488-503 PR00456E 3.06 8.125e- 10 489-504  BL00674 AAA-protein family BL00674C 22.60 8.043e-			SIGNATURE	
10 420-435 PR00456 RIBOSOMAL PROTEIN P2 SIGNATURE PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e-10 488-503 PR00456E 3.06 8.125e- 10 489-504 RIBOSOMAL PROTEIN P2 BL00674 AAA-protein family BL00674C 22.60 8.043e-				
PR00456 RIBOSOMAL PROTEIN P2 PR00456E 3.06 7.281e- 10 487-502 PR00456E 3.06 7.281e-10 488-503 PR00456E 3.06 8.125e- 10 489-504  BL00674 AAA-protein family BL00674C 22.60 8.043e-		}		
SIGNATURE 10 487-502 PR00456E 3.06 7.281e-10 488-503 PR00456E 3.06 8.125e-10 489-504  BL00674 AAA-protein family BL00674C 22.60 8.043e-	1692	PR00456	RIBOSOMAL PROTEIN P2	L
3.06 7.281e-10 488-503 PR00456E 3.06 8.125e- 10 489-504 BL00674 AAA-protein family BL00674C 22.60 8.043e-			I	
10 489-504 1693 BL00674 AAA-protein family BL00674C 22.60 8.043e-		1	[	3.06 7.281e-10 488-503
BL00674 AAA-protein family BL00674C 22.60 8.043e-			1	
BL006/4C 22.60 8.043e-	1693	BLODE 74		
		5000074		
			Processis.	24 2/4-317 BL00674B

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		4.46 4.000e-23 241-263 BL00674D 23.41 8.560e- 18 338-385 BL00674E 15.24 1.720e-15 414- 434
1697	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409F 12.70 4.388e- 10 427-447 PR00466C 10.17 3.443e-
1698	PR00466	CYTOCHROME B-245 HEAVY CHAIN SIGNATURE	PRO0466C 10.17 3.4436- 13 187-208 PR00466B 5.03 5.500e-11 162-186 PR00466F 9.16 6.159e- 09 498-517 BL00028 16.07 9.217e-
1699	BL00028	Zinc finger, C2H2 type, domain proteins.	12 283-300 BL00028 16.07 3.769e-11 255- 272 BL00028 16.07 5.154e-11 171-188 BL00028 16.07 5.500e- 11 227-244 BL00028 16.07 1.600e-10 199- 216
1700	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 3.348e- 15 62-102 BL01019B 19.49 4.000e-15 107- 162
1703	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.484e- 12 200-239 PR00109B 12.27 4.558e-
1707	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PROOTISM 12.27 4.3556 14 134-153 PROOTISM 11.19 2.565e-
1710	PR00019	LEUCINE-RICH REPEAT SIGNATURE	10 116-130 PR00019B 11.36 4.600e-09 113- 127 PR00019B 11.36 7.120e-09 204-218
1711	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 6.523e- 11 232-247 BL01159 13.85 5.408e-10 613- 628
1712	PF00023	Ank repeat proteins.	PF00023A 16.03 7.000e- 10 187-203 PF00642 11.59 9.550e-
1713	PF00642	Zinc finger C-x8-C-x5-C- x3-H type (and similar). Zinc finger C-x8-C-x5-C-	11 230-241
1714	PF00642	x3-H type (and similar).  GTP-binding nuclear	
1715	BL00353	protein ran proteins.  HMG1/2 proteins.	09 7-51 BL00353C 14.83 6.018e-
1775			10 136-183 BL00353B 11.47 8.866e-09 86-136 BL00412D 16.54 5.408e-
1719	BL00412	Neuromodulin (GAP-43) proteins.	09 432-483 BL00038B 16.97 8.448e-
1721	BL00038	Myc-type, 'helix-loop- helix' dimerization domain proteins.	12 79-100 BL00038A 13.61 4.000e-11 52-68 PD00567C 9.17 8.500e-
1723	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	09 418-428 BL01279A 24.27 5.663e-
1724	BL01279	Protein-L- isoaspartate(D- aspartate) O- methyltransferase signa	12 233-281
1728	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.059e-11 73-86 BL00018 7.41 4.176e-11 157-170 BL00594A 16.75 1.089e-
1730	BL00594	Aromatic amino acids permeases proteins.	09 17-61

SEQ ID N	O: ACCESSION	DESCRIPTION	RESULTS*
1731	NO. BL01160		<b>,</b>
	BE01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e- 10 296-350
1732	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e-
1733	PF00850	Histone deacetylase	10 316-370 PF00850F 15.70 4.349e-
		family.	22 246-279 PF00850D 14.76 6.850e-20 177-
			201 PF00850E 8.88
			8.691e-18 209-235 PF00850G 22.75 4.098e-
1734	BL00354	HMG-I and HMG-Y DNA-	14 281-323
ļ	2200334	binding domain proteins	BL00354C 6.61 5.932e- 09 292-307
1735	DM00179	(Ahook) w KINASE ALPHA ADHESION	D400170
1743		T-CELL.	DM00179 13.97 5.263e- 10 492-502
1/43	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e- 11 5-27 PR00449D
			10.79 2.241e-10 109-
			123 PR00449E 13.50 9.289e-10 144-167
1744	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e-
		AAS SIGNATURE	11 5-27 PR00449D 10.79 2.241e-10 109-
			123 PR00449E 13.50 9.289e-10 144-167
1745	BL00720	Guanine-nucleotide	BL00720B 16.57 8.297e-
		dissociation stimulators CDC25 family sign.	15 136-160
1746	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY	PR00081B 10.38 6.727e-
		SIGNATURE	11 45-57 PR00081E 17.54 3.935e-10 150-
1747	BL00439	Acyltransferases	168 BL00439H 18.24 8.435e-
		ChoActase / COT / CPT	14 65-91 BL00439G
1749	PR00819	family proteins.  CBXX/CFQX SUPERFAMILY	13.40 2.895e-12 3-14 PR00819B 10.83 7.158e-
1751	PD00066	SIGNATURE PROTEIN ZINC-FINGER	11 4-20
İ		METAL-BINDI.	PD00066 13.92 3.400e- 14 33-46 PD00066
		·	13.92 1.000e-13 89-102 PD00066 13.92 7.000e-
			13 61-74 PD00066
4850			13.92 6.571e-12 117- 130
1753	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 6.516e- 18 33-77
1754	BL00790	Receptor tyrosine kinase	BL00790I 20.01 2.393e-
		class V proteins.	09 490-521 BL00790I 20.01 2.821e-09 60-91
			BL007901 20.01 6.357e-
1756	PD01066	PROTEIN ZINC FINGER	09 287-318 PD01066 19.43 9.750e-
		ZINC-FINGER METAL- BINDING NU.	35 10-49
1758	DM00406	GLIADIN.	DM00406 7.73 7.600e-09
1762	PD02929	ADHESION GLYCOPROTEIN	653-666 PD02929A 28.27 4.529e-
1765	PR00326	PRECURSOR I.	09 224-278
		GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 5.950e- 11 146-167
1775	PF00023	Ank repeat proteins.	PF00023A 16.03 3.077e-
1776	BL00942	glpT family of	14 523-539 BL00942F 15.07 4.343e-
		transporters proteins.	10 371-389 BL00942B
1777	DM00215	PROLINE-RICH PROTEIN 3.	20.36 8.040e-09 94-137 DM00215 19.43 2.373e-
			09 279-312

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1778	BL00084	Copper type II, ascorbate-dependent monooxygenases proteins.	BL00084D 25.11 3.700e- 20 169-224 BL00084B 24.26 8.134e-16 10-58 BL00084C 27.71 8.412e- 11 107-158
1779	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 3.758e- 18 611-655 BL01013A 25.14 2.891e-15 344- 380 BL01013C 9.97 6.308e-13 435-445 BL01013B 11.33 3.717e- 12 409-420
1783	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515
1784	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515

^{*} results include in order: accession number subtype; raw score; p-value; postion of signature in amino acid sequence.

TRADOCS:1416223.1(%CRJ0!!.DOC)

TABLE 4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:			b-varge	SCORE
2	ig	Immunoglobulin domain	2.1e-32	109.5
3	pkinase	Eukaryotic protein kinase domain	1.3e-29	110.7
4	zf-C2H2	Zinc finger, C2H2 type	1.6e-21	84.9
5	fn3	Fibronectin type III domain	0	1097.1
6	fn3	Fibronectin type III domain	0	1035.0
7	fn3	Fibronectin type III domain	<del>  0</del>	1090.4
8	fn3	Fibronectin type III domain	10	1097.1
9	TBC	TBC domain	4e-40	146.7
10	p450	Cytochrome P450	9.5e-17	62.0
12	ank	Ank repeat	6e-20	79.7
14	ig	Immunoglobulin domain	1.7e-05	22.7
15	zf-MYND	MYND finger	1.3e-06	35.4
16	zf-MYND	MYND finger	1.3e-06	35.4
17	zf-C2H2	Zinc finger, C2H2 type	1.7e-99	343.9
18	CAP_GLY	CAP-Gly domain	1.2e-25	98.7
20	IMPDH_C	IMP dehydrogenase / GMP	1.6e-119	410.5
	_	reductase C terminus	1.00-115	1 310.3
21	IMPDH C	IMP dehydrogenase / GMP	4.3e-102	352.6
		reductase C terminus		"""
22	pkinase	Eukaryotic protein kinase domain	2.4e-79	277.0
23	pkinase	Eukaryotic protein kinase domain	8.4e-74	258.6
25	RNA_pol_A	RNA polymerase alpha subunit	10	1077.7
26	Clq	Clq domain	1.9e-10	44.4
27	Ribosomal_L2	Ribosomal protein L23	7.8e-32	111.2
28	Ribosomal_L2	Ribosomal protein L23	le-29	104.2
30	zf-A20	A20-like zinc finger	1.5e-10	48.5
31	zf-A20	A20-like zinc finger	1.5e-10	48.5
32	FMN_dh	FMN-dependent dehydrogenase	5.4e-179	608.1
34	PID	Phosphotyrosine interaction domain (PTB/PID)	3.8e-59	209.9
35	ig	Immunoglobulin domain	1.4e-13	48.8
36	ig	Immunoglobulin domain	1.4e-13	48.8
40	kinesin	Kinesin motor domain	6.7e-76	265.6
44	Ets	Ets-domain	1.4e-56	182.1
45	Ets	Ets-domain	1.4e-56	182.1
46	LRR	Leucine Rich Repeat	1.7e-13	58.3
48	zf-C2H2	Zinc finger, C2H2 type	2.3e-162	552.8
49	ITAM	Immunoreceptor tyrosine-based activation mot	1.4e-05	31.9
50		FYInd and Jan	<del> </del>	1 200 0
	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
	UCH-2	hydrolase family   Ubiquitin carboxyl-terminal	1.1e-26	102.0
51		hydrolase family Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
51	UCH-2	hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family	1.1e-26 8.5e-45	102.0
51 52 53	UCH-2	hydrolase family Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
51 52 53 54	UCH-2 ras PRK myb_DNA-	hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain	1.1e-26 8.5e-45 2.1e-65 0.096	102.0 162.3 230.7 15.2
51 52 53 54	UCH-2 ras PRK myb_DNA- binding	hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain Voltage gated chloride channels	1.1e-26 8.5e-45 2.1e-65 0.096	102.0 162.3 230.7 15.2
52 53 54	ras PRK myb_DNA- binding voltage_CLC	hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain	1.1e-26 8.5e-45 2.1e-65 0.096 3.3e-186 0.00015	102.0 162.3 230.7 15.2 631.9 -64.3
52 53 54 55 66 57	ras PRK myb_DNA- binding voltage_CLC sugar_tr	hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain  Voltage gated chloride channels Sugar (and other) transporter TBC domain	1.1e-26 8.5e-45 2.1e-65 0.096 3.3e-186 0.00015 2.2e-37	102.0 162.3 230.7 15.2 631.9 -64.3
551 552 553 554 55 66 67 68	ras PRK myb_DNA- binding voltage_CLC sugar_tr TBC	hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain  Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat	1.1e-26 8.5e-45 2.1e-65 0.096 3.3e-186 0.00015 2.2e-37 5.9e-25	102.0 162.3 230.7 15.2 631.9 -64.3 137.6 96.3
51 52 53 54 55 66 57 58	ras PRK myb_DNA- binding voltage_CLC sugar_tr TBC ank	hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain  Voltage gated chloride channels Sugar (and other) transporter TBC domain	1.1e-26 8.5e-45 2.1e-65 0.096 3.3e-186 0.00015 2.2e-37	102.0 162.3 230.7 15.2 631.9 -64.3 137.6
551 52 53 54 55 56 57 58 59	UCH-2  ras  PRK  myb_DNA- binding  voltage_CLC  sugar_tr  TBC  ank  ank  PMP22_Claudi	hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain  Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat  PMP-22/EMP/MP20/Claudin family	1.1e-26 8.5e-45 2.1e-65 0.096 3.3e-186 0.00015 2.2e-37 5.9e-25 5.9e-25 7.9e-49	102.0 162.3 230.7 15.2 631.9 -64.3 137.6 96.3 96.3 175.6
551 52 53 54 55 56 57 58 59 57	ras PRK myb_DNA- binding voltage_CLC sugar_tr TBC ank ank PMP22_Claudi n	hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain  Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat PMP-22/EMP/MP20/Claudin family  C2 domain	1.1e-26 8.5e-45 2.1e-65 0.096 3.3e-186 0.00015 2.2e-37 5.9e-25 5.9e-25 7.9e-49	102.0 162.3 230.7 15.2 631.9 -64.3 137.6 96.3 96.3 175.6
51 52 53 54 55 66 67 58 59 57	ras PRK myb_DNA- binding voltage_CLC sugar_tr TBC ank ank PMP22_Claudi n C2	hydrolase family Ubiquitin carboxyl-terminal hydrolase family Ras family Phosphoribulokinase Myb-like DNA-binding domain  Voltage gated chloride channels Sugar (and other) transporter TBC domain Ank repeat Ank repeat PMP-22/EMP/MP20/Claudin family  C2 domain C2 domain	1.1e-26 8.5e-45 2.1e-65 0.096 3.3e-186 0.00015 2.2e-37 5.9e-25 7.9e-49 7.9e-54 2.3e-54	102.0 162.3 230.7 15.2 631.9 -64.3 137.6 96.3 96.3 175.6
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NO:	PFAM NAME	DESCRIPTION			PCT/U
160	Jacalin				
165	Zn_carbOpe	Jacalin-like led	et in a	p-value	PFAM
167	- Lase	ot Zinc carboxypept  Eukaryotic pro-	idase	0.09	SCORE
	zf-C3IIC4	I down :- Fryte	7 10	E	-24.9
168	Ribosomal_Si	finger) C3HC	C4 F3	5.1e-67	471.9 236.1
169		Ribosomal protein	The (RING	5.3e-07	
171	DEAD DUF59	DEAD/DES	\$15	1	27.0
177		DEAD/DEAH box hel	icase	1.1e-06	29.0
[ P	kinase	I DOEG - TOTAL OWN	filmed	le-48	157.0
173 g.	obin	Eukaryotic protein	Kinn	0.07	-17.4
175 WA		1 01001h		3.7e-15	1
178 ra	5	WW domain		1	58.6
179 AT	PIG1_PLM_M	Ras family ATPIGION		4.6e-18 7.3e-06	67.4
180 2f-	C2H2	ATP1G1/PLM/MAT8 fam:	ily	le-31	32.9
190 Ciq		Zinc fines		2.5e-17	118.8 71.0
	hosphatas	Clq domain Protein	pe	1.5e-99	- 1
103 efha	ind	Protein-tyrosine phos	sphatase	8.8e-72	344.2
Pkin	ase E	F hand		90 300	67.0
194 brond	odomain R	ukaryotic protein ki	nasa 7	50.16	- 1
Lamp	Bi	comodomain	6	E	5.1
197 Dnay	en	ridoxal-phosphate de zyme		1 - 9	35.6
199 RrnaAi	Dn.	aJ domain	pendent 2.	8e-31 11 5e-64 23	1.4
200	1 1/11	20S0m-1		1 42	7.1
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204 VATP-	home	Aldrich sime	_   4.5	e-10 37.	<del>-</del>
205 Synt_AC	39 ATP	Synthase (C/AC39) su	0.00	10.40	- 1
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206 Idl_rece	.3	Archase (C/AC30)	1.3e	-159 543.	7
209	Low-d	ensity lipoprotein tor domain	1.6e-	139 476.5	1
210 Rhomboid	- I state ye	DO:	2.4e-		' ]
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213 UQ_con 215 UQ_con	Clq do	main	1.4e-1	9 78.4	$ \rightarrow $
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1 210	PMP-227	AH box helicase EMP/MP20/Claudin fam	1e-53	258.8 191.9	$\exists$
Glycos_train f_2	ns Glycosy	transferases	ily 1.8e-43 4.5e-21		
222 19	- Image	cransferases		83.4	7
The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	WD domest	obulin domain	4e-21	83.6	1
DnaJ CXXCVC	TPR Des	veta ron	0.092	_1	1
	DnaJ cent	ral domai	7.4e-23	10.7 89.4	1
DnaJ_CXXCXGX G	Dnaul com	ral domain (4 repeat	1.2e-08 (s) 1.5e-38	42.1	1
230 HSP70	_	di domain //	_1	141.5	
231 GSHPX	Hsp70 prot	ein	s) 1.5e-38	141.5	
233 cyclin	Thrombos	e peroxidases	2.4e-54	1 1	
235 ras	Cyclin	e peroxidases ndin type 1 domain	3.4e-47	194.0	
236 LRR	Ras family		0.0075	170.2 17.1	
237 PDZ	Leucine Ric	h Repeat	4.6e-144 4.8e-50	492.0	
	Leucine Rici	Repeat Also known as DHR	1.2e-30	179.7	
	or GLGF).	ALSO KNOWN as DHR	6.7e-29	115.3	
			1.7e-09	5.0	
		248			

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
244	dCMP_cyt_dea	Cytidine and deoxycytidylate	2.5e-05	31.1
0.0	m	deaminase Immunoglobulin domain	6.7e-08	30.5
245	ig	wnt family of developmental	9.1e-270	742.6
248	wnt	signaling protei		
250	mito_carr	Mitochondrial carrier proteins	1.3e-55	193.6
254	adenylatekin ase	Adenylate kinase	1.8e-14	55.7
255	Cation_efflu x	Cation efflux family	2.8e-33	124.0
256	SH3	SH3 domain	3.9e-14	60.4
257	Aa_trans	Transmembrane amino acid	2.6e-52	187.2
	<u> </u>	transporter protein		
258	adenylatekin ase	Adenylate kinase	2.1e-110	380.2
259	HIT	HIT family	8.2e-07	25.3
260	Bacterial_PQ	PQQ enzyme repeat	1.6e-15	65.0
262	proteasome	Proteasome A-type and B-type	6.5e-64	225.7
267	pkinase	Eukaryotic protein kinase domain	6.3e-27	101.0
270	filament	Intermediate filament proteins	3.2e-150	512.5
271	Choline_kina	Choline/ethanolamine kinase	2e-67	237.4
277	Ribosomal S7	Ribosomal protein S7p/S5e	3.3e-20	80.6
279	pkinase	Eukaryotic protein kinase	3.3e-77	269.9
280	WD40	WD domain, G-beta repeat	7.8e-73	255.4
281	WD40	WD domain, G-beta repeat	7.8e-73	255.4
284	zf-DHHC	DHHC zinc finger domain	4.6e-24	93.4
287	Exonuclease	Exonuclease	1.4e-67	238.0
291	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
292	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
294	zf-C2H2	Zinc finger, C2H2 type	1.4e-29	111.7
295	zf-C2H2	Zinc finger, C2H2 type	2.2e-125	430.0
296	mito_carr	Mitochondrial carrier proteins	4.1e-59	205.5
297	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
302	Glycos_trans f_4	Glycosyl transferase	5e-87	302.5
304	tRNA-synt_2	tRNA synthetases class II (D, K and N)	1.1e-84	294.8
305	KRAB	KRAB box	2e-44	161.0
306	rrm	RNA recognition motif.	2.7e-44	160.6
308	7tm_1	7 transmembrane receptor (rhodopsin family)	5.2e-39	126.1
309	DNA_polymera	DNA polymerase X family	2.4e-64	227.2
311	F-box	F-box domain.	9.5e-08	39.2
312	ig	Immunoglobulin domain	6.8e-19	65.9
313	Ets	Ets-domain	8.le-60	192.3
315	Kelch	Kelch motif	1.3e-106	367.6
317	arf	ADP-ribosylation factor family	3.2e-35	130.4
318	sugar_tr	Sugar (and other) transporter	0.0003	-73.1
320	pkinase	Eukaryotic protein kinase domain	8.1e-83	288.6
322	pkinase	Eukaryotic protein kinase domain	4.9e-81	282.6
324	Xlink	Extracellular link domain	4.5e-143	331.5
326	ARID	ARID DNA binding domain	5.1c-37	136.4
327	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
328	cadherin	Cadherin domain	8.1e-81	281.9
331	chromo	'chromo' (CHRromatin Organization MOdifier)	4e-18	66.7
333	Peptidase M2	Glycoprotease family	1.2e-136	467.4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
335			<u> </u>	SCORE
335	∨wa	von Willebrand factor type A	2.3e-07	37.9
339	ras	Ras family	7.8e-07	-59.1
340	zf-C2H2	Zinc finger, C2H2 type	8.2e-64	225.4
342	zf-C2H2	Zinc finger, C2H2 type	2.4e-85	297.0
343	ig	Immunoglobulin domain	0.0005	
346	pkinase			18.0
	1-	Eukaryotic protein kinase domain	6.5e-65	229.1
347	pkinase	Bukaryotic protein kinase domain	6.5e-65	229.1
351	EGF	EGF-like domain	8.5e-20	79.2
352	ank	Ank repeat	2.5e-101	350.0
354	TBC	TBC domain	5.1e-15	63.3
355	PHD	PHD-finger	3.2e-07	37.4
358	DUF6	Integral membrane protein DUF6		
359	zf-C2H2	Threegral membrane process Dors	0.033	15.8
361		Zinc finger, C2H2 type	7.4e-20	79.4
	ank	Ank repeat	6.6e-34	126.1
362	ArfGap	Putative GTP-ase activating protein for Arf	4.7e-53	189.7
363	efhand	EF hand	5.4e-10	+46.6
367	LRR .	Leucine Rich Repeat		46.6
368	laminin G		8.8e-44	158.9
369	PP2C PP2C	Laminin G domain	1.5e-33	121.7
	1	Protein phosphatase 2C	5.3e-20	73.9
372	LIM	LIM domain containing proteins	9.9e-15	57.1
373	KRAB	KRAB box	4.8e-23	90.0 .
376	ion_trans	Ion transport protein	2.9e-09	-4.2
377	Beach	Beige/BEACH domain	4.9e-208	704.5
380	pkinase	Eukaryotic protein kinase	1.6e-94	327.5
381	AMP-binding		<u> </u>	
382	HECT	AMP-binding enzyme	1.4e-07	-140.3
	HECI	HECT-domain (ubiquitin- transferase).	1.3e-07	-13.5
384	ank	Ank repeat	2.5e-101	350.0
386	ig	Immunoglobulin domain	9.5e-06	23.6
388	zf-C2H2	Zinc finger, C2H2 type	1.7e-42	154.6
389	ig	Immunoglobulin domain	2.8e-15	54.3
390	mito carr	Mitochondrial carrier proteins	3.5e-67	233.2
392	TPR	TPR Domain	6.1e-17	69.7
393	SH3	SH3 domain		
394	AAA	ATPases associated with various	3.5e-09 4.le-21	83.6
396	CDOOD CO	cellular act		
396	spectrin	Spectrin repeat	2.1e-67	237.3
	zf-C2H2	Zinc finger, C2H2 type	0.0066	23.1
399	fn3	Fibronectin type III domain	4.le-102	352.6
400	WD40	WD domain, G-beta repeat	0.00049	26.8
401	El_dehydrcg	Dehydrogenase El component	3e-119	409.6
402	fn3	Fibronectin type III domain	0	1719.6
404	LRR	Leucine Rich Repeat	2.1e-10	48.0
400			<b></b>	
405	cadherin	Cadherin domain	8 76-81	281 0
405	<del></del>	Cadherin domain	8.1e-81	281.9
406	zf-CXXC	CXXC zinc finger	5e-15	63.4
406 410	zf-CXXC RhoGEF	CXXC zinc finger RhoGEF domain	5e-15 1.1e-23	63.4 92.1
406 410 411	zf-CXXC RhoGEF F-box	CXXC zinc finger RhoGEF domain F-box domain.	5e-15 1.1e-23 4.2e-06	63.4 92.1 33.7
406 410 411 412	zf-CXXC RhoGEF	CXXC zinc finger RhoGEF domain F-box domain. SNF2 and others N-terminal domain	5e-15 1.1e-23	63.4 92.1
406 410 411	zf-CXXC RhoGEF F-box	CXXC zinc finger RhoGEF domain F-box domain. SNF2 and others N-terminal domain	5e-15 1.1e-23 4.2e-06 5.8e-16	63.4 92.1 33.7 61.6
406 410 411 412	zf-CXXC RhoGEF F-box SNF2_N	CXXC zinc finger RhoGEF domain F-box domain. SNF2 and others N-terminal	5e-15 1.1e-23 4.2e-06	63.4 92.1 33.7
406 410 411 412	zf-CXXC RhoGEF F-box SNF2_N CPSase_L_cha	CXXC zinc finger RhoGEF domain F-box domain. SNF2 and others N-terminal domain Carbamoyl-phosphate synthase (CPSase)	5e-15 1.1e-23 4.2e-06 5.8e-16	63.4 92.1 33.7 61.6
406 410 411 412 415	zf-CXXC RhoGEF F-box SNF2_N CPSase_L_Cha in LRR	CXXC zinc finger RhoGEF domain F-box domain. SNF2 and others N-terminal domain Carbamoyl-phosphate synthase (CPSase) Leucine Rich Repeat	5e-15 1.1e-23 4.2e-06 5.8e-16 1.5e-172 3.8e-24	63.4 92.1 33.7 61.6 586.6
406 410 411 412 415 418 419	zf-CXXC RhoGEF F-box SNF2_N CPSase_L_Cha in LRR	CXXC zinc finger RhoGEF domain F-box domain. SNF2 and others N-terminal domain Carbamoyl-phosphate synthase (CPSase) Leucine Rich Repeat DENN (AEX-3) domain	5e-15 1.1e-23 4.2e-06 5.8e-16 1.5e-172 3.8e-24 2e-58	63.4 92.1 33.7 61.6 586.6
406 410 411 412 415 418 419 420	zf-CXXC RhoGEF F-box SNF2_N CPSase_L_Cha in LRR DENN RasGEF	CXXC zinc finger RhoGEF domain F-box domain. SNF2 and others N-terminal domain Carbamoyl-phosphate synthase (CPSase) Leucine Rich Repeat DENN (AEX-3) domain RasGEF domain	5e-15 1.1e-23 4.2e-06 5.8e-16 1.5e-172 3.8e-24 2e-58 8.1e-43	63.4 92.1 33.7 61.6 586.6 93.6 207.5 155.7
406 410 411 412 415 418 419 420 421	zf-CXXC RhoGEF F-box SNF2_N CPSase_L_Cha in LRR DENN RasGEF ank	CXXC zinc finger RhoGEF domain F-box domain. SNF2 and others N-terminal domain Carbamoyl-phosphate synthase (CPSase) Leucine Rich Repeat DENN (AEX-3) domain RasGEF domain Ank repeat	5e-15 1.1e-23 4.2e-06 5.8e-16 1.5e-172 3.8e-24 2e-58	63.4 92.1 33.7 61.6 586.6
406 410 411 412 415 418 419 420 421 424	zf-CXXC RhoGEF F-box SNF2_N CPSase_L_cha in LRR DENN RasGEF ank G-patch	CXXC zinc finger RhoGEF domain F-box domain. SNF2 and others N-terminal domain Carbamoyl-phosphate synthase (CPSase) Leucine Rich Repeat DENN (AEX-3) domain RasGEF domain	5e-15 1.1e-23 4.2e-06 5.8e-16 1.5e-172 3.8e-24 2e-58 8.1e-43	63.4 92.1 33.7 61.6 586.6 93.6 207.5 155.7
406 410 411 412 415 418 419 420 421	zf-CXXC RhoGEF F-box SNF2_N CPSase_L_Cha in LRR DENN RasGEF ank	CXXC zinc finger RhoGEF domain F-box domain. SNF2 and others N-terminal domain Carbamoyl-phosphate synthase (CPSase) Leucine Rich Repeat DENN (AEX-3) domain RasGEF domain Ank repeat G-patch domain Eukaryotic protein kinase	5e-15 1.1e-23 4.2e-06 5.8e-16 1.5e-172 3.8e-24 2e-58 8.1e-43 1.4e-153	63.4 92.1 33.7 61.6 586.6 93.6 207.5 155.7 523.7
406 410 411 412 415 418 419 420 421 424	zf-CXXC RhoGEF F-box SNF2_N CPSase_L_cha in LRR DENN RasGEF ank G-patch	CXXC zinc finger RhoGEF domain F-box domain. SNF2 and others N-terminal domain Carbamoyl-phosphate synthase (CPSase) Leucine Rich Repeat DENN (AEX-3) domain RasGEF domain Ank repeat G-patch domain	5e-15 1.1e-23 4.2e-06 5.8e-16 1.5e-172 3.8e-24 2e-58 8.1e-43 1.4e-153 1e-19	63.4 92.1 33.7 61.6 586.6 93.6 207.5 155.7 523.7 78.9

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:	<u> </u>			SCORE
429	zf-C3HC4	Zinc finger, C3HC4 type (RING	8.6e-11	39.2
427	21-C3RC4	finger)	8.66-11	39.2
431	DEAD	DEAD/DEAH box helicase	1e-66	214.0
432	SH3	SH3 domain	3.4e-16	67.2
433	GTP_CDC	Cell division protein	2.1e-114	393.5
436	Collagen	Collagen triple helix repeat	4.6e-194	658.1
		(20 copies)		
438	Ricin_B_lect	Similarity to lectin domain of ricin b	0.0085	10.5
441	Alpha_adapti	Alpha adaptin carboxyl-terminal domai	1.2e-256	866.0
442	Alpha_adapti n_C	Alpha adaptin carboxyl-terminal domai	1.8e-235	795.7
443	PDZ	PDZ domain (Also known as DHR or GLGF).	1.9e-65	230.9
445	LON	ATP-dependent protease La (LON)	0.00012	-17.1
446	ig	Immunoglobulin domain	0.00011	20.1
451	sushi	Sushi domain (SCR repeat)	1.4e-18	75.2
452	fn3	Fibronectin type III domain	1.5e-06	35.2
454	pyridoxal_de	Pyridoxal-dependent	8.3e-14	50.3
	C	decarboxylase conse		
456	kinesin	Kinesin motor domain	4.9e-217	734.4
457	neur_chan	Neurotransmitter-gated ion- channel	1e-175	597.1
458	Josephin	Josephin	0.0002	18.7
468	bzip	bZIP transcription factor	1.7e-07	31.8
470	NTP_transfer ase	Nucleotidyl transferase	6.3e-06	-26.3
471	WD40	WD domain, G-beta repeat	2e-28	107.9
473	LIM	LIM domain containing proteins	0.00021	20.7
477	zf-RanBP	Zn-finger in Ran binding protein and others.	0.028	21.0
479	WD40	WD domain, G-beta repeat	6.5e-18	73.0
480	KRAB	KRAB box	1e-31	118.8
481	ArfGap	Putative GTP-ase activating protein for Arf	8.4e-66	232.0
485	SH2	Src homology domain 2	0.011	11.4
486	Clq	Clq domain	4.3e-74	259.6
487	dsrm	Double-stranded RNA binding motif	1.le-47	171.9
489	zf-C2H2	Zinc finger, C2H2 type	4.8e-153	521.9
490	Alpha_adapti n_C	Alpha adaptin carboxyl-terminal domai	3.4e-222	751.6
492	SKI	Shikimate kinase	1.2e-10	48.8
497	ENV_polyprot ein	ENV polyprotein (coat polyprotein)	2.6e-22	77.6
498	abhydrolase_ 2	Phospholipase/Carboxylesterase	0.041	-48.1
500	rrm	RNA recognition motif.	5.4e-34	126.4
501	WW	WW domain	4.6e-18	73.4
502	ig	Immunoglobulin domain	1.1e-10	39.5
504	abhydrolase	alpha/beta hydrolase fold	0.045	-3.6
505	vwa	von Willebrand factor type A domain	7.1e-62	219.0
508	Na_K_ATPase_ C	Na+/K+ ATPase C-terminus	2.3e-145	496.3
509	Exonuclease	Exonuclease	1.3e-56	201.5
510	Glycos_trans f_1	Glycosyl transferases group 1	2.9e-06	27.0
511	Glycos_trans f 1	Glycosyl transferases group 1	2.9e-06	27.0
512	Glycos_trans f 1	Glycosyl transferases group 1	1.9e-09	38.5
514	pro isomeras	Cyclophilin type peptidyl-	1.8e-63	221.4
	e	prolyl cis-tr	2.00.00	""" ' "

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:	TOTAL MANEE	pbock11110M	p-varue	SCORE
515	EGF	EGF-like domain	1.9e-18	74.7
516	Surp	Surp module	4.3e-38	140.0
523	ig	Immunoglobulin domain	3.3e-06	25.0
526	UBX	UBX domain	1.1e-34	128.6
528	adh zinc	Zinc-binding dehydrogenases	2.7e-34	127.4
530	SAM	SAM domain (Sterile alpha	0.046	10.0
	1	motif)		
531	adh_short	short chain denydrogenase	0.0025	-34.1
532	mito carr	Mitochondrial carrier proteins	2.5e-81	281.7
533	mito carr	Mitochondrial carrier proteins	2e-61	213.5
534	thiolase	Thiolase	3.5e-183	622.0
535	FMO-like	Flavin-binding monooxygenase- like	0	1153.7
536	SCAN	SCAN domain	4e-55	196.6
537	tRNA-synt 1	tRNA synthetases class I (I. L.	3.1e-136	466.0
		M and V)		
538	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.1e-136	466.0
539	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	1.9e-117	403.6
540	tRNA-synt_1	tRNA synthetases class I (I, L, M and V)	3.1e-136	466.0
541	vATP-synt_E	ATP synthase (E/31 kDa) subunit	5.9e-85	295.7
543	zf-C2H2	Zinc finger, C2H2 type	5.5e-69	242.6
544	DUF101	Protein of unknown function DUF101	8.5e-38	139.0
545	TGFb_propept ide	TGF-beta propeptide	1.le-67	238.2
547	WD40	WD domain, G-beta repeat	2.6e-32	120.8
548	RHD	Rel homology domain (RHD).	·1.6e-238	686.2
549	MMR_HSR1	GTPase of unknown function	5.4e-67	236.0
551	HECT	HECT-domain (ubiquitin-	4.3e-127	435.6
554	MHC_II_alpha	transferase). Class II histocompatibility	3.5e-74	259.8
555	zf-UBR1	antigen, alp Putative zinc finger in N-	3.3e-16	67.3
		recognin	L	
556	Kelch	Kelch motif	5.5e-29	109.7
561 562	AMP-binding PABP	AMP-binding enzyme	2.8e-06	-163.7
		Poly-adenylate binding protein, unique domai	4.9e-38	139.8
564	Gag_p30	Gag P30 core shell protein	1.2e-67	238.2
566	PWWP	PWWP domain	8.1e-16	66.0
567	SCAN	SCAN domain	7.3e-68	238.9
569	pkinase	Eukaryotic protein kinase domain	1.5e-84	294.3
570	pkinase	Bukaryotic protein kinase domain	1.5e-84	294.3
571	CN_hydrolase	Carbon-nitrogen hydrolase	0.00081	-79.7
572	myosin_head	Myosin head (motor domain)	0	1495.2
573	myosin_head	Myosin head (motor domain)	0	1490.4
575	Surp	Surp module	1.7e-23	91.5
576	Surp	Surp module	1.7e-23	91.5
577	DNA_pol_B	DNA polymerase family B	0	1138.6
578	PDZ	PDZ domain (Also known as DHR or GLGF).	8.3e-09	42.7
579	LRR	Leucine Rich Repeat	4.9e-21	83.3
580 ·	neur_chan	Neurotransmitter-gated ion- channel	5.9e-177	601.3
583	sushi	Sushi domain (SCR repeat)	<del>  0</del>	1673.0
584	DEAD	DEAD/DEAH box helicase	7.3e-36	116.3
	KH-domain	KH domain	2.9e-13	57.5
586			~ - 3 <del>C</del> ~ T 3	1 31.3
		G-patch domain	2.36-14	61 2
587	G-patch LIM	G-patch domain	2.3e-14	61.2
586 587 589 590	G-patch	G-patch domain LIM domain containing proteins Bromodomain	2.3e-14 2.3e-36 6.6e-32	61.2 133.4 114.7

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
592	hormone_rec	Ligand-binding domain of	3.5e-22	87.1
		nuclear hormone	3.8e-12	<del>  </del>
593	PHD	PHD-finger	4.2e-99	53.8
594	cadherin	Cadherin domain	5e-92	319.2
596	pkinase	Eukaryotic protein kinase domain		
597	WD40	WD domain, G-beta repeat	0.00054	26.7
600	FG-GAP	FG-GAP repeat	4.3e-75	262.9
602	G_Adapt_CT	Gamma-adaptin, C-terminus	1.1e-53	191.8
603	pkinase	Eukaryotic protein kinase domain	2.3e-86	300.4
605	Collagen	Collagen triple helix repeat (20 copies)	8e-42	152.4
606	mito_carr	Mitochondrial carrier proteins	6.3e-67	232.3
608	PWWP	PWWP domain	2.6e-28	107.5
609	PWWP	PWWP domain	2.6e-28	107.5
613	CAP GLY	CAP-Gly domain	0.0046	20.1
615	RFX_DNA_bind	RFX DNA-binding domain	5.2e-54	192.9
616	kinesin	Kinesin motor domain	1.1e-81	284.8
617	kinesin	Kinesin motor domain	8.4e-80	278.5
618	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0098	13.1
620	MATH	MATH domain	7.8e-05	22.2
621	Y_phosphatas	Protein-tyrosine phosphatase	1.4e-32	121.6
622	pkinase	Eukaryotic protein kinase domain	4.4e-40	146.6
623	BNR	BNR repeat	2.1e-11	51.3
624	molybdopteri n	Prokaryotic molybdopterin oxidoreductas	1.4e-12	42.2
625	TPR	TPR Domain	1.1e-17	72.2
627	cNMP_binding	Cyclic nucleotide-binding domain	3.7e-58	206.6
630	adh short	short chain dehydrogenase	5e-17	70.0
631	zf-C2H2	Zinc finger, C2H2 type	2.1e-88	307.1
632	rrm	RNA recognition motif.	4e-05	30.5
635	pkinase	Eukaryotic protein kinase domain	1.6e-104	360.7
636	Fork head	Fork head domain ,	5.9e-27	103.0
637	pkinase	Eukaryotic protein kinase domain	3.8e-70	246.5
642	TPR	TPR Domain	4.8e-08	40.1
643	efhand	EF hand	1.9e-27	104.6
647	SNF2_N	SNF2 and others N-terminal domain	1.2e-101	351.1
648	PseudoU_synt h 2	RNA pseudouridylate synthase	1.9e-55	197.6
650	zf-C2H2	Zinc finger, C2H2 type	0.0087	22.7
651	ank	Ank repeat	1.3e-17	71.9
652	I_LWEQ	I/LWEQ domain	9.5e-101	341.0
653	neur_chan	Neurotransmitter-gated ion- channel	4.1e-171	581.8
654	tsp 1	Thrombospondin type 1 domain	4.1e-47	169.9
659	FH2	Formin Homology 2 Domain	1e-107	371.2
661	рои	Pou domain - N-terminal to homeobox domain	5.3e-45	162.9
662	C2	C2 domain	6.7e-19	76.2
663	C2	C2 domain	6.7e-19	76.2
664	C2	C2 domain	6.7e-19	76.2
667	GST	Glutathione S-transferases.	9.3e-34	114.4
668	LRR	Leucine Rich Repeat	9.3e-31	115.6
670	spectrin	Spectrin repeat	4e-57	203.2
671	I_LWEQ	I/LWEQ domain	9.5e-101	341.0
672	ABC_tran	ABC transporter	5.3e-60	212.8
674	WD40	WD domain, G-beta repeat	4.8e-24	93.3

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
675	WD40	WD domain, G-beta repeat	4.8e-24	93.3
676	LRR	Leucine Rich Repeat		
679		Leucine Rich Repeat	0.0015	25.2
	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-29	107.7
680	zf-C2H2	Zinc finger, C2H2 type	5.2e-05	30.1
681	CH	Calponin homology (CH) domain	2.4e-17	71.1
682	DSPC	Dual specificity phosphatase,	4.3e-43	156.6
683		catalytic doma		
683	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.051	10.8
687	Synapsin	Synapsin	0	1890.8
689	PR55	Protein phosphatase 2A	0	1038.8
	1	regulatory subunit PR	1	
691	homeobox	Homeobox domain	8.5e-30	112.4
696	Peptidase M2	metallopeptidase family M24	2.6e-59	210.5
	4			
697	RhoGEF	RhoGEF domain	9.5e-35	128.9
698	PHD	PHD-finger	0.008	9.3
701	zf-C2H2	Zinc finger, C2H2 type	5.5e-123	422.0
702	Sulfatase	Sulfatase	3e-231	781.6
703	zf-C2H2	Zinc finger, C2H2 type	5.7e-20	79.8
707	Acyl transf	Acyl transferase domain	1.1e-22	88.8
708	WD40	WD domain, G-beta repeat	4.8e-19	76.7
710	Ran BP1	RanBP1 domain.		
713	DEAD DEAD		8.4e-06	-7.3
714	PH	DEAD/DEAH box helicase	9.9e-42	134.9
		PH domain	1.6e-09	39.0
715	DSPc	Dual specificity phosphatase, catalytic doma	1.5e-37	138.2
717	Sialyltransf	Sialyltransferase family	7.5e-31	115.9
718	ig	Immunoglobulin domain	1e-29	100.8
719	integrin B	Integrins, beta chain	0	1125.4
720	zf-C3HC4	Zinc finger, C3HC4 type (RING	1.1e-08	32.4
722		finger)		
	Peptidase_C2	Calpain family cysteine protease	3e-145	495.9
723	ig	Immunoglobulin domain	2.2e-05	22.4
724	F-box	F-box domain.	0.007	23.0
725	Nop	Putative snoRNA binding domain	8.1e-58	205.5
726	Nop	Putative snoRNA binding domain	8.1e-58	205.5
727	WD40	WD domain, G-beta repeat	7.5e-26	99.3
730	darm	Double-stranded RNA binding	0.027	12.1
731		motif		<u> </u>
	dynamin	Dynamin family	4.2e-16	66.9
733	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.8e-10	41.7
735	CDP-	CDP-alcohol	4.2e-26	100.1
_	OH_P_transf	phosphatidyltransferase	]	
738	DEAD	DEAD/DEAH box helicase	8.6e-57	182.5
739	TSC22	TSC-22/dip/bun family	6.5e-32	119.5
742	ras	Ras family	2.2e-100	346.9
743	PMI typeI	Phosphomannosc isomerase type I		
747	trypsin		1.2e-243	822.9
748		Trypsin	6.4e-88	279.4
_	kazal	Kazal-type serine protease inhibitor domain	2.2e-52	187.4
749	efhand	EF hand	6.3e-06	33.1
751	PHD	PHD-finger	4.9e-16	66.7
752	zf-CZHZ	Zinc finger, C2H2 type	3.2e-21	183.9
753	Hydrolase	haloacid dehalogenase-like	6.le-11	49.8
754	Ribosomal_L3	Ribosomal L39 protein	0.00018	26.7
/54		į.	ł	1
	9		l	
755	PH	PH domain	3.6e-14	55.7
755 758	PH SCAN	PH domain SCAN domain	3.6e-14 1.4e-53	55.7 191.5
755 758	PH	SCAN domain PA domain		191.5
755 758 759 760	PH SCAN	SCAN domain	1.4e-53	

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
NO:	histone	Core histone H2A/H2B/H3/H4	9.9e-53	188.6
762		MYND finger	4.1e-14	60.3
763	zf-MYND	Pou domain - N-terminal to	1e-52	188.6
764	pou	homeobox domain	2.9e-34	127.3
767	VWC	von Willebrand factor type C domain		
769	efhand	EF hand	4.8e-11	50.1
770	zf-C4	Zinc finger, C4 type (two domains)	2.4e-53	181.6
	ras	Ras family	7e-90	312.0
772	Sulfatase	Sulfatase	le-142	487.5
773	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
775	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
776	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
777		RNA recognition motif.	2.1e-32	121.1
778	rrm	Glucose-6-phosphate	1.5e-76	236.6
779	G6PD ·	dehydrogenase	3.7e-29	110.3
780	spectrin	Spectrin repeat		198.5
781	mito_carr	Mitochondrial carrier proteins	4.6e-57	95.2
782	SCAN	SCAN domain	1.3e-24	37.1
783	PDZ	PDZ domain (Also known as DHR or GLGF).	4.1e-07	1
785	DEAD	DEAD/DEAH box helicase	6e-06	21.7
786	ras	Ras family	5.3e-39	143.0
787	RNase HII	Ribonuclease HII	2.5e-67	237.1
790	PI3_PI4_kina	Phosphatidylinositol 3- and 4-	5.4e-108	372.2
l	se	Cadherin domain	2.5e-40	147.4
795	cadherin	ARID DNA binding domain	1.6e-20	81.6
796	ARID		9.9e-20	64.8
797	trypsin	Trypsin Calponin homology (CH) domain	3.7e-15	63.B
799	CH	Vertebrate galactoside-binding	4.1e-25	88.7
801	Gal-		1	1
	bind_lectin	lectin WD domain, G-beta repeat	0.00082	26.1
803	WD40	TBC domain	1.8e-26	101.4
806	TBC		1.8e-26	101.4
807	TBC	TBC domain Carbon-nitrogen hydrolase	8.8e-80	278.5
808	CN_hydrolase	Histone-like transcription	6e-14	59.8
811	CBFD_NFYB_HM	factor		
L	F	short chain dehydrogenase	8.1e-20	79.3
812	adh_short	Domain of unknown function	3.3e-71	250.0
814	IMP4	Zinc finger, C2H2 type	8.2e-66	232.1
815	zf-C2H2		1.6e-37	138.0
816	Pept_tRNA_hy	peptidy1-ckwx mydioidae		
		ARID DNA binding domain	2.5e-18	74.3
817	ARID		1.6e-32	121.5
826	IF5_eIF4_eIF 2		1.5e-53	191.3
830	ArfGap	Putative GTP-ase activating protein for Arf	_	
831	LRR	Leucine Rich Repeat	2.1e-26	101.1
832	laminin_EGF	Laminin EGF-like (Domains III and V)	2e-57	204.2
839	rrm	RNA recognition motif.	1.3e-22	88.5
840	Y_phosphatas		2.6c-119	409:8
841	pkinase	Eukaryotic protein kinase domain	3.4e-100	346.3
844	Ribosomal_L2		1e-64	228.4
1	2e	TDP domain	9e-15	62.5
846	IBR	IBR domain Zinc finger, C3HC4 type (RING	7.4e-07	26.5
849	zf-C3HC4	finger)		18.9
850	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.00016	
851	SET	SET domain	5e-30	113.2
		Scavenger receptor cysteine-	0	

SEQ II	PFAM NAME	DESCRIPTION	p-value	PFAM
140:	<del></del>			SCORE
853		rich domain	<del></del>	
653	SRCR	Scavenger receptor cysteine-	To	1025.
055		rich domain		1023.
857	lactamase_B	Metallo-beta-lactamase	0.012	-6.0
		superfamily	10.012	1 -0.0
858	COX6A	Cytochrome c oxidase subunit	3.4e-58	206.7
		VIa	3.46-36	206.7
859	rrm	RNA recognition motif.	5.4e-45	
861	PRK	Phosphoribulokinase		162.9
863	mito carr	Mitochondrial carrier proteins	5.1e-62	219.4
864	HSP90	Hsp90 protein	2.9e-53	185.5
866	iq	Aspau protein	4.7e-158	538.5
867	zf-C2H2	Immunoglobulin domain	4e-12	44.1
872		Zinc finger, C2H2 type	7e-135	461.5
	histone	Core histone H2A/H2B/H3/H4	4.9e-41	149.8
874	CPSase_L_cha	Carbamoyl-phosphate synthase	2.1e-218	739.0
	in	(CPSase)	3.10-210	133.0
879	Ribosomal_S1	Ribosomal protein S12e	1 2 2 2 2 2 2	
	2e	procon ouze	2.1e-98	340.3
882	serpin	Serpins (serine protease		
		inhibitors)	2.5e-42	145.7
883	Patatin	Patatin		1
884	RA		1.2e-51	182.0
004	I RA	Ras association (RalGDS/AF-6)	0.044	8.0
887		domain		1
	DUF92	Integral membrane protein DUF92	2.7e-12	54.3
889	sugar_tr	Sugar (and other) transporter	8.2e-63	222.1
893	DUF28	Domain of unknown function	1.3e-43	
	i	DUF28	1.3e-43	158.3
896	IP trans	Phosphatidylinositol transfer		
		protein	6.5e-98	338.7
898	DEAD		ł	
899	KE2	DEAD/DEAH box helicase	1.5e-48	156.5
900	KE2	KE2 family protein	7e-61	215.7
901		KE2 family protein	4.3e-51	183.2
	zf-C2H2	Zinc finger, C2H2 type	2.7e-57	203.8
902	ras	Ras family	2.3e-75	263.8
904	TPR	TPR Domain	3.2e-22	87.2
906	GBP	Guanylate-binding protein	8.9e-253	
907	GBP	Guanylate-binding protein		853.1
908	WD40	WD domain, G-beta repeat	1.1e-239	809.6
909	PH	PH domain	2.6e-26	100.8
910	2f-C2H2		1.3e-09	39.4
913	Epimerase	Zinc finger, C2H2 type	2.50-39	144.1
	ppimerase	NAD dependent	5e-07	-88.5
21	1 7000	epimerase/dehydratase family		
22	TBC	TBC domain	1.5e-09	30.7
	WD40	WD domain, G-beta repeat	1.6e-25	98.2
23	WD40	WD domain, G-beta repeat	8.2e-07	36.1
24	Hydrolase	haloacid dehalogenase-like	2.9e-05	_
	j	hydrolase	2.96-05	29.1
25	UQ_con	Ubiquitin-conjugating enzyme		
26	CH	Calponia home	0.00033	-27.6
28	WD40	Calponin homology (CH) domain	3.3e~53	190.2
29	1_	WD domain, G-beta repeat	5.9e-48	172.7
	zf-C3HC4	Zinc finger, C3HC4 type (RING	3.1e-10	37.4
20		finger)	-	· · · •
30	Ribul_P_3_ep	Ribulose-phosphate 3 epimerase	7.2e-105	361.8
	im	family		301.8
31	Ribul_P_3_ep	Ribulose-phosphate 3 epimerase	1.2e-96	224
	im	family	4.2C-36	334.4
36	C2 -	C2 domain		
37	NAP family		2.2e-62	220.7
		Nucleosome assembly protein	1.1e-22	84.6
10	abbredye3	(NAP)		
4	abhydrolase	alpha/beta hydrolase fold	0.011	3.1
	Tropomyosin	Tropomyosins	3.2e-07	25.1
18	pkinase	Eukaryotic protein kinase	3.4e-75	263.2
		domain	46-/3	203.2
9	WD40	WD domain, G-beta repeat	1 0 22	
0	Acyltransfer	Acyltransferase	1.8e-27	104.7
		**** / ~ = = QUID   CLUSH	1.6e-07	38.4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
951	SAM	SAM domain (Sterile alpha motif)	0.014	14.5
954	GFO IDH MocA	Oxidoreductase family	1.3e-11	52.0
955	BTB	BTB/POZ domain	7e-22	86.1
956	BTB	BTB/POZ domain	7e-22	86.1
957	CDP-	CDP-alcohol phosphatidyltransferase	0.053	-22.2
	OH_P_transf		2.4e-97	336.8
959	ras	Ras family	8.4e-43	155.6
960	ras	Ras family	1.2e-08	42.2
961	Acetyltransf	Acetyltransferase (GNAT) family	1	117.6
962	adh_short	short chain dehydrogenase	2.4e-31	26.2
963	mutT	Bacterial mutT protein	5.6e-06	653.9
969	IF-2B	Initiation factor 2 subunit family	8.4e-193	
970	RNase PH	3' exoribonuclease family	9e-24	92.4
975	WW	WW domain	5.7e-25	96.4
977	PDZ	PDZ domain (Also known as DHR or GLGF).	3.6e-21	83.7
978	Ribosomal_L1	Ribosomal protein L17	2.4e-20	81.0
979	LIM	LIM domain containing proteins	5.8c-42	152.8
980	Calsequestri	Calsequestrin	1.7e-297	1001.7
~~~	n	Hsp20/alpha crystallin family	1.2e-10	43.2
982 983	HSP20 oxidored_q6	NADH ubiquinone oxidoreductase,	4.8e-63	222.9
			2.2e-50	180.8
988	TBC	TBC domain	2.2e-50	180.8
989 993	TBC tRNA_int_end	TBC domain tRNA intron endonuclease	0.0017	-34.2
	0		4e-18	73.6
994	homeobox	Homeobox domain	0.012	11.6
997	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	İ	421.2
1000	mito_carr	Mitochondrial carrier proteins	9.7e-123	65.4
1001	RA	Ras association (RalGDS/AF-6) domain	1.2e-15	
1004	DUF81	Domain of unknown function DUF81	0.099	10.2
1005	actin	Actin	1.3e-174	574.3
1006	actin	Actin	3.1e-130	428.6
1007	cpn60_TCP1	TCP-1/cpn60 chaperonin family	3.7e-195	661.8
1008	TPR	TPR Domain	8.1e-44	159.0
1009	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1011	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1012	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.7e-15	53.1
1016	tRNA-synt 2c	tRNA synthetases class II (A)	2.3e-15	55.2
	RhoGAP	RhoGAP domain	1.6e-78	274.3
1018	PGAM	Phosphoglycerate mutase family	3.8e-18	69.7
1022		HMG (high mobility group) box	8.4e-20	79.2
1026	HMG_box	TBC domain	7.3e-45	162.5
1027	TBC	Ubiquitin-conjugating enzyme	1.4e-49	178.1
1028	UQ_con		0.028	16,3
1032	PDZ	PDZ domain (Also known as DHR	0.020	
	PDZ Hydrolase	or GLGF). haloacid dehalogenasc-like	2e-21	84.6
1032	Hydrolase	or GLGF). haloacid dehalogenasc-like hydrolase	2e-21	84.6
1032		or GLGF). haloacid dehalogenasc-like	}	
1032 1034 1037 1038	Hydrolase KRAB Cation_efflu x	or GLGF). haloacid dehalogenasc-like hydrolase KRAB box Cation efflux family	2e-21 4.8e-06	84.6
1032 1034 1037	Hydrolase KRAB Cation_efflu	or GLGF). haloacid dehalogenase-like hydrolase KRAB box Cation efflux family NAD:arginine ADF- ribosyltransferase	2e-21 4.8e-06 7.1e-42 4.7e-47	32.4 152.5
1032 1034 1037 1038	Hydrolase KRAB Cation_efflu x ART	or GLGF). haloacid dehalogenase-like hydrolase KRAB box Cation efflux family NAD:arginine ADP- ribosyltransferase WD domain, G-beta repeat	2e-21 4.8e-06 7.1e-42 4.7e-47	32.4 152.5 169.1
1032 1034 1037 1038	Hydrolase KRAB Cation_efflu x ART	or GLGF). haloacid dehalogenasc-like hydrolase KRAB box Cation efflux family NAD:arginine ADP- ribosyltransferase WD domain, G-beta repeat Zinc finger, C2H2 type	2e-21 4.8e-06 7.1e-42 4.7e-47 1.9e-18 3.7e-24	84.6 32.4 152.5 169.1 74.7 93.7
1032 1034 1037 1038 1040	Hydrolase KRAB Cation_efflu x ART	or GLGF). haloacid dehalogenase-like hydrolase KRAB box Cation efflux family NAD:arginine ADP- ribosyltransferase WD domain, G-beta repeat	2e-21 4.8e-06 7.1e-42 4.7e-47	32.4 152.5 169.1

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:			p value	SCORE
1047	ligase-CoA	CoA-ligases	4.5e-80	279.4
1049	ig	Immunoglobulin domain	1.7e-09	35.6
1050	Ribosomal_L2	Ribosomal protein L24e	2e-33	124.5
1054	4e		ľ	
	Amidase	Amidase	4.3e-152	518.7
1055	rrm	RNA recognition motif.	3.8e-26	100.3
1058	annexin	Annexin	6.9e-14	159.2
1059	PMP22_Claudi	PMP-22/EMP/MP20/Claudin family	0.023	-23.6
1060	n			
1060	homeobox	Homeobox domain	3.2e-31	117.2
1062	Acyltransfer ase	Acyltransferase	0.00065	10.5
1064	AMP-binding			ł
1065	LRR	AMP-binding enzyme	6.6e-100	345.3
1066		Leucine Rich Repeat	3.3e-14	60.6
1071	GTP1_OBG	GTP1/OBG family	4.8e-41	141.8
1072	ig	Immunoglobulin domain	8.4e-48	159.1
1072	PHD	PHD-finger	6.8e-07	36.3
1074	DENN	DENN (AEX-3) domain	8.3e-33	121.5
1075	SCP	SCP-like extracellular protein	4.7e-41	149.8
1078		Olfactomedin-like domain	2.2e-66	234.0
1078	mito_carr	Mitochondrial carrier proteins	1e-42	149.3
1087	START	WD domain, G-beta repeat	6.2e-45	162.7
1093	DSPC	START domain	1.5e-48	174.7
1000	DSPC	Dual specificity phosphatase,	3.3e-63	223.4
1094	GSHPx	catalytic doma		
1095	DUF25	Glutathione peroxidases	9.6e-41	148.8
	20123	Domain of unknown function	2e-75	264.0
1096	DUF25	Domain of unknown function		
	. 201 23	DUF25	6e-75	262.4
1105	Nitroreducta	Nitroreductase family		
	se	mility	1.3e-13	58.6
1106	PTE	Phosphotriesterase family	1 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	
1107	DAGKC	Diacylglycerol kinase catalytic	1.3e-179	610.1
		domain	0.00049	19.6
1109	ras	Ras family	1.3e-15	40.7
1115	ArfGap	Putative GTP-ase activating	9.7e-47	168.7
		protein for Arf	3.70-47	100.7
1116	HMG14_17	HMG14 and HMG17	4.4e-21	83.5
1117	HMG14_17	HMG14 and HMG17	9.9e-12	52.4
1119	FAA_hydrolas	Fumarylacetoacetate (FAA)	2e-83	290.6
	е	hydrolase fam		1
1120	pkinase	Eukaryotic protein kinase	1.4e-94	327.6
1100		domain	1	1
1123 1129	abhydrolase	alpha/beta hydrolase fold	9.2e-23	89.0
116A	pro_isomeras	Cyclophilin type peptidyl-	2.2e-56	197.1
1131	e	prolyl cis-tr	1	
1132	DnaJ	DnaJ domain	1.6e-30	114.9
1132	WD40	WD domain, G-beta repeat	1.3e-19	78.6
1133	WD40	WD domain, G-beta repeat	1.8e-15	64.9
1134	PH	PH domain	0.0015	17.8
++20	Adap_comp_su	Adaptor complexes medium	1.2e-256	866.0
1137	b	subunit family		İ
/	Adap_comp_su b	Adaptor complexes medium	2.5e-209	708.8
1139	ras	subunit family		
1141	pkinase	Ras family	1.5e-86	301.0
	buttigae	Eukaryotic protein kinase	9.4e-74	258.4
152	Acyltransfer	domain	•	
	ase	Acyltransferase	1.2e-05	29.9
.153	IRS			İ
	ig	PTB domain (IRS-1.type)	5.4e-55	196.1
	TC7 1	Immunoglobulin domain	1.3e-31	106.9
			T.36-37	
155	Asparaginase	Asparaginase	6.4e-72	252.3
.157	Asparaginase _2	Asparaginase		
	Asparaginase			

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1163	linker_histo	linker histone H1 and H5 family	3.8e-14	60.4
	ne	Death effector domain	3.9e-05	30.5
1164	DED	PTB domain (IRS-1 type)	2.6e-43	157.3
1165	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1166	IRS	SAM domain (Sterile alpha	0.04	10.5
1168	SAM	motif)		
1170	abhydrolase	alpha/beta hydrolase fold	0.098	-7.5
1174	SAP	SAP domain	3.9∈-10	47.1
1177	PP2C	Protein phosphatase 2C	5.3e-31	112.5
1178	WD40	WD domain, G-beta repeat	4.7e-35	129.9
1180	Ets	Ets-domain	1.8e-09	33.3
1181	Collagen	Collagen triple helix repeat (20 copies)	0.00016	24.7
1182	TCL1 MTCP1	TCL1/MTCP1 family	9.5e-56	198.6
1184	RasGEF	RasGEF domain	1.7e-88	307.4
1185	mito carr	Mitochondrial carrier proteins	1.5e-62	217.3
1187	UPAR LY6	u-PAR/Ly-6 domain	0.0042	15.6
1188	Orn DAP Arg	Pyridoxal-dependent decarboxylase	6.2e-128	430.6
1193	Stathmin	Stathmin family	1.8e-90	314.0
1194	Stathmin	Stathmin family	1.8e-90	314.0
1195	Secl	Sec1 family	3.2e-183	622.1
1196	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	3.1e-32	111.8
1197	Glyco_transf	Glycosyl transferase family 8	1.2e-09	45.5
1202	K_tetra	K+ channel tetramerisation	0.022	-16.8
1202	adh short	short chain dehydrogenase	8.3e-45	162.3
1203	Ubie_methylt	ubiE/COQ5 methyltransferase family	1.3e-121	417.4
1208	7tm 3	7 transmembrane receptor	7.2e-09	29.0
1209	ank	Ank repeat	3.9e-15	63.7
1210	vATP- synt AC39	ATP synthase (C/AC39) subunit	2.5e-128	439.7
1212	zf-C2H2	Zinc finger, C2H2 type	5.5e-17	69.9
1213	efhand	EF hand	3.2e-07	37.4
1219	rim	RNA recognition motif.	2.1e-40	147.7
1220	DUF6	Integral membrane protein DUF6	0.015	21.5
	SCAN	SCAN domain	1.5e-71	251.1
1222 1223	G-gamma	GGL domain	3.6e-36	129.5
		Catalase	0	1158.9
1227	catalase	Catalase	1 0	
		ny desain	2 20-15	64 5
	PX	PX domain	2.2e-15	64.5
1233	PX	PX domain	2.2e-15	64.5
	PX FCH Peptidase_M2		· · - · · · - ·	
1233 1236 1241	PX FCH Peptidase_M2 0	PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40	2.2e-15 3.3e-09 2e-63	64.5 44.0 224.1
1233 1236	PX FCH Peptidase_M2	PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown	2.2e-15 3.3e-09	64.5
1233 1236 1241 1243	PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans	PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain	2.2e-15 3.3e-09 2e-63	64.5 44.0 224.1
1233 1236 1241 1243 1247	PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2	PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases	2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10	64.5 44.0 224.1 17.9 215.8
1233 1236 1241 1243 1247 1248	PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand	PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases EF hand	2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10	64.5 44.0 224.1 17.9 215.8 46.9
1233 1236 1241 1243 1247 1248 1249	PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand UQ_con	PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases EF hand Ubiquitin-conjugating enzyme	2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73	64.5 44.0 224.1 17.9 215.8 46.9 50.4 257.3
1233 1236 1241 1243 1247 1248	PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand UQ_con ras formyl_trans	PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases EF hand	2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10	64.5 44.0 224.1 17.9 215.8 46.9
1233 1236 1241 1243 1247 1248 1249 1254 1255	PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand UQ_con ras	PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases EF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase Zinc finger, C3HC4 type (RING	2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62	64.5 44.0 224.1 17.9 215.8 46.9 50.4 257.3 220.7
1233 1236 1241 1243 1247 1248 1249 1254 1255 1256	PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand UQ_con ras formyl_trans f zf-C3HC4 DiHfolate_re	PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases EF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase	2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62 4.9e-30	64.5 44.0 224.1 17.9 215.8 46.9 50.4 257.3 220.7 108.3
1233 1236 1241 1243 1247 1248 1249 1254 1255 1256	PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand UQ_con ras formyl_trans f zf-C3HC4 DiHfolate_re d G_glu_transp	PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases EF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase Zinc finger, C3HC4 type (RING finger)	2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62 4.9e-30 5.3e-13	64.5 44.0 224.1 17.9 215.8 46.9 50.4 257.3 220.7 108.3
1233 1236 1241 1243 1247 1248 1249 1254 1255 1256 1259	PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand UQ_con ras formyl_trans f zf-C3HC4 DiHfolate_re d	PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases EF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase Zinc finger, C3HC4 type (RING finger) Dihydrofolate reductase	2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62 4.9e-30 5.3e-13	64.5 44.0 224.1 17.9 215.8 46.9 50.4 257.3 220.7 108.3 46.4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
1266	SCP	SCP-like extracellular protein		SCORE
1267	K tetra	K+ channel tetramerisation	6e-29	108.0
	1-00014	domain	2.8e-2/	104.0
1269	ras	Ras family	1.3e-85	297.9
1275	zf-C3HC4	Zinc finger, C3HC4 type (RING	4.2e-10	37.0
		finger)	1	37.0
1276	abhydrolase	alpha/beta hydrolase fold	5.4e-23	89.8
1277	abhydrolase	alpha/beta hydrolase fold	5.6e-21	83.1
1279	trypsin	Trypsin	4.4e-41	132.0
1280	PBP	Phosphatidylethanolamine-	1.3e-13	58.7
		binding protein		j
1285	zf-C3HC4	Zinc finger, C3HC4 type (RING	5.6e-14	49.6
		finger)		
1287	ank	Ank repeat	1.7e-52	187.8
1294	fn3	Fibronectin type III domain	0.026	20.9
1295	GBP	Guanylate-binding protein	0.00026	-70.0
1296	PMP22_Claudi	PMP-22/EMP/MP20/Claudin family	6.9e-41	149.3
1202	n			
1297 1298	Rhodanese LIM	Rhodanese-like domain	3.2e-14	60.7
1301	rnaseA	LIM domain containing proteins	5.8e-21	79.1
1301		Pancreatic ribonucleases	4.9e-43	145.2
1307	mito_carr WD40	Mitochondrial carrier proteins WD domain, G-beta repeat	2.1e-53	186.0
1310	UPAR LY6	u-PAR/Ly-6 domain	1.6e-17	71.6
1313	thiored	Thioredoxin	7.1e-20	75.5
1314	Aa trans	Transmembrane amino acid	3.6e-05	21.6
-5-4	na_craiis	transporter protein	1.5e-67	237.9
1316	trypsin	Trypsin	4.4e-41	132.0
1320	Ribosomal L1	Ribosomal protein L13	3.9e-62	219.8
	3	ALLOSSINGI PICCEIN 113	3.96-62	219.0
1327	Armadillo se	Armadillo/beta-catenin-like	0.0054	23.4
	g	repeats	1	23.1
1328	KRAB	KRAB box	0.052	-5.6
1329	rrm	RNA recognition motif.	2.1e-40	147.7
1330	Bcl-2	Apoptosis regulator proteins,	0.014	-1.6
		Bcl-2 family		
1331	PX	PX domain	2.1e-10	48.0
1333 1334	KRAB	KRAB box	1.8e-36	134.6
1334	UPP_syntheta	Putative undecaprenyl	2.3e-89	310.3
1335	ge UPP_syntheta	diphosphate synt Putative undecaprenyl		
2000	'se	diphosphate synt	1.8e-59	211.0
1336	DSPC	Dual specificity phosphatase,	1.2e-31	118.6
	12020	catalytic doma	1.26-31	118.6
1337	DSPc	Dual specificity phosphatase,	2.3e-12	54.5
		catalytic doma	2.36-12	33.3
1338	TPR	TPR Domain	0.00021	28.1
1340	metalthio	Metallothionein	0.013	20.3
1341	mutT	Bacterial mutT protein	5.8e-09	36.5
1343	Band_41	FERM domain (Band 4.1 family)	1.3e-38	122.5
1344	Kelch	Kelch motif	1.4e-44	161.5
1345	Antifreeze	Antifreeze protein	1.2e-10	48.8
1347	3Beta_HSD	3-beta hydroxysteroid	0.086	-177.2
		dehydrogenase/isomera	1	J
1348	BTB	BTB/POZ domain	5.3e-28	106.5
1349	DUF6	Integral membrane protein DUF6	0.033	15.8
1350	myosin_head	Myosin head (motor domain)	0	1088.7
1352	Nramp	Natural resistance-associated	1.2e-202	686.6
1252	1000	macrophage pro		1
1353	S_100	S-100/ICaBP type calcium	5.3e-23	89.9
1355	DEAD	binding domain		<u></u>
1355 1356	DEAD	DEAD/DEAH box helicase	3.6e-65	209.0
1356	C2 RBD	C2 domain	2.4e-15	64.4
1360		Raf-like Ras-binding domain	4.2e-57	203.1
1361	zf-C2H2 HMG14_17	Zinc finger, C2H2 type	7.4e-141	481.4
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	HMG14 and HMG17	7.9e-40	145.7

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:				SCORE
1362	SIS	SIS domain	3.8e-30	113.6
1363	SIS	SIS domain	1.3e-28	108.5
1364	ig	Immunoglobulin domain	0.00026	19.0
1368	K tetra	K+ Channel tetramerisation	1.1e-16	68.9
1300	1	domain		
1371	Collagen	Collagen triple helix repeat	2.2e-113	390.1
2372	00==030!!	(20 copies)		1
1372	DnaJ	DnaJ domain	6.6e-36	132.7
	KRAB	KRAB box	2.1e-38	141.0
1376			2e-23	91.3
1378	ELM2	ELM2 domain	1.2e-23	82.8
1380	thiored	Thioredoxin		290.4
1381	ank	Ank repeat	2.3e-83	1
1382	BTB	BTB/POZ domain	3e-11	50.8
1383	WD40	WD domain, G-beta repeat	1.6e-19	78.3
1384	WD40	WD domain, G-beta repeat	6.3e-24	92.9
1387	zf-C3HC4	Zinc finger, C3HC4 type (RING	1.le-09	35.6
		finger)		İ
1389	zf-C2H2	Zinc finger, C2H2 type	5.5e-50	179.5
1390	zf-C2H2	Zinc finger, C2H2 type	2.5e-85	296.9
1393	kinesin	Kinesin motor domain	7.8e-188	637.4
	zf-C2H2	Zinc finger, C2H2 type	1.2e-49	178.4
1394			5.1e-22	86.6
1398	KRAB	KRAB box	0.035	13.1
1402	bZIP	bZIP transcription factor	0.035	-101.5
1405	sugar_tr	Sugar (and other) transporter		1
1406	RhoGAP	RhoGAP domain	8.9e-47	168.8
1407	rrm	RNA recognition motif.	1e-35	132.1
1408	LRR	Leucine Rich Repeat	2.le-13	58.0
1409	Nebulin repe	Nebulin repeat	6e-54	192.6
	at	<u>-</u>	1	l
1410	ank	Ank repeat	1.6e-17	71.6
1412	Ribosomal L5	ribosomal L5P family C-terminus	8.2e-58	205.5
1412	C C	Libosowar Bar raming a committee	}	
1415	trypsin	Trypsin	4.7e-85	.270.4
1416	aminotran 1	Aminotransferases class-I	4.4e-05	-91.2
		S1 RNA binding domain	1.6e-07	33.1
1417	S1		2.2e-09	44.6
1419	WD40	WD domain, G-beta repeat	8.3e-42	152.3
1422	cadherin	Cadherin domain		280.3
1424	SH3	SH3 domain	2.5e-80	
1425	PHD	PHD-finger	3.2e-17	70.6
1426	PHD	PHD-finger	3.2e-17	70.6
1427	ArfGap	Putative GTP-ase activating	1e-37	138.8
	i i	protein for Arf		
1428	helicase C	Helicases conserved C-terminal	le-26	102.2
-	_	domain	ļ	
1429	WD40	WD domain, G-beta repeat	3.9e-07	37.2
1430	inositol P	Inositol monophosphatase family	2.5e-10	40.2
1431	mito carr	Mitochondrial carrier proteins	4.3e-83	287.7
1431	Clq	Clq domain	2.9e-16	66.2
			1.6e-13	58.3
1434	WD40	WD domain, G-beta repeat	7e-228	770.4
1435	Inos-1-	Myo-inositol-1-phosphate	16-220	1,,0.3
	P_synth	synthase	 	13003
1436	rrm	RNA recognition motif.	1.4e-34	128.3
1438	ig	Immunoglobulin domain	1.3e-12	45.6
1440	G_Adapt_CT	Gamma-adaptin, C-terminus	3.4e-67	236.7
1441	G Adapt CT	Gamma-adaptin, C-terminus	3.4e-67	236.7
1443	Kelch	Kelch motif	0.00013	28.7
1446	ARID	ARID DNA binding domain	1.8e-21	84.7
,	zf-C2H2	Zinc finger, C2H2 type	9.4e-28	105.6
1447			2.6e-07	-145.1
1447				
1448	AMP-binding	AMP-binding enzyme		
1448 1451	AMP-binding rrm	RNA recognition motif.	6.5e-21	82.9
1448 1451 1454	AMP-binding rrm ig	RNA recognition motif. Immunoglobulin domain	6.5e-21 5.6e-44	82.9 146.7
1448 1451	AMP-binding rrm ig Sialyltransf	RNA recognition motif.	6.5e-21 5.6e-44 5.4e-21	82.9 146.7 83.2
1448 1451 1454	AMP-binding rrm ig	RNA recognition motif. Immunoglobulin domain	6.5e-21 5.6e-44 5.4e-21 1.9e-35	82.9 146.7 83.2 131.2
1448 1451 1454 1455	AMP-binding rrm ig Sialyltransf	RNA recognition motif. Immunoglobulin domain Sialyltransferase family Aldose 1-epimerase	6.5e-21 5.6e-44 5.4e-21	82.9 146.7 83.2
1448 1451 1454 1455 1460	AMP-binding rrm ig Sialyltransf Aldose_epim	RNA recognition motif. Immunoglobulin domain Sialyltransferase family	6.5e-21 5.6e-44 5.4e-21 1.9e-35	82.9 146.7 83.2 131.2

SEQ ID	PFAM NAME	DESCRIPTION		
NO:		DESCRIPTION	p-value	PFAM
	h_2			SCORE
1474	DENN	DENN (AEX-3) domain	1.3e-44	161.6
1475	Cation_efflu	Cation efflux family	4.6e-49	176.4
1477	×			1 - / - / -
1478	TBC	TBC domain	8e-47	169.0
1480	rrm	RNA recognition motif.	2e-21	84.6
1484	Ig Telo_bind al	Immunoglobulin domain	5.5e-06	24.3
1204	pha pind_ar	Telomere-binding protein alpha subuni	0.028	-225.9
1485	zf-C2H2	Zinc finger, C2H2 type		L
1486	pkinase	Eukaryotic protein kinase	1.8e-68	240.9
	Firence	domain grotein kinase	9.5e-13	49.9
1488	helicase C	Helicases conserved C-terminal	\	
		domain	1.4e-15	65.2
1489	DUF89	Protein of unknown function	0.079	135
Ĺ		DUF89	0.079	-132.4
1490	ECH	Enoyl-CoA hydratase/isomerase	5.2e-41	149.7
		family		149.7
1491	guanylate_cy	Adenylate and Guanylate cyclase	5.9e-46	166.1
L	C	catalyt		1 200.1
1492	LRR	Leucine Rich Repeat	3.4e-19	77.2
1495	zf-C3HC4	Zinc finger, C3HC4 type (RING	7.1e-10	36.3
1497	mle i man	finger)		
143,	pkinase	Eukaryotic protein kinase	le-22	85.8
1500	SH3	domain SH3 domain		
1502	homeobox	Homeobox domain	9.3e-05	27.2
1503	homeobox	Homeobox domain	0.084	13.8
1505	EGF	EGF-like domain	0.084	13.8
1506	UCH-2	Ubiquitin carboxyl-terminal	2.7e-23 2.7e-21	90.8
<u> </u>		hydrolase family	2.7e-21	84.2
1508	Peptidase_M2	Peptidase family M20/M25/M40	2.8e-28	101.8
	0		2.00 20	101.0
1511	PX	PX domain	1.9e-11	51.5
1512 1516	Sulfatase	Sulfatase	2.8e-35	130.7
1518	Syntaxin aminotran 3	Syntaxin	0.011	-62.3
1318	aminotran_3	Aminotransferases class-III	9.7e-106	305.6
1520	ig	pyridoxal-pho		
1521	RA	Immunoglobulin domain Ras association (RalGDS/AF-6)	0.075	11.0
]	domain (kaighs/AF-6)	0.013	13.3
1523	RhoGAP	RhoGAP domain	2.5e-05	
1528	WD40	WD domain, G-beta repeat	5.4e-24	18.7
1535	IMS	impB/mucB/samB family	7.8e-95	328.5
1538	FYVE	FYVE zinc finger	3.2e-27	101.5
1539	DAGKC	Diacylglycerol kinase catalytic	6e-07	36.5
3540		domain		1
1540 1653	Ocular_alb	Ocular albinism type 1 protein	0	1184.7
1654	1	SAP domain	6e-06	33.2
7074	Amino_oxidas	Flavin containing amine oxidase	3.2e-43	157.0
1655	Amino oxidas	Plant	<u> </u>	<u> </u>
	e e	Flavin containing amine oxidase	3.2e-43	157.0
1656	RhoGEF	RhoGEF domain		
1657	MMR HSR1	GTPase of unknown function	1.4e-24	95.1
1659	UCH-2	Ubiquitin carboxyl-terminal	0.0011	-45.5
_		hydrolase family	2.5e-11	51.1
1660	actin	Actin	6 60 33	100
1661	BAH	BAH domain	6.6e-21 1.7e-82	69.9
1662	vwa	von Willebrand factor type A	1.7e-82	287.5
		domain	•	1909.4
1663	WD40	WD domain, G-beta repeat	1.4e-67	237.9
1667	zf-C2H2	Zinc finger, C2H2 type	1.3e-93	324.4
1669	Nol1_Nop2_Su	NOL1/NOP2/sun family	1.3e-23	84.3
1671	n	_		
1671	SH2	Src homology domain 2	5.4e-15	46.9

SEQ ID No:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1672	chromo	'chromo' (CHRromatin	2.1e-18	67.7
		Organization MOdifier)	}	
1674	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	0.0025	17.6
1676	Glyco_hydro_	Glycosyl hydrolase family 47	1.8e-187	636.2
1677	Glyco_hydro_ 47	Glycosyl hydrolase family 47	4.5e-74	259.5
1680	WD40	WD domain, G-beta repeat	1.le-27	105.5
1681	WD40	WD domain, G-beta repeat	1.le-27	105.5
1683	MMR HSR1	GTPase of unknown function	1.8e-78	274.1
1691	rrm	RNA recognition motif.	1.8e-37	137.9
1692	rrm	RNA recognition motif.	1.8e-37	137.9
1693	AAA	ATPases associated with various cellular act	1.3e-81	284.5
1697	Ferric_reduc	Ferric reductase like	8.4e-82	285.2
1698	Ferric_reduc	Ferric reductase like	3.5e-53	190.1
1699	zf-C2H2	Zinc finger, C2H2 type	4.4e-34	126.6
1700	arf	ADP-ribosylation factor family	9e-19	75.8
1702	GTP EFTU	Elongation factor Tu family	0.014	11.4
1702	SCAN	SCAN domain	1.8e-54	194.4
1707	pkinase	Eukaryotic protein kinase domain	1.2e-88	307.9
1709	WD40	WD domain, G-beta repeat	0.0035	24.0
1710	LRR	Leucine Rich Repeat	1.2e-30	115.3
1711	WW	WW domain	7.6e-12	52.8
1712	ank	Ank repeat	4.2e-34	126.7
1713	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	2.6e-09	38.3
		type		38.3
1714	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	_
1715	ras	Ras family	4.4e-41	149.9
1718	HMG_box	HMG (high mobility group) box	8.3e-21	82.6
1719	TBC	TBC domain	1.1e-45	165.2
1721	HLH	Helix-loop-helix DNA-binding domain	9.2e-10	45.9
1723	dsim	Double-stranded RNA binding motif	2.9e-05	30.9
1724	RrnaAD	Ribosomal RNA adenine dimethylases	0.045	9.2
1725	CIDE-N	CIDE-N domain	5.9e-40	146.2
1726	HAT	HAT (Half-A-TPR) repeats	2.9e-44	160.5
1728	efhand	EF hand	5.1e-20	79.9
1733	Hist_deacety	Histone deacetylase family	1.7e-104	360.6
1735	LRR	Leucine Rich Repeat	4.6e-34	126.6
1739	PI-PLC-X	Phosphatidylinositol-specific phospholipase	0.0023	16.1
1743	ras	Ras family	3.7e-10	-21.3
1744	ras	Ras family	3.7e-10	-21.3
1745	RasGEF	RasGEF domain	3.2e-49	176.9
1746	adh short	short chain dehydrogenase	7.1e-08	34.6
1751	zf-C2H2	Zinc finger, C2H2 type	9e-39	142.2
1754	fn3	Fibronectin type III domain	5.5e-101	348.9
1756	zf-C2H2	Zinc finger, C2H2 type	6.3e-93	322.1
1758	rrm	RNA recognition motif.	0.017	21.2
1760	Nop	Putative snoRNA binding domain	6.1e-95	328.8
1761	дор дом	Putative snorma binding domain	6.1e-95	328.8
1765	MMR HSR1	GTPase of unknown function	6.4e-41	149.4
				-43.9
1769	CN_hydrolase	Carbon-nitrogen hydrolase	3e-06	
1775	ank	Ank repeat	4.1e-07	37.1
1779	Oxysterol_BP	Oxysterol-binding protein	4.7e-56	199.6
1783	RhoGEF	RhoGEF domain	1.6e-23	91.6
1784	RhoGEF	RhoGEF domain	1.6e-23	91.6

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
				SCORE
1785	rrm	RNA recognition motif.	6.4e-14	59.7

TRADOCS:1416227.1(%CRN01!.DOC)

TABLE 5

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	Maxs (MAXIMUM SCORE)	MeanS (MEAN SCORE)
	1-21	0.991	0.955
2	1-31	0.995	0.944
3	1-33	0.949	0.736
4	1-19	0.970	0.951
5	1-26	0.971	0.863
	1-26	0.971	0.863
6	1-26	0.971	0.863
7	1-26	0.971	0.863
8	1-46	0.982	0.901
9		0.991	0.955
10	1-21	0.989	0.899
11	1-23	0.955	0.803
12	1-25		0.625
13	1-18	0.932	0.876
14	1-18	0.938	
15	1-25	0.941	0.811
16	1-17	0.972	0.939
17	1-27	0.964	0.777
18	1-16	0.914	0.657
19	1-19	0.953	0.840
20	1-20	0.935	0.701
21	1-22	0.974	0.850
22	1-33	0.961	0.895
23	1-19	0.991	0.959
24	1-31	0.995	0.944
25	1-22	0.976	0.935
26	1-27	0.996	0.928
27	1-24	0.953	0.739
28	1-21	0.906	0.688
29	1-31	0.986	0.841
30	1-28	0.980	0.893
31	1-19	0.993	0.976
32	1-22	0.998	0.909
	1-33	0.949	0.736
35	1-33	0.949	0.736
36	1-19	0.570	0.951
46		0.968	0.848
67	1-25	0.949	0.845
71	1-18	0.991	0.919
72	1-30	0.958	0.854
75	1-29		0.945
88	1-20	0.986	0.943
94	1-33	0.994	0.595
97	1-46	0.964	
103	1-49	0.983	0.570
108	1-26	0.978	0.885
111	1-23	0.989	0.899
126	1-25	0.955	0.803
129	1-19	0.963	0.918
138	1-29	0.971	0.844
143	1-18	0.914	0.628
148	1-20	0.969	0.904
156	1-25	0.941	0.811
158	1-22	0.979	0.927
160	1-17	0.972	0.939
161	1-48	0.903	0.571
162	1-25	0.937	0.729
168	1-16	0.939	0.826
	1-27	0.964	0.777
1 7 7 1		0.945	0.825
171	11-21		
178	1-21		
178 180	1-27	0.981	0.941
178 180 187	1-27 1-28	0.981	0.941 0.936
178 180	1-27	0.981	0.941

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
199	1-20	0.935	0.701
200	1-23	0.977	0.701
206	1-30	0.984	0.890
207	1-19	0.990	0.924
208	1-22	0.974	0.850
210	1-40	0.940	0.670
211	1-28	0.971	0.849
216	1-24	0.986	0.956
218	1-33	0.961	0.895
219	1-19	0.970	0.871
221	1-19	0.904	0.553
222	1-21	0.917	0.555
230	1-19	0.991	0.959
231	1-26	0.953	0.800
232	1-25	0.988	0.826
239	1-23	0.969	0.828
240	1-17	0.982	0.955
241	1-17	0.982	0.955
245	1-30	0.970	0.722
248	1-22	0.976	0.935
249	1-23	0.968	0.940
252	1-18	0.971	0.923
261	1-24	0.883	0.587
265	1-18	0.939	0.868
272	1-24	0.953	0.739
283	. 1-21	0.906	0.688
284	1-29	0.997	0.854
290	1-31	0.986	0.841
302	1-28	0.980	0.893
304 312	1-16	0.907	0.635
313	1-19	0.993	0.976
323	1-17	0.930	0.753
324	1-22	0.998	0.909
328	1-17	0.982	0.954
329	1-19	0.971	0.865
330	1-33	0.963	0.924
331	1-33	0.978	0.841
332	1-24	0.920	0.712
333	1-19	0.975	0.881
334	1-20	0.984	0.941
335	1-27	0.942	0.567
336	1-20	0.952	0.813
337	1-38	0.942	0.850
338	1-27	0.973	0.653
339	1-36	0.979	0.772
340	1-27	0.888	0.804
343	1-19	0.971	0.865
344	1-22	0.994	0.928
345	1-17	0.966	0.687
346	1-19	0.936	0.822
347	1-22	0.963	0.924
349	1-24	0.982	0.966
351	1-21	0.918	0.815
352	1-31	0.988	0.013
354	1-31	0.974	0.839
355	1-29	0.932	0.632
356	1-15	0.994	0.969
357	1-33	0.935	0.726
360	1-27	0.938	0.827
361	1-25	0.954	0.674
362	1-22	0.929	0.788
363	1-21	0.881	0.715
] - 	, 0.001	
364 365	1-33	0.978	0.841

10 10 NO	POSITION OF	MaxS (MAXIMUM	MeanS (MEAN
SEQ ID NO:	SIGNAL IN AMINO	SCORE)	SCORE)
	ACID SEQUENCE) beauty,	
366	1-21	0.916	0.820
367	1-19	0.936	0.822
368	1-29	0.972	0.874
370	1-24	0.920	0.712
371	1-24	0.961	0.773
372	1-27	0.919	0.768
373	1-19	0.986	0.945
375	1-32	0.994	0.932
376	1-34	0.987	0.810
377	1-17	0.995	0.950
378	1-49	0.971	0.749
380	1-20	0.968	0.874
381	1-20	0.928	0.782
382	1-19	0.986	0.934
383	1-28	0.965	0.829
384	1-39	0.970	0.551
386	1-24	0.975	0.881
388	1-30	0.989	0.868
389	1-19	0.984	0.941
390	1-26	0.971	0.782
392	1-20	0.981	0.900
393	1-16	0.968	0.890
394	1-23	0.937	0.701
397	1-22	0.985	0.854
399	1-46	0.977	0.698
401	1-20	0.899	0.567
402	1-22	0.967	0.931
403	1-27	0.992	0.934
404	1-19	0.991	0.973
405	1-23	0.994	0.921
407	1-35	0.987	0.658
408	1-39	0.976	0.551
409	1-33	0.897	0.570
410	1-25	0.990	0.962
411	1-38	0.977	0.827
412	1-20	0.944	0.768
413	1-20	0.988	0.965
414	1-46	0.993	0.638
415	1-23	0.981	
417	1-29	0.941	0.672
418	1-20	0.952	0.850
419	1-19	0.986	0.861
420	1-29	0.965	0.785
421	1-22	0.889	0.862
422	1-48	0.982	0.862
424	1-19		0.653
428	1-38	0.942	0.595
430	1-18	0.957	0.789
432	1-33	0.957	0.904
433	1-26	0.979	0.777
434	1-27	0.962	0.977
435	1-24	0.973	0.772
436	1-27	0.973	0.940
443	1-15	0.979	0.804
448	1-36	0.979	0.609
453	1-41	0.938	0.606
455		0.888	` 0.597
457	1-27	0.888	0.681
462	1-16	0.925	0.845
486	1-27	0.912	0.636
495	1-24	0.917	0.890
498	1-26	0.993	0.926
505	1-20	0.976	0.687
507	1-17	0.986	0.593
510	1-23	0.930	10.000

SEQ ID NO:	POSITION OF	Mond (MANUFACTOR)	1.00
	SIGNAL IN AMINO	MaxS (MAXIMUM SCORE)	MeanS (MEAN
1	ACID SEQUENCE	SCORE)	SCORE)
511	1-23	0.930	0.593
512	1-23	0.930	0.593
515	1-18	0.978	0.956
523	1-19	0.936	0.822
529	1-22	0.963	0.924
545	1-24	0.982	0.966
550	1-30	0.933	0.713
552	1-21	0.973	0.912
554	1-23	0.969	0.784
571	1-21	0.918	
574	1-31	0.988	0.815
580	1-39	0.925	0.912
594	1-31	0.974	0.556
608	1-29	0.932	0.839
609	1-29		0.632
610	1-21	0.932	0.632
621	1-15	0.990	0.948
623		0.994	0.969
653	1-33	0.935	0.726
669		0.938	0.827
677	1-22	0.929	0.788
685		0.948	0.807
699	1-21	0.881	0.715
702	1-22	0.975	0.816
707	1-31	0.968	0.898
713	1-16	0.880	0.562
718	1-25	0.966	0.743
719	1-19	0.936	0.822
729	1-20	0.961	0.824
735	1-29	0.972	0.874
746	1-46	0.903	0.598
747	1-14	0.916	0.730
	1-22	0.965	0.876
748	1-29	0.968	0.785
759	1-24	0.961	0.773
767 768	1-27	0.919	0.768
L	1-33	0.900	0.585
773	1-42	0.959	0.702
779	1-19	0.986	0.945
797	1-19	0.944	0.759
798	1-19	0.900	0.568
820 827	1-17	0.995	0.950
	1-49	0.971	0.749
848	1-20	0.968	0.874
864	1-20	0.928	0.782
866	1-19	0.986	0.934
873	1-23	0.948	0.886
881	1-28	0.965	0.829
887	1-39	0.970	0.551
927	1-30	0.989	0.868
934	1-48	0.988	0.777
939	1-39	0.994	0.889
944	1-26	0.971	0.782
950	1-29	0.957	0.845
963	1-20	0.981	0.900
964	1-20	0.886	0.558
973	1-16	0.968	0.890
980	1-34	0.961	0.749
981	1-20	0.953	0.822
984	1-12	0.938	0.780
1015	1-22	0.985	0.854
1040	1-46	0.977	0.698
1052	1-18	0.977	
1059	1-20	0.989	0.842
1065	1-33	0.927	0.867
1069	1-22	0.983	0.918
	<u> </u>	4.333	0.935

SEO ID NO:	POSITION OF	MaxS (MAXIMUM	MeanS (MEAN
SEQ ID NO.	SIGNAL IN AMINO	SCORE)	SCORE)
	ACID SEQUENCE	0.992	0.934
1075	1-27	0.931	0.829
1080	1-19	0.991	0.973
1092	1-19	0.992	0.653
1094	1-46	0.974	0.929
1095	1-30	0.994	0.921
1105	1-23	0.987	0.658
1123	1-35	0.954	0.613
1138	1-32	0.989	0.789
1140		0.897	0.570
1142	1-33	0.990	0.962
1152	1-38	0.977	0.827
1170	1-38	0.944	0.768
1176		0.988	0.965
1187	1-20	0.967	0.839
1189		0.993	0.638
1192	1-46	0.925	0.710
1193	1-16	0.985	0.853
1197	1-29	0.981	0.940
1208	1-23	0.941	0.672
1225	1-29	0.986	0.967
1245	1-19	0.965	0.861
1258	1-29	0.889	0.785
1265	1-22	0.944	0.809
1266		0.982	0.862
1276	1-48	0.979	0.933
1292		0.984	0.944
1296	1-21	0.984	0.953
1297	1-19	0.942	0.653
1332	1-38	0.947	0.595
1358	1-18	0.957	0.789
1371	1-33	0.979	0.904
1380	1-26	0.962	0.777
1397	1-23	0.997	0.960
1399	1-24	0.998	0.977
1404	1-15	0.946	0.845
1410	1-24	0.913	0.588
1414	1-19	0.982	0.929
	1-12	0.931	0.891
1416	1-30	0.933	0.563
	1-20	0.881	0.561
1420	1-19	0.990	0.968
1421	1-17	0.968	0.863
1424	1-21	0.885	0.591
1425	1-24	0.913	0.588
1425	1-24	0.913	0.588
1428	1-25	0.957	0.899
1430	1-34	0.977	0.819
1431	1-34	0.979	0.923
1431	1-36	0.957	0.613
1432	1-30	0.921	0.753
1433	1-32	0.983	0.621
1434	1-25	0.910	0.631
1436	1-42	0.988	0.868
1437	1-22	0.998	0.980
1442	1-20	0.918	0.753
1448	1-12	0.931	0.891
1462	1-18	0.968	0.888
1490	1-20	0.881	0.561
1518	1-17	0.968	0.863
1525	1-21	0.885	0.591
	1-28	0.974	0.891
1547	1-25	0.967	0.899
1561	1-25	0.923	0.824
1580		0.979	0.923
1593	1-28		

ACID SEQUENCE	SCORE)	SCORE)
	0.929	0.709
1-36	0.957	0.613
1-22		
1-20		0.831
		0.770
		0.753
		0.829
<u></u>	_ 1	0.869
	0.983	0.621
<u> </u>	0.910	0.631
	0.897	0.591
1-42	0.988	0.868
1-20	0.927	0.568
1-17		0.742
1-22		0.742
	1-20 1-32 1-33 1-20 1-39 1-25 1-33 1-42 1-20 1-17	1-22 0.979 1-20 0.974 1-32 0.921 1-33 0.969 1-20 0.959 1-39 0.983 1-25 0.910 1-33 0.897 1-42 0.988 1-20 0.927 1-17 0.923

TRADOCS:1416234.1(%CR%01!.DOC)

TABLE 6

TABLE 6					
SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N. 09/488,725
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	1	sedneuce	priority application	
	sequence			784CIP2 1	1103
1	1787	3573	5359		2673
2	1788	3574	5360	784CIP2_2	4117
3	1789	3575	5361	784CIP2_3	5556
4	1790	3576	5362	784CIP2_4	
5	1791	3577	5363	784CIP2_5	5562
6	1792	3578	5364	784CIP2_6	5562
7	1793	3579	5365	784CIP2_7	5562
8	1794	3580	5366	784CIP2_8	5562
9	1795	3581	5367	784CIP2_9	5563
10	1796	3582	5368	784CIP2_10	5564
11	1797	3583	5369	784CIP2_11	5565
12	1798	3584	5370	784CIP2_12	5689
13	1799	3585	5371	784CIP2_13	5729
14	1830	3586	5372	784CIP2_14	5745
15	1801	3587	5373	784CIP2_15	5777
16	1802	3588	5374	784CIP2_16	5777
17	1803	3589	5375	784CIP2_17	5789
18	1804	3590	5376	784CIP2_18	5792
19	1805	3591	5377	784CIP2_19	5804
20	1806	3592	5378	784CIP2_20	5805
21	1807	3593	5379	784CIP2_21	5805
22	1808	3594	5380	784CIP2_22	5844
23	1809	3595	5381	784CIP2_23	5844
24	1810	3596	5382	784CIP2_24	5850
25	1811	3597	5383	784CIP2_25	5867
26	1812	3598	5384	784CIP2_26	5973
27	1813	3599	5385	784CIP2_27	5995
28	1814	3600	5386	784CIP2_28	5995
29	1815	3601	5387	784CIP2_29	6005
30	1815	3602	5388	784CIP2 30	6007
31	1817	3603	5389	784CIP2_31	6007
32	1818	3604	5390	784CIP2_32	6009
33	1819	3605	5391	784CIP2_33	6012
34	1820	3606	5392	784CIP2_34	6015
35	1821	3607	5393	784CIP2 35	6016
36	1822	3608	5394	784CIP2 36	6016
37	1823	3609	5395	784CIP2_37	6018
38	1824	3610	5396	784CIP2_38	6018
39	1825	3611	5397	784CIP2_39	6018
40	1826	3612	5398	784CIP2_40	6023
41	1827	3613	5399	784CIP2_41	6070
. 42	1828	3614	5400	784CIP2 42	6081
43	1829	3615	5401	784CIP2 43	6089
44	1830	3616	5402	784CIP2 44	6118
45	1831	3617	5403	784CIP2 45	6118
46	1832	3618	5404	784CIP2 46	6130
47	1833	3619	5405	784CIP2 47	6177
48	1834	3620	5406	784CIP2 48	6189
49	1835	3621	5407	784CIP2 49	6191
50	1836	3622	5408	784CIP2 50	6204
	1837	3623	5409	784CIP2 51 -	6204
51	1838		5410	784CIP2 52	6284
52		3624	5411	784CIP2 53	6367
53	1839	3625		784CIP2_54	6436
54	1840	3626	5412	784CIP2 55	6442
55	1841	3627	5413		6445
56	1842	3628	5414	784CIP2_56	6457
57	1843	3629	5415	784CIP2_57	6458
58	1844	3630	5416	784CIP2_58	6458
59	1845	3631	5417	784CIP2_59	L 0430

of full- length nucleotide sequence 60	SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	1 000 70
Length eng	of full-					SEQ ID
sequence seq	length		,			_
Sequence Sequence	nucleotide	length	•	peptide		
Sequence	sequence	peptide				03/400,123
60	1	sequence				
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101 1887 3673 5458 784CIP2_102 7029 102 1888 3674 5460 784CIP2_103 7031 103 1889 3675 5461 784CIP2_104 7032 104 1890 3676 5462 784CIP2_105 7033 105 1891 3677 5463 784CIP2_106 7035 106 1892 3678 5464 784CIP2_107 7036 107 1893 3679 5465 784CIP2_108 7039 108 1894 3680 5466 784CIP2_109 7043 109 1895 3681 5467 784CIP2_110 7044 110 1896 3682 5468 784CIP2_110 7044 111 1897 3683 5459 764CIP2_111 7054 112 1898 3684 5470 784CIP2_113 7061 113 1899 3685 5471 784CIP2_114 7077				5457	784CIP2_100	7027
102 1888 3674 5460 784CIP2_103 7031 103 1689 3675 5461 784CIP2_104 7032 104 1890 3676 5462 784CIP2_105 7033 105 1891 3677 5463 784CIP2_106 7035 106 1892 3678 5464 784CIP2_107 7036 107 1893 3679 5465 784CIP2_108 7039 108 1894 3680 5466 784CIP2_109 7043 109 1895 3681 5467 784CIP2_110 7044 110 1896 3682 5468 784CIP2_110 7044 111 1897 3693 5459 764CIP2_111 7046 111 1898 3684 5470 784CIP2_113 7061 113 1899 3685 5471 784CIP2_114 7077 14 1900 3686 5472 784CIP2_115 7092				5458	784CIP2_101	7028
102 1888 3674 5460 784CIP2_103 7031 103 1889 3675 5461 784CIP2_104 7032 104 1890 3676 5462 784CIP2_105 7033 105 1891 3677 5463 784CIP2_106 7035 106 1892 3678 5464 784CIP2_107 7036 107 1893 3679 5465 784CIP2_108 7039 108 1894 3680 5466 784CIP2_109 7043 109 1895 3681 5467 784CIP2_109 7043 109 1896 3682 5468 784CIP2_110 7044 110 1896 3682 5468 784CIP2_111 7046 111 1897 3693 5469 764CIP2_112 7054 112 1898 3684 5470 784CIP2_113 7061 113 1899 3685 5471 784CIP2_114 7077				5459		7029
103 1889 3675 5461 784CIP2_104 7032 104 1890 3676 5462 784CIP2_105 7033 105 1891 3677 5463 784CIP2_106 7035 106 1892 3678 5464 784CIP2_107 7036 107 1893 3679 5465 784CIP2_108 7039 108 1894 3680 5466 784CIP2_109 7043 109 1895 3681 5467 784CIP2_109 7043 109 1896 3682 5468 784CIP2_110 7044 110 1896 3682 5468 784CIP2_111 7046 111 1897 3683 5469 784CIP2_112 7054 112 1898 3684 5470 784CIP2_113 7061 113 1899 3685 5471 784CIP2_114 7077 114 1900 3686 5472 784CIP2_116 7094				5460	784CIP2 103	7031
104 1890 3676 5462 784CIP2_105 7033 105 1891 3677 5463 784CIP2_106 7035 106 1892 3678 5464 784CIP2_107 7036 107 1893 3679 5465 784CIP2_108 7039 108 1894 3680 5466 784CIP2_109 7043 109 1895 3681 5467 784CIP2_110 7044 110 1896 3682 5468 784CIP2_111 7046 111 1897 3683 5469 764CIP2_112 7054 112 1898 3684 5470 784CIP2_113 7061 113 1899 3685 5471 784CIP2_114 7077 114 1900 3686 5472 784CIP2_115 7092 115 1901 3687 5473 784CIP2_116 7094 116 1902 3688 5474 784CIP2_116 7094 116 1903 3689 5475 784CIP2_119 7111 119 1905 3691 5476 784CIP2_120 7123 120 1906 3692 5478 784CIP2_121 <t< td=""><td></td><td></td><td>3675</td><td>5461</td><td></td><td></td></t<>			3675	5461		
105 1891 3677 5463 784CIP2 106 7035 106 1892 3678 5464 784CIP2 107 7036 107 1893 3679 5465 784CIP2 108 7039 108 1894 3680 5466 784CIP2 109 7043 109 1895 3681 5467 784CIP2 110 7044 110 1896 3682 5468 784CIP2 111 7046 111 1897 3683 5459 764CIP2 112 7054 112 1898 3684 5470 784CIP2 113 7061 113 1899 3685 5471 784CIP2 114 7077 114 1900 3686 5472 784CIP2 115 7092 115 1901 3687 5473 784CIP2 116 7094 116 1902 3688 5474 784CIP2 117 7106 117 1903 3689 5475 784CIP2 118 7107			3676	5462		
106 1892 3678 5464 784CIP2_107 7036 107 1893 3679 5465 784CIP2_108 7039 108 1894 3680 5466 784CIP2_109 7043 109 1895 3681 5467 784CIP2_110 7044 110 1896 3682 5468 784CIP2_111 7046 111 1897 3683 5469 764CIP2_112 7054 112 1898 3684 5470 784CIP2_113 7061 113 1899 3685 5471 784CIP2_114 7077 114 1900 3686 5472 784CIP2_115 7092 115 1901 3687 5473 784CIP2_116 7094 116 1902 3688 5474 784CIP2_117 7106 117 1903 3689 5475 784CIP2_118 7107 118 1904 3690 5476 784CIP2_119 7111		1891	3677	5463		
107 1893 3679 5465 784CIP2 108 7039 108 1894 3680 5466 784CIP2 109 7043 109 1895 3681 5467 784CIP2 110 7044 110 1896 3682 5468 784CIP2 111 7046 111 1897 3683 5469 764CIP2 112 7054 112 1898 3684 5470 784CIP2 113 7061 113 1899 3685 5471 784CIP2 114 7077 114 1900 3686 5472 784CIP2 115 7092 115 1901 3687 5473 784CIP2 116 7094 116 1902 3688 5474 784CIP2 117 7106 117 1903 3689 5475 784CIP2 118 7107 118 1904 3690 5476 784CIP2 119 7111 119 1905 3691 5477 784CIP2 120 7123		1892	3678	1		
108 1894 3680 5466 784CIP2 109 7043 109 1895 3681 5467 784CIP2 110 7044 110 1896 3682 5468 784CIP2 111 7046 111 1897 3683 5469 764CIP2 112 7054 112 1898 3684 5470 784CIP2 113 7061 113 1899 3685 5471 784CIP2 114 7077 114 1900 3686 5472 784CIP2 115 7092 115 1901 3687 5473 784CIP2 116 7094 116 1902 3688 5474 784CIP2 117 7106 117 1903 3689 5475 784CIP2 118 7107 118 1904 3690 5476 784CIP2 119 7111 119 1905 3691 5477 784CIP2 120 7123 120 1906 3692 5478 784CIP2 121 7142 <td>107</td> <td>1893</td> <td>3679</td> <td></td> <td></td> <td></td>	107	1893	3679			
109 1895 3681 5467 784CIP2 110 7044 110 1896 3682 5468 784CIP2 111 7046 111 1897 3693 5469 764CIP2 112 7054 112 1898 3684 5470 784CIP2 113 7061 113 1899 3685 5471 784CIP2 114 7077 114 1900 3686 5472 784CIP2 115 7092 115 1901 3687 5473 784CIP2 116 7094 116 1902 3688 5474 784CIP2 117 7106 117 1903 3689 5475 784CIP2 118 7107 118 1904 3690 5476 784CIP2 119 7111 119 1905 3691 5477 784CIP2 120 7123 120 1906 3692 5478 784CIP2 121 7142	108	1894				
110 1896 3682 5468 784CIP2_111 7046 111 1897 3683 5469 764CIP2_112 7054 112 1898 3684 5470 784CIP2_113 7061 113 1899 3685 5471 784CIP2_114 7077 114 1900 3686 5472 784CIP2_115 7092 115 1901 3687 5473 784CIP2_116 7094 116 1902 3688 5474 784CIP2_117 7106 117 1903 3689 5475 784CIP2_118 7107 118 1904 3690 5476 784CIP2_119 7111 119 1905 3691 5477 784CIP2_120 7123 120 1906 3692 5478 784CIP2_121 7142	109	1895				
111 1897 3693 5469 764CIF2_112 7054 112 1898 3684 5470 784CIF2_113 7061 113 1899 3685 5471 784CIF2_114 7077 114 1900 3686 5472 784CIF2_115 7092 115 1901 3687 5473 784CIF2_116 7094 116 1902 3688 5474 784CIF2_117 7106 117 1903 3689 5475 784CIF2_118 7107 118 1904 3690 5476 784CIF2_119 7111 119 1905 3691 5477 784CIF2_120 7123 120 1906 3692 5478 784CIF2_121 7142	110					
112 1898 3684 5470 784CIP2_112 7054 113 1899 3685 5471 784CIP2_113 7061 114 1900 3686 5472 784CIP2_114 7077 115 1901 3687 5473 784CIP2_115 7092 116 1902 3688 5474 784CIP2_116 7094 117 1903 3689 5475 784CIP2_117 7106 118 1904 3690 5476 784CIP2_119 7111 119 1905 3691 5477 784CIP2_120 7123 120 1906 3692 5478 784CIP2_121 7142	111					
113 1899 3685 5471 784CIP2_113 7061 114 1900 3686 5471 784CIP2_114 7077 115 1901 3687 5472 784CIP2_115 7092 116 1902 3688 5474 784CIP2_116 7094 117 1903 3689 5475 784CIP2_117 7106 118 1904 3690 5476 784CIP2_119 7111 119 1905 3691 5477 784CIP2_120 7123 120 1906 3692 5478 784CIP2_121 7142	112					
114 1900 3686 5471 784CIP2 114 7077 115 1901 3687 5472 784CIP2 115 7092 116 1902 3688 5474 784CIP2 116 7094 117 1903 3689 5475 784CIP2 117 7106 118 1904 3690 5476 784CIP2 119 7111 119 1905 3691 5477 784CIP2 120 7123 120 1906 3692 5478 784CIP2 121 7142						
115 1901 3687 5473 784CIP2_115 7092 116 1902 3688 5474 784CIP2_116 7094 117 1903 3689 5474 784CIP2_117 7106 118 1904 3690 5475 784CIP2_118 7107 119 1905 3691 5476 784CIP2_119 7111 120 1906 3692 5478 784CIP2_121 7142						
116 1902 3688 5474 784CIP2_116 7094 117 1903 3689 5475 784CIP2_117 7106 118 1904 3690 5475 784CIP2_118 7107 119 1905 3691 5476 784CIP2_119 7111 119 1905 3691 5477 784CIP2_120 7123 120 1906 3692 5478 784CIP2_121 7142						
117 1903 3689 5474 784CIP2 117 7106 118 1904 3690 5475 784CIP2 118 7107 119 1905 3690 5476 784CIP2 119 7111 119 1905 3691 5477 784CIP2 120 7123 120 1906 3692 5478 784CIP2 121 7142						
118 1904 3690 5476 784CIP2 118 7107 119 1905 3691 5476 784CIP2 119 7111 120 1906 3691 5477 784CIP2 120 7123 120 1906 3692 5478 784CIP2 121 7142						
119 1905 3691 5477 784CIP2 119 7111 120 1906 3692 5478 784CIP2 121 7142						7107
120 1906 3692 5478 784CIP2_121 7142						7111
120 1906 3692 5478 784CIP2 121 7142				5477	784CIP2_120	7123
121 1907 3693 5479 784CTP2 122 7142				5478		7142
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124	1910	3697	5483	784CIP2 126	7185
125	1911	3698	5484	784CIP2 127	7197
126		3699	5485	784CIP2 128	7219
127	1913	3700	5486	784CIP2 129	7226
128	1914	3701	5487	784CIP2 130	7229
129	1915	3702	5488	784CIP2 131	7234
130	1917	3703	5489	784CIP2 132	7235
131	1917	3704	5490	784CIP2 133	7235
132	1918	3705	5491	784CIP2 134	7238
133	1920	3706	5492	784CIP2 135	7247
134	1920	3707	5493	784CIP2 136	7261
135	1921	3707	5494	784CIP2 137	7262
136	1922	3709	5495	784CIP2 138	7267
137	1923	3710	5496	784CIP2 139	7272
138	1924	3711	5497	784CIP2_140	7273
140	1926	3712	5498	784CIP2 141	7282
141	1927	3713	5499	784CIP2 142	7288
141	1928	3714	5500	784CIP2 143	7291
143	1929	3715	5501	784CIP2 144	7293
144	1930	3716	5502	784CIP2_145	7294
145	1931	3717	5503	784CIP2_146	7299
146	1932	3718	5504	784CIP2_147	7300
147	1933	3719	5505	784CIP2_148	7312
148	1934	3720	5506	784CIP2_149	7313
149	1935	3721	5507	784CIP2_150	7315
150	1936	3722	5508	784CIP2_151	7318
151	1937	3723	5509	784CIP2_152	7321
152	1938	3724	5510	784CIP2_153	7330
153	1939	3725	5511	784CIP2_154	7331
154	1940	3726	5512	784CIP2_155	7333
155	1941	3727	5513	784CIP2_156	7350
156	1942	3728	5514	784CIP2_157	7352
157	1943	3729	5515	784CIP2_158	7384
158	1944	3730	5516	784CIP2_159	7403
159	1945	3731	5517	784C1P2_160	7431
160	1946	3732	5518	784CIP2_161	7441
161	1947	3733	5519	784CIP2_162	7453
162	1948	3734	5520	784CIP2_163	7467 7471
163	1949	3735	5521	784CIP2_164	7471
164	1950	3736	5522	784CIP2_165	7502
165	1951	3737	5523	784CIP2_166	7511
166	1952	3738	5524	784CIP2_167	7514
167	1953	3739	5525	784CIP2_168	7520
168	1954	3740	5526	784CIP2_169	7541
169	1955	3741	5527	784CIP2_170	7570
170	1956	3742	5528	784CIP2_171	7578
171	1957	3743	5529	784CIP2_172	7583
172	1958	3744	5530	784CIP2_173	7592
173	1959	3745	5531	784CIP2_174	7601
174	1960	3746	5532	784CIP2_175	7602
175	1961	3747	5533	784CIP2_176	7602
176	1962	3748	5534	784CIP2_177	7615
177	1963	3749	5535	784CIP2_178	7617
178	1964	3750	5536	784CIP2_179	
179	1965	3751	5537	784CIP2_181	7624 7626
180	1966	3752	5538	784CIP2_182	7640
181	1967	3753	5539	784CIP2_183	7641
182	1968	3754	5540	784CIP2_184	7641
183	1969	3755	5541	784CIP2_185	1041

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length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
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184	sequence	<u> </u>		application	
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185	1971	3757	5543	784CIP2_187	7642
186	1972	3758	5544	784CIP2_188	7649
	1973	3759	5545	784CIP2_189	7656
188 189	1974	3760	5546	784CIP2_190	7657
190	1975	3761	5547	784CIP2_191	7657
191	1976	3762	5548	784CIP2_192	7662
192	1977	3763	5549	784CIP2_193	7668
193	1978	3764	5550	784CIP2_194	7673
193	1979	3765	5551	784CIP2_195	7690
194	1980	3766	5552	784CIP2_196	7700
196	1981	3767	5553	784CIP2_197	7709
196	1982	3768	5554	784CIP2_198	7736
198	1983	3769	5555	784CIP2_199	7737
	1984	3770	5556	784CIP2_200	7744
199 200	1985	3771	5557	784CIP2_201	7771
	1986	3772	5558	784CIP2_202	7786
201 202	1987	3773	5559	784CIP2_203	7791
	1988	3774	5560	784CIP2_204	7797
203 204	1989	3775	5561	784CIP2_205	7806
205	1990	3776	5562	784CIP2_206	7812
206	1991	3777	5563	784CIP2_207	7812
207	1992	3778	5564	784CIP2_208	7818
207	1993	3779	5565	784CIP2_209	7822
208	1994	3780	5566	784CIP2_210	7827
210	1995	3781	5567	784CIP2_211	7830
211	1995	3782	5568	784CIP2_212	7835
212	1997	3783	5569	784CIP2_214	7840
212	1998	3784	5570	784CIP2_215	7858
213	1999	3785	5571	784CIP2_216	7858
215	2000	3786	5572	784CIP2_217	7861
216	2002	3787	5573	784CIP2_218	7866
217	2002	3788	5574	784CIP2_219	7868
218	2004	3789	5575	784CIP2_220	7896
219	2004	3790	5576	784CIP2_221	7898
220	2005	3791	5577	784CIP2_222	7900
221	2007	3792	5578	784CIP2_223	7906
222	2007	3793	5579	784CIP2_224	7908
223	2009	3794	5580	784CIP2_225	7909
224	2010	3795 3796	5581	784CIP2_226	7917
225	2010	3797	5582	784CIP2_227	7932
226	2012	3798	5583	784CIP2_228	7940
227	2013		5584	784CIP2_229	7940
228	2014	3799 3800	5585	784CIP2_230	7984
229	2015	3801	5586	784CIP2_231	7984
230	2016		5587	784CIP2_232	8001
231	2017	3802	5588	784CIP2_233	8021
232	2017	3803	5589	784CIP2_234	8029
233	2019	3804	5590	784CIP2_235	8033
234	2020	3805	5591	784CIP2_236	8040
235	2021	3806	5592	784CIP2_237	8052
236	2022	3807	5593	784CIP2 238	8096
237	2022	3808	5594	784CIP2_239	8096
238	2024	3809	5595	784CIP2_240	8113
		3810	5596	784CIP2_241	8126
230		201-			
239	2025	3811	5597	784CIP2_242	8132
240	2025 2026	3812	5598	784CIP2_242 784CIP2_243	8132
240 241	2025 2026 2027	3812 3813	5598 5599		
240 241 242	2025 2026 2027 2028	3812 3813 3814	5598 5599 5600	784CIP2_243	8137
240 241 242 243	2025 2026 2027 2028 2029	3812 3813 3814 3815	5598 5599 5600 5601	784CIP2_243 784CIP2_244	8137 8137
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248	2034	3820	5606	784CIP2 251	8212
249	2035	3821	5607	784CIP2_252	8220
	2036	3822	5608	784CIP2_253	8238
250		3823	5609	784CIP2 254	8254
251	2037	3824	5610	784CIP2 255	8255
252	2038	3825	5611	784CIP2 256	8288
253	2039		5612	784CIP2 257	8296
254	2040	3826	5613	784CIP2 258	8329
255	2041	3827	5614	784CIP2 259	8362
256	2042	3828		784CIP2 260	8429
257	2043	3829	5615	784CIP2 261	8436
258	2044	3830	5616		8448
259	2045	3831	5617	784CIP2_262	8472
260	2046	3832	5618	784CIP2_263	8502
261	2047	3833	5619	784CIP2_264	8504
262	2048	3834	5620	784CIP2_265	
263	2049	3835	5621	784CIP2_266	8507
264	2050	3836	5622	784CIP2_268	8509
265	2051	3837	5623	784CIP2_269	8515
266	2052	3838	5624	784CIP2_270	8519
267	2053	3839	5625	784CIP2_271	8530
268	2054	3840	5626	784CIP2_272	8532
269	2055	3841	5627	784CIP2_273	8532
270	2056	3842	5628	784CIP2_274	8539
271	2057	3843	5629	784CIP2_275	8541
272	2058	3844	5630	784CIP2_276	8543
273	2059	3845	5631	784CIP2_277	8593
274	2060	3846	5632	784CIP2_278	8595
275	2061	3847	5633	784CIP2_279	8615
276	2062	3848	5634	784CIP2_280	8620
277	2063	3849	5635	784CIP2_281	8621
278	2064	3850	5636	784CIP2 282	8623
279	2065	3851	5637	784CIP2_283	8625
280	2066	3852	5638	784CIP2 284	8628
281	2067	3853	5639	784CIP2_285	8628
282	2068	3854	5640	784CIP2 286	8629
283	2069	3855	5641	784CIP2_287	8630
	2070	3856	5642	784CIP2 288	8631
284	2071	3857	5643	784CIP2 289	8633
285		3858	5644	784CIP2 290	8634
286	2072	1	5645	784CIP2 291	8635
287	2073	3859	5646	784CIP2_292	8636
288	2074	3860		784CIP2 293	8659
289	2075	3861	5647	784CIP2_293	8660
290	2076	3862	5648	784CIP2 295	8667
291	2077	3863	5649		8667
292	2078	3864	5650	784CIP2_296 784CIP2_297	8685
293	2079	3865	5651		8805
294	2080	3866	5652	784CIP2_298	8896
295	2081	3867	5653	784C1P2_299	
296	2082	3868	5654	784CIP2_300	8978
297	2083	3869	5655	784CIP2_301	9046
298	2084	3870	5656	784CIP2_302	9048
299	2085	3871	5657	784CIP2_303	9116
300	2086	3872	5658	784CIP2_304	9195
301	2087	3873	5659	784CIP2_305	9201
302	2088	3874	5660	784CIP2_306	9307
303	2089	3875	5661	784CIP2 307	9321
	2090	3876	5662	784CIP2 308	9397
304	2090	3877	5663	784CIP2 309	9405
305			5664	784CIP2 310	9406
306	2092	3878	5665	784CIP2 311	9422
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312	2098	3884	5670	784CIP2_315 784CIP2_316	9661
313	2099	3885	5671		9664
314	2100	3886	5672		9691
315	2101	3887	5673	784CIP2_318 784CIP2_319	9700
316	2102	3888	5674	784CIP2_319	9716
317	2103	3889	5675	784CIP2_320	9721
318	2104	3890	5676	784CIP2_321	9870
319	2105	3891	5677	784CIP2_322 784CIP2_323	9887
320	2106	3892	5678	784CIP2_323 784CIP2_324	9923
321	2107	3893	5679	784CIP2_324 784CIP2_325	9938
322	2108	3894	5680	784CIP2_325	9964
323	2109	3895	5681	784CIP2_326	10007
324	2110	3896	5682	784CIP2_327 784CIP2_328	10009
325	2111	3897	5683	784CIP2_328	10046
326	2112	3898	5684	784CIP2_329	10156 10276
327	2113	3899	5685	784CIP2_330	102/6
328	2114	3900	5686	784CIP2B 1	152
329	2115	3901	5687	784CIP2B 2	167
330	2116	3902	5688	784CIP2B 3	205
331	2117	3903	5689	784CIP2B 4	210
332	2118	3904	5690	784CIP2B 5	225
333	2119	3905	5691	784CIP2B 6	226
334	2120	3906	5692	784CIP2B 7	264
335	2121	3907	5693	784CIP2B 8	268
336	2122	3908	5694	784CIP2B 9	293
337	2123	3909	5695	784CIP2B 10	293
338	2124	3910	5696	784CIP2B 11	293
339	2125	3911	5697	784CIP2B_12	302
340	2126	3912	5698	784CIP2B_13	311
341	2127	3913	5699	784CIP2B_14	352
342 343	2128	3914	5700	784CIP2B_15	358
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345	2130	3916	5702	784CIP2B_17	393
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349	2134	3920	5706	784CIP2B_21	515
350	2136	3921	5707	784CIP2B_22	578
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352	2138	3923	5709	784CIP2B_24	591
353	2139	3925	5710 5711	784CIP2B_25	593
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365	2151	3937	5722 5723	784CIP2B_37	891
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367	2153	3939	5724 5725	784CIP2B_39	921
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370	2156	3943	5729	784CIP2B 44	968
371	2157	3944	5730	784CIP2B_45	992
372	2159	3945	5731	784CIP2B 46	1025
373	2160	3946	5732	784CIP2B 47	1074
374	2161	3947	5733	784CIP2B_48	1104
375	2162	3948	5734	784CIP2B 49	1114
376 377	2163	3949	5735	784CIP2B_50	1144
378	2164	3950	5736	784CIP2B_51	1262
378	2165	3951	5737	784CIP2B_52	1318
	2166	3952	5738	784CIP2B_53	1319
380	2167	3953	5739	784CIP2B_54	1328
381 382	2168	3954	5740	784CIP2B_55	1436
383	2169	3955	5741	784CIP2B_56	1464
384	2170	3956	5742	784CIP2B_57	1584
385	2171	3957	5743	784CIP2B_58	1617
386	2172	3958	5744	784CIP2B_59	1724
387	2173	3959	5745	784CIP2B_60	1728
388	2174	3960	5746	784CIP2B_61	1772
389	2175	3961	5747	784CIP2B_62	1809
390	2176	3962	5748	784C1P2B_63	1868
391	2177	3963	5749	784CIP2B_64	1898
392	2178	3964	5750	784CIP2B_65	1926
393	2179	3965	5751	784CIP2B_66	1965
394	2180	3966	5752	784CIP2B_67	1967
395	2181	3967	5753	784CIP2B_68	1995
396	2182	3968	5754	784CIP2B_69	2005.
397	2183	3969	5755	784CIP2B_70	2027
398	2184	3970	5756	784CIP2B_71	2103
399	2185	3971	- 5757	784CIP2B_72	2106
400	2186	3972	5758	784CIP2B_73	2166
401	2187	3973	5759	784CIP2B_74 784CIP2B_75	2175
402	2188	3974	5760	784CIP2B_75	2176
403	2189	3 9 7 5	5761	784CIP2B_78	2236
404	2190	3976	5762	784CIP2B_78	2250
405	2191	3977	5763	784CIP2B_73	2300 .
406	2192	3978	5764	784CIP2B 81	2323
407	2193	3979	5765	784CIP2B 82	2340
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409	2195	3981	5767 5768	784CIP2B 84	2399
410	2196	3982	5769	784CIP2B 85	2411
411	2197	3983	5770	784CIP2B 86	2428
412	2198	3984	5771	784CIP2B_87	2430
413	2199	3985	5772	784CIP2B 88	2439
414	2200	3986	5773	784CIP2B_89	2447
415	2201	3987	5774	784CIP2B 90	2461
416	2202	3988	5773	784CIP2B_91	2487
417	2203	3989	5776	784CIP2B 92	2492
418	2204	3990	5777	784CIP2B 93	2512
419	2205	3991	5778	784CIP2B 94	2564
420	2206	3992 3993	5779	784CIP2B_95	2678
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422	2208	3994	5781	784CIP2B_97	2818
423	2209	3995	5782	784CIP2B 98	2819
424	2210	3996	5783	784CIP2B_99	2943
425	2211	3997	5784	784CIP2B 100	3137
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435	2221	4007	5793	784CIP2B_108	3442
436	2222	4008		784CIP2B_109	3442
437	2223	4009	5794 5795	784CIP2B_110	3444
438	2224	4010		784CIP2B_111	3855
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440	2226	4012	5798	784CIP2B_113	4090
441	2227 .	4013	5799	784CIP2B_114	4105
442	2228	4014		784CIP2B_115	4142
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444	2230	4016	5801	784CIP2B_117	4149
445	2231	4017	5802 5803	784CIP2B_118	4196
446	2232	4018	5804	784CIP2B_119	4202
447	2233	4019	5805	784CIP2B_120	4274
448	2234	4020	5806	784CIP2B_121	4304
449	2235	4021	5807	784CIP2B_122	4306
450	2236	4022	5807	784CIP2B_123	4311
451	2237	4023	5809	784CIP2B_124	4321
452	2238	4024	5810	784CIP2B_125 784CIP2B_126	4323
453	2239	4025	5811	784CIP2B 126	4332
454	2240	4026	5812	784CIP2B 127	4488
455	2241	4027	5813	784CIP2B 129	4588
456	2242	4028	5814	784CIP2B 130	5569 5573
457	2243	4029	5815	784CIP2B 131	5577
458	2244	4030	5816	784CIP2B 132	5579
459 460	2245	4031	5817	784CIP2B 133	5582
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462	2247 2248	4033	5819	784CIP2B_135	5584
463	2249	4034	5820	784CIP2B_136	5585
464	2250	4035 4036	5821	784CIP2B_137	5591
465	2251	4037	5822	784CIP2B_138	5593
466	2252	4038	5823 5824	784CIP2B_139	5594
467	2253	4039	5825	784CIP2B_140	5594
468	2254	4040	5826	784CIP2B_141	5598
469	2255	4041	5827	784CIP2B_142	5602
470	2256	4042	5828	784CIP2B_143 784CIP2B_144	5605
471	2257	4043	5829	784CIP2B 145	5608
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473	2259	4045	5831	784CIP2B 147	5620 5622
474	2260	4046	5832	784CIP2B 148	5623
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476	2262	4048	5834	784CIP2B 150	5625
477	2263	4049	5835	784CIP2B_151	5627
478	2264	4050	5836	784CIP2B 152	5628
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481	2266	4052	5838	784CIP2B_154	5632
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483	2269	4054	5840	784CIP2B_156	5641
494	2270	4055	5841	784CIP2B_157	5643
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486	2272	4057	5843	784CIP2B_159	5649
487	2273	4059	5844	784CIP2B_160	5658
488	2274	4059	5845	784CIP2B_161	5659
489	2275	4060	5846	784CIP2B_162	5667
490	2276	4062	5847 5848	784CIP2B_163	5672
_491	2277	4063	5848	784CIP2B 164	5674
492	2278	4064	5850	784CIP2B_165 784CIP2B_166	5678
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length	full-	nucleotide	of contig	SEQ ID NO: in	09/488,725
nucleotide	length	sequence	peptide sequence	priority	
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	sequence	4066	5852	784CIP2B 168	5686
494	2280	4067	5853	784CIP2B_169	5694
495	2281	4068	5854	784CIP2B 170	5698
496	2282	4069	5855	784CIP2B 171	5699
497		4070	5856	784CIP2B 172	5712
498	2284	4071	5857	784CIP2B 173	5719
499	2286	4072	5858	784CIP2B 174	5720
500	2286	4073	5859	784CIP2B 175	5727
501	2288	4074	5860	784CIP2B 176	5730
502	2289	4075	5861	784CIP2B 177	5734
503	2290	4076	5862	784CIP2B 178	5738
504	2291	4077	5863	784CIP2B 179	5739
505	2292	4078	5864	784CIP2B 180	5740
506	2293	4079	5865	784CIP2B 181	5744
507	2294	4080	5866	784CIP2B 182	5748
508	2294	4081	5867	784CIP2B_183	5749
509	2295	4082	5868	784CIP2B 184	5750
510	2297	4083	5869	784CIP2B_185	5750
511	2298	4084	5870	784CIP2B 186	5750
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513 514	2300	4086	5872	784CIP2B_188	5762
515	2300	4087	5873	784CIP2B 189	5767
516	2302	4088	5874	784CIP2B 190	5773
517	2302	4089	5875	784CIP2B 191	5783
	2304	4090	5876	784CIP2B 192	5784
518	2305	4091	· 5877	784CIP2B 193	5788
519 520	2306	4092	5878	784CIP2B 194	5798
520	2307	4093	5879	784CIP2B 196	5807
522	2308	4094	5880	784CIP2B_197	5818
523	2309	4095	5881	784CIP2B 198	5819
524	2310	4096	5882	784CIP2B_199	5827
525	2311	4097	5883	784CIP2B_200	5828
526	2312	4098	5884	784CIP2B_201	5842
527	2313	4099	5885	784CIP2B_202	5853
528	2314	4100	5886	784CIP2B_203	5861
529	2315	4101	5887	784CIP2B_204	5864
530	2316	4102	5888	784CIP2B_205	5865
531	2317	4103	5889	784CIP2B_206	5871
532	2318	4104	5890	784CIP2B_207	5873
533	2319	4105	5891	784CIP2B_208	5873
534	2320	4106	5892	784CIP2B_209	5875
535	2321	4107	5893	784CIP2B_210	5878
536	2322	4108	5894	784CIP2B_211	5879
537	2323	4109	5895	784CIP2B_212	5880
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539	2325	4111	5897	784CIP2B_214	5880
540	2326	4112	5898	784CIP2B_215	5880
541	2327	4113	5899	784CIP2B_216	5885
542	2328	4114	5900	784CIP2B_217	5895
543	2329	4115	5901	784CIP2B_218	5898
544	2330	4116	5902	784CIP2B_219	5902
545	2331	4117	5903	784CIP2B_220	5904
546	2332	4118	5904	784CIP2B_221	5918
547	2333	4119	5905	784CIP2B_222	5921
548	2334	4120	5906	784CIP2B_223	5927
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550	2336	4122	5908	784CIP2B_225	5939
551	2337	4123	5909	784CIP2B_226	5945
552	2338	4124	5910	784CIP2B_227	5946
553	2339	4125	5911	784CIP2B_228	5947
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562	2348	4134	5920	784CIP2B 238	5989
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566	2352	4138	5924	784CIP2B_241	5998
567	2353	4139	5925	784CIP2B 242	6003
568	2354	4140	5926		6004
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570	2356	4142	5928	784CIF2B_245	6028
571	2357	4143	5929	784CIP2B_246	6028
572	2358	4144		784CIP2B_247	6029
573	2359	4145	5930 5931	784CIP2B_248	6031
574	2360	4146	5932	784CIP2B_249	6031
575	2361	4147		784CIP2B_250	6032
576	2362	4148	5933	784CIP2B_251	6037
577	2363	4149	5934	784CIP2B_252	6037
578	2364	4150	5935	784CIP2B_253	6043
579	2365	4151	5936	784CIP2B_254	6044
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582	2368	4154	5939	784CIP2B_257	6049
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585	2371	4157	5942 5943	784CIP2B_260	6060
586	2372	4158	5944	784CIP2B_261	6063
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592	2378	4164	5950	784CIP2B_267	6076
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606	2392	4178	5963	784CIP2B_282	6126
607	2393	4179	5964	784CIP2B_283	6128
608	2394	4180	5965	784CIP2B_284	6129
609	2395	4181	5966	784CIP2B_285	6133
610	2396		5967	784CIP2B_286	6133
611	2397	4182	5968	784CIP2B_287	6135
612	2398	4183	5969	784CIP2B_288	6139
613	2398	4184	5970	784CIP2B_289	6141
614		4185	5971	784CIP2B_290	6145
615	2400	4186	5972	784CIP2B_291	6146
616	2401	4187	5973	784CIP2B_292	6148
617	2402	4188	5974	784CIP2B_293	6149
	2403	4189	5975	784CIP2B 294	6149

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619	2405	4191	5977	784CIP2B_298	6164
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621	2407	4193	5979	784CIP2B_298	6167
622	2408	4194	5980	784CIP2B_299	6172
623	2409	4195	5981	784CIP2B_300	6173
624	2410	4196	5982	784CIP2B_301	6190
625	2411	4197	5983	784CIP2B_302	6194
626	2412	4198	5984	784CIP2B_303	6196
627	2413	4199	5985	784CIP2B_304	6197
628	2414	4200	5986	784CIP2B_305	6198
629	2415	4201	5987	784CIP2B_306	6198
630	2416	4202	5988	784CIP2B_308	6214
631	2417	4203	5989	784CIP2B 309	6215
632	2418	4204	5990	784CIP2B 310	6219
633	2419	4205	5991	784CIP2B 311	6226
634	2420	4206	5992	784CIP2B 312	6229
635	2421	4207	5993	784CIP2B 313	6234
636	2422	4208	5994	784CIP2B 314	6237
637	2422	4208	5995	784CIP2B 315	6238
638	2423	4210	5996	784CIP2B 316	6239
		4211	5997	784CIP2B 317	6239
639	2425	4211	5998	784CIP2B 318	6239
640	2426		5999	784CIP2B 319	6240
641	2427	4213	1	784CIP2B 320	6244
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643	2429	4215	6001	784CIP2B_321 784CIP2B 322	6250
644	2430	4216	6002		6252
645	2431	4217	6003	784CIP2B_323	
646	2432	4218	6004	784CIP2B_324	6252
647	2433	4219	6005	784CIP2B_325	6256
648	2434	4220	6006	784CIP2B_326	6260
649	2435	4221	6007	784CIP2B_327	6251
650	2436	4222	6008	784CIP2B_328	6264
651	2437	4223	6009	784CIP2B_329	6265
652	2438	4224	6010	784CIP2B_330	6266
653	2439	4225	6011	784CIP2B_331	6270
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656	2442	4228	6014	784C1P2B_335	6276
657	2443	4229	6015	784CIP2B 336	6281
658	2444	4230	6016	784CIP2B 337	6281
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		4237	6023	784CIP2B 346	6322
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669	2455	4241	6027	784CIP2B_351	
670	2456	4242	6028	784CIP2B_352	6334
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672	2458	4244	6030	784CIP2B_354	6339
	2459	4245	6031	784CIP2B_355	6346
673			6032	784CIP2B 356	634B
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		4246 4247	6033	784CIP2B_357	6348
674	2460			_ =	
674 675 676	2460 2461 2462	4247 4248	6033	784CIP2B_357	6348
674 675	2460 2461	4247	6033 6034	784CIP2B_357 784CIP2B_358	6348 6350

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683	2469	4255	6041	784CIP2B 365	6376
684	2470	4256	6042	784CIP2B 366	6379
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686	2472	4258	6044	784CIP2B 368	6381
687	2473	4259	6045	784CIP2B 369	6392
688	2474	4260	6046	784CIP2B 370	6395
689	2475	4261	6047	784CIP2B 371	6397
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691	2477	4263	6049	784CIP2B 373	6401
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694	2480	4266	6052	784CIP2B_376	6411
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696	2482	4268	6054	784CIP2B 378	6418
697	2483	4269	6055	784CIP2B 379	6422
698	2484	4270	6056	784CIP2B_379	6423
699	2485	4271	6057	784CIP2B_380 784CIP2B_381	6426
700	2486	4272	6058	784CIP2B_381	6426
701	2487	4273	6059	784CIP2B 383	6428
702	2438	4274	6060	784CIP2B 384	6429
703	2489	4275	6061	784CIP2B 385	6430
704	2490	4276	6062	784CIP2B 386	6432
705	2491	4277	6063	784CIP2B 387	6432
706	2492	4278	6064	784CIP2B 388	6438
707	2493	4279	6065	784CIP2B 389	6441
708	2494	4280	6066	784CIP2B 390	6446
709	2495	4281	6067	784CIP2B 391	6454
710	2496	4282	6068	784CIP2B 392	6459
711	2497	4283	6069	784CIP2B 394	6461
712	2498	4284	6070	784CIP2B 395	6467
713	2499	4285	6071	784CIP2B 396	6468
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715	2501	4287	6073	784CIP2B 398	6491
716	2502	4288	6074	784CIP2B_399	6506
717	2503	4289	6075	784CIP2B 401	6514
718	2504	4290	6076	784CIP2B_402	6519
719	2505	4291	6077	784CIP2B_403	6521
720	2506	4292	6078	784CIP2B_404	6532
721	2507	4293	6079	784CIP2B_405	6536
722	2508	4294	6080	784CIP2B_406	6543
723	2509	4295	6081	784CIP2B_407	6544
724	2510	4296	6082	784CIP2B_408	6548
725	2511	4297	6083	784CIP2B_409	6551
726	2512	4298	6084	784CIP2B_410	6551
727	2513	4299	6085	784CIP2B_411	6552
728	2514	4300	6086	784CIP2B_412	6554
729	2515	4301	6987	784CIP2B_413	6556
730	2516	4302	6088	784CIP2B_414	6560
731	2517	4303	6089	784CIP2B_415	6563
732	2518	4304	6090	784CIP2B_416	6564
733	2519	4305	6091	784CIP2B_417	6567
734	2520	4306	6092	784CIP2B_418	6573
735	2521	4307	6093	784CIP2B_419	6575
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737	2523	4309	6095	784CIP2B_421	6593
738	2524	4310	6096	784CIP2B_422	6595
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743	2529	4315	6101	784CIP2B 428	6631
744	2530	4316	6102	784CIP2B 429	6632
745	2531	4317	6103	784CIP2B_430	6633
746	2532	4318	6105	784CIP2B_431	6634
747	2533	4319	6106	784CIP2B 432	6638
748	2534	4320	6107	784CIP2B 433	6641
749	2535	4321	6108	784CIP2B 434	6644
750	2536	4322	6109	784CIP2B 435	6646
751	2537	4323	6110	784CIP2B 436	6648
752	2538	4324	6111	784CIP2B 437	6652
753	2539	4325 4326	6112	784CIP2B 438	6654
754	2540	4327	6113	784CIP2B 439	6657
755	2541	4328	6114	784CIP2B 440	6658
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764	2550	4336	6122	784CIP2B 448	6689
765	2551	4337	6123	784CIP2B_449	6693
766	2552	4338	6124	784CIP2B_450	6698
767	2553	4339	6125	784CIP2B_451	6699
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769	2555	4341	6127	784CIP2B_453	6711
770	2556	4342	6128	784CIP2B_454	6713
771	2557	4343	6129	784CIP2B_455	6716
772	2558	4344	6130	784CIP2B_456	6725
773	2559	4345	6131	784CIP2B_457	6726
774	2560	4346	6132	784C1P2B_458	6727
775	2561	4347	6133	784CIP2B_459	6730
776	2562	4348	6134	784CIP2B_460	6730
777	2563	4349	6135	784CIP2B_461	6730
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780	2566	4352	6138	784CIP2B_464	6745
781	2567	4353	6139	784CIP2B_465	6751
782	2568	4354	6140	784CIP2B_466	6754
783	2569	4355	6141	784CIP2B_467 784CIP2B_468	6758
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786	2572	4356	6144	784CIP2B_470	6768
787	2573	4359	6145	784CIP2B_471 784CIP2B_472	6773
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789	2575	4361	6147	784CIP2B 474	6796
790	2576	4362	6148	784CIP2B_474 784CIP2B_475	6798
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792	. 2578	4364	6150	784CIP2B_478	6825
793	2579	4365	6151	784CIP2B 478	6826
794	2580	4366	6152	784CIP2B_478	6839
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796	2582	4368	6154	784CIP2B_480 784CIP2B 482	
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	2584	4370	6156	784CIP2B_483 784CIP2B_484	
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SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	I Day out to	
of full-	NO: of	of contig	NO:	Priority docket number	SEQ ID
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nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
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809	2595	4381	6167	784CIP2B 494	6901
810	2595	4382	6168	784CIP2B 495	6904
811	2597	4383	6169	784CIP2B 496	6907
812	2598	4384	6170	784CIP2B 497	6914
813	2599	4385	6171	784CIP2B 498	6917
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815	2601	4387	6173	784CIP2B 500	6929
816	2602	4388	6174	784CIP2B 501	6931
817	2603	4389	6175	784CIP2B 502	6935
818	2604	4390	6176	784CIP2B 503	6940
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820	2606	4392	6178	784CIP2B 505	6946
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832	2617	4403	6189	784CIP2B_516	7003
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835	2621	4406 4407	6192	784CIP2B 519	7025
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856	2642	4428	6214	784CIP2B_540 784CIP2B_541	7109
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858	2644	4430	6215	784CIP2B_542	7120
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861	2647	4433	6218	784CIP2B_545	7127
862	2648	4434	6219	784CIP2B_546	7130
863	2649	4434	6220	784CIP2B_547	7131
864	2650	4436	6221	784CIP2B_548	7144
865	2651	4437	6222	784CIP2B 549	7159
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868	2654	4440	6226	784CIP2B_553	7189
869	2655	4441	6227	784CIP2B_554	7190
870	2656	4442	6228	784CIP2B_555	7191
871	2657	4443	6229	·784CIP2B_556	7203
872	2658	4444	6230	784CIP2B_557	7204
873	2659	4445	6231	784CIP2B_558	7208
874	2660	4446	6232	784CIP2B_559	7209
875	2661	4447	6233	784CIP2B_560	7210
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878	2664	4450	6236	784CIP2B_563	7230
879	2665	4451	6237	784CIP2B_564	7237
880	2666	4452	6238	784CIP2B_565	7240 7245
881	2667	4453	6239	784CIP2B_566	7250
882	2668	4454	6240	784CIP2B_567	7251
883	2669	4455	6241	784CIP2B_568	7255
884	2670	4456	6242	784CIP2B_569	7260
885	2671	4457	6243	784CIP2B_570	7265
886	2672	4458	6244	784CIP2B_571	7268
887	2673	4459	6245	784CIP2B_572	7275
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890	2676	4462	6248	784CIP2B_575	7283
891	2677	4463	6249	784CIP2B_576	7287
892	2678	4464	6250	784CIP2B 578	7301
893	2679	4465	6251	784CIP2B_578	7308
894	2680	4466	6252	784CIP2B_575	7308
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897	2683	4469	6255 6256	784CIP2B 583	7320
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899	2685	4471	6258	784CIP2B 585	7326
900	2686	4472	6259	784CIP2B 586	7334
901	2687	4474	6260	784CIP2B_587	7337
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917	2702	4489	6275	784CIP2B 604	7393
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919	2705	4491	6277	784CIP2B_606	7397
920	2706	4492	6278	784CIP2B_607	7399
920	2707	4493	6279	784CIP2B 608	7405
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939	2725	4511	6297	784CIP2B_625	7435
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1006	2792	4578	6364	784CIP2B 695	7674
1007	2793	4579	6365	1 .0.10	7675
1008	2794	4580	6366	784CIP2B_696	7676
1009	2795	4581	6367	784CIP2B_697	7681
1010	2796	4582	6368	784CIP2B_698	
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1012	2798	4584	6370	784CIP2B_700	7693
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1016	2802	4588	6374	784CIP2B_704	7718
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1241	3027	4813	6599	784CIP2B_931 784CIP2B_932	8409
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1251	3037	4823	6609	784CIP2B_941	8433
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1261	3047	4833	6619	784CIP2B_951	
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1284	3070	4856	6642	784CIP2B_974	8531
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1290	3076	4862	6648	784CIP2B 980	8572
1291	3077	4863	6649	784CIP2B 981	8576
1292	3078	4864	6650	784CIP2B 982	8578
			6651	784CIP2B 983	8584
1293	3079	4865		784CIP2B 984	8598
1294	3080	4866	6652		8602
1295	3081	4867	6653	784CIP2B_985	8604
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1299	3085	4871	6657	784CIP2B 989	8637

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1420	3205	4992	6778	784CIP2C_7	980
1421	3207	4993	6779	784CIP2C 8	1595
1422	3208	4994	6780	784CIP2C 9	1697
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	3214	5000	6786	784CIP2C_15	2889
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1430	3216	5002	6788	784CIP2C_17	2902
1431	3217	5003	6789	784CIP2C_18	2905
1432	3218	5004	6790	784CIP2C_19	2948
1433	3219	5005	6791	784CIP2C_20	2956
1434	3220	5006	6792	784CIP2C_21	2959
1435	3221	5007	6793	784CIP2C 22	2965
1436	3222	5008	6794	784CIP2C 23	2966
1437	3223	5009	6795	784CIP2C 24	2970
1438	3224	5010	6796	784CIP2C 25	2985
1439	3225	5011	6797	784CIP2C 26	2987
1440	3226	5012	6798	784CIP2C 27	2993
1441	3227	5013	6799	784CIP2C_27	2993
1442	3228	5014	6800	784CIP2C_28	3017
1443	3229	5015	6801	784CIP2C 30	3046
1444	3230	5016	6802	784CIP2C_30	
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1446	3232	5018		L	3357
1447	3232		6804	784CIP2C_33	3359
1448		5019	6805	784CIP2C_34	3432
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1451	3236	5022	6808	784CIP2C_39	3463
	3237	5023	6809	784CIP2C_40	3466
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1453	3239	5025	6911	784CIP2C_42	3467
1454	3240	5026	6912	784CIP2C_43	3468
1455	3241	5027	6813	784CIP2C_44	3483
1456	3242	5028	6814	784CIP2C_45	3484
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1458	3244	5030	6816	784CIP2C_47	3491
1459	3245	5031	6817	784CIP2C_48	34 <i>9</i> 3
1460	3246	5032	6818	784CIP2C_49	3494
1461	3247	5033	6819	784CIP2C_50	3495
1462	3248	5034	6820	784CIP2C 51	3496
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1468	3254	5040	6826	784CIP2C 57	3536
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1470	3256	5042	6828	784CIP2C 59	3548
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1472	3258	5044	6830	784CIP2C 61	3553
1473	3259	5045	6831	784CIP2C 62	3564
1474	3260	5046	6832		
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1482	3268	5054	6840	784CIP2C_71	3666
1483	3269	5055	6841	784CIP2C_72	3667
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1490	3276	5062	6848	784CIP2C_79 784CIP2C_80	3989
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1492	3278	5064	6850	784CIP2C 82	4300
1493	3279	5065	6851	784CIP2C_82	4360
1494	3280	5066	6852		4362
1495	3281	5067	6853	784CIP2C_84	4371
1496	3282	5068	6854	784CIP2C_85	4373
1497	3283	5069	6855	784CIP2C_86	4376
1498	3284	5070	6856	784CIP2C_87 784CIP2C 89	4378
1499	3285	5071	6857		4382
1500	3286	5072	6858	784CIP2C_90	4409
1501	3287	5073	6859	784CIP2C_91 784CIP2C 92	4421
· 1502	.3288	5074	6860	784C1P2C_92 784C1P2C_93	4421
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1504	3290	5076	6862	784C1P2C_94 784C1P2C_95	4430
1505	3291	5077	6863	784CIP2C 96	4435
1506	3292	5078	6864	784CIP2C 97	4436
1507	3293	5079	6865	784CIP2C 98	4439
1508	3294	5080	6866 6867	784CIP2C 99	4440
1509	3295	5081	6868	784CIP2C 100	4441
1510	3296	5082	6869	784CIP2C 101	4442
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1518	3305	5091	6877	784CIP2C 109	4484
1520	3306	5092	6878	784CIP2C 110	4486
1521	3307	5093	6879	784CIP2C 111	4490
1522	3308	5094	6880	784CIP2C 112	4499
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1528	3314	5100	6886	784CIP2C_118	4522
1529	3315	5101	6887	784CIP2C_119	4525
1530	3316	5102	6888	784CIP2C_120	4527
1531	3317	5103	6889	784CIP2C_121	4528
1532	3318	5104	6890	784CIP2C_122	4529
1533	3319	5105	6891	784CIP2C_123	4532
1534	3320	5106	6892	784CIP2C_124	4537
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1536	3322	5108	6894	784CIP2C 126	4551
1537	3323	5109	6895	784CIP2C 127	4552
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1539	3325	5111	6897	784CIP2C 129	4567
	3325	5112	6898	784CIP2C 130	4568
		5113	6899	784CIP2C 132	4585
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1541	3327		6900	784CIP2C 133	4592
1541 1542	3328	5114	6900	784CIP2C 133	
1541 1542 1543	3328 3329	5114 5115	6901	784CIP2C_134	4592 4609 4616
1541 1542 1543 1544	3328 3329 3330	5114 5115 5116	6901 6902	784CIP2C_134 784CIP2C_135	4609
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1551	3337	5123	6909	784CIP2C_142	4638
1552	3338	5124	6910	784CIP2C 143	4639
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1556	3342	5128	6914	784CIP2C 147	4668
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1560	3346	5132	6918	784CIP2C 152	4682
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1569	3355	5141	6927	784CIP2C 161	4793
1570	3356	5142	6928	784CIP2C 162	4825
1571	3357	5143	6929	784CIP2C 163	4826
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1574	3360	5146	6932	784CIP2C 166	4855
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1577	3363	5149	6935	784CIP2C 169	4869
1578	3364	5150	6936	784CIP2C 170	4878
1579	3365	5151	6937	784CIP2C 171	4880
1580	3366	5152	6938	784CIP2C 172	4942
1581	3367	5153	6939	784CIP2C 173	4945
1582	3368	5154	6940	784CIP2C 174	4950
1583	3369	5155	6941	784CIP2C 175	4952
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1588	3374	5160	6946	784CIP2C 180	5599
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1591	3377	5163	6949	784CIP2C 183	5765
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1595	3381	5167	6953	784CIP2C 187	5806
1596	3382	5168	6954	784CIP2C 188	5852
1597	3383	5169	6955	784CIP2C 189	5892
1598	3384	5170	6956	784CIP2C 190	6057
1599	3385	5171	6957	784CIP2C 191	6061
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1601	3387	5173	6959	784CIP2C_192 784CIP2C_193	6160
1602	3388	5174	6960	784CIP2C 193	
1603	3389	5175	6961		6297
1604	3390	5176		784CIP2C_195	6398
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1607	3393	5178	6964	784CIP2C_198	6448
		5179	6965 6966	784CIP2C_199	6469
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1608	3394 3395	5180 5181	6967	784CIP2C_200 784CIP2C_201	6476 6561

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1613	3399	5185	6971	784CIP2C_205	6572
1614	3400	5186	6972	784CIP2C_206	6691
1615	3401	5187	6973	784CIP2C_207	6695 6746
1616	3402	5188	6974	784CIP2C_208	1
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1618	3404	5190	6976	784CIP2C_210	6943
1619	3405	5191	6977	784CIP2C_211	7110
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1621	3407	5193	6979	784CIP2C_213	7200 7212
1622	3408	5194	6980	784CIP2C_214	7212
1623	3409	5195	6981	784CIP2C_215	7249
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1625	3411	5197	6983	784CIP2C_217	7509
1626	3412	5198	6984	784CIP2C_218	7523
1627	3413	5199	6985	784CIP2C_219	7544
1628	3414	5200	6986	784CIP2C_220	7564
1629	3415	5201	6987	784CIP2C_221	7568
1630	3416	5202	6988	784CIP2C_222	7631
1631	3417	5203	6989	784CIP2C_223	7813
1632	3418	5204	6990	784CIP2C_224	7831
1633	3419	5205	6991	784CIP2C_225	
1634	3420	5206	6992	784CIP2C_226	7843
1635	3421	5207	6993	784CIP2C_227	7907
1636	3422	5208	6994	784CIP2C_228	7943
1637	3423	5209	6995	784CIP2C_229	8175
1638	3424	5210	6996	784CIP2C_230	8216
1639	3425	5211	6997	784CIP2C_231	8225
1640	3426	5212	6998	784CIP2C_232	8271
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1644	3430	5216	7002	784CIP2C_236	8953
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1646	3432	5218	7004	784CIP2C_238	9139
1647	3433	5219	7005	784CIP2C_239	9555
1648	3434	5220	7006	784CIP2C_240	9650
1649	3435	5221	7007	784CIP2C_241	9889
1650	3436	5222	7008	784CIP2C_242	9933
1651	3437	5223	7009	784CIP2C_243	9953
1652	3438	5224	7010	784CIP2C_244	9981
1653	3439	5225	7011	784C1P2D_1	746
1654	3440	5226	7012	784CIP2D_2	3558
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1656	3442	5228	7014	784CIP2D_4	3633
1657	3443	5229	7015	784CIP2D_5	3658
1658	3444	5230	7016	784CIP2D_6	3732
1659	3445	5231	7017	784CIP2D_7	4004
1660	3446	5232	7018	784CIP2D_8	4700
1661	3447	5233	7019	784CIP2D_9	4703
1662	3448	5234	7020	784CIP2D_10	4774
1663	3449	5235	7021	784CIP2D_11	4894
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1665	3451	5237	7023	784CIP2D_13	5159
1666	3452	5238	7024	784CIP2D 14	7443
1667	3453	5239	7025	784CIP2D_15	8673
	3454	5240	7026	784CIP2D_16	8679
1 7669		, , , , , , ,	1		8727
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nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
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	sequence		-	application	İ
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1673	3459	5245	7031	784CIP2D 21	8844
1674	3460	5246	7032	784CIP2D 22	8846
1675	3461	5247	7033	784CIP2D 23	8912
1676	3462	5248	7034	784CIP2D 24	8918
1677	3463	5249	7035	784CIP2D 25	8918
1678	3464	5250	7036	784CIP2D 26	8941
1679	3465	5251	7037	784CIP2D 27	8941
1680	3466	5252	7038	784CIP2D 28	8951
1681	3467	5253	7039	784CIP2D 29	8951
1682	3468	5254	7040	784CIP2D 30	9007
1683	3469	5255	7041	784CIP2D_31	9012
1684	3470	5256	7042	784CIP2D 32	9013
1685	3471	5257	7043	784CIP2D_33	9025
1686	3472	5258	7044	784CIP2D_34	9053
1687	3473	5259	7045	784CIP2D_35	9054
1688	3474	5260	7046	784CIP2D_36	9054
1689	3475	5261	7047	784CIP2D_37	9113
1690	3476	5262	7048	784CIP2D_38	9134
1691 1692	3477	5263	7049	784CIP2D_39	9152
1692	3478	5264	7050	784CIP2D_40	9152
1694	3479	5265	7051	784CIP2D_41	9211
1695	3480	5266	7052	784CIP2D_42	9223
1696	3481 3482	5267	7053	784CIP2D_43	9223
1697	3482	5268	7054	784CIP2D_44	9231
1698	3484	5269 5270	7055	784CIP2D_45	9236
1699	3485	5271	7056	784CIP2D_46	9236
1700	3486	5272	7057	784CIP2D_47	9303
1701	3487	5273	7058 7059	784CIP2D_48	9309
1702	3488	5274	7060	784CIP2D_49 784CIP2D_50	9314
1703	3489	5275	7061	784CIP2D_50	9326
1704	3490	5276	7062	784CIP2D_51	9339 9348
1705	3491	5277	7063	784CIP2D_53	9376
1706	3492	5278	7064	784CIP2D 54	9382
1707	3493	5279	7065	784CIP2D 55	9407
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1709	3495	5281	7067	784CIP2D 57	9439
1710	3496	5282	7068	784CIP2D 58	9485
1711	3497	5283	7069	784CIP2D 59	9493
1712	3498	5284	7070	784CIP2D 60	9501
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1718	3504	5290	7076	784CIP2D_66	9588
1719	3505	5291	7077	784CIP2D_67	9597
1720	3506	5292	7078	784CIP2D_68	9615
1721	3507	5293	7079	784CIP2D_69	9628
1722	3508	5294	7080	784CIP2D_70	9649
1723	3509	5295	7081	784CIP2D_71	9652
1724	3510	5296	7082	764CIP2D_72	9660
1725	3511	5297	7083	784CIP2D_73	9662
1726	3512	5298	7084	784CIP2D_74	9725
1727	3513	5299	7085	784CIP2D_75	9746
1728	3514	5300	7086	784CIP2D_76	9777
1729	3515	5301	7087	784CIP2D_77	9787
1730	3516	5302	7088	784CIP2D 78	9790
1774	(
1731	3517	5303	7089	784CIP2D_79	9842
1731 1732 1733	(

SEO ID NO:	SEO ID	SEQ ID NO:	SEQ ID	Priority	SEO ID
of full-	NO: Of	of contig	NO:	docket number	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	0040000	sequence	priority	,,
beganne	sequence	}		application	Ì
1734	3520	5306	7092	784CIP2D 82	9867
1735	3521	5307	7093	7B4CIP2D 83	10010
1736	3522	5308	7094	784CIP2D 84	10011
1737	3523	5309	7095	784CIP2D 85	10052
1738	3524	5310	7096	784CIP2D 86	10057
1739	3525	5311	7097	784CIP2D 87	10085
1740	3526	5312	7098	784CIP2D 89	10139
1741	3527	5313	7099	784CIP2D 90	10142
L.—————	3528	5314	7100	784CIP2D 92	10165
1742	3528	5314	7101	784CIP2D 93	10173
		5316	7101	784CIP2D 94	10173
1744	3530	I	1	784CIP2D_94	10273
1745	3531	5317	7103	784CIP2E 1	3121
1746	3532	5318	7104	784CIP2E_1 784CIP2E_2	3628
1747	3533	5319 5320	7105	784CIP2E_2 784CIP2E_4	3628
1748	3534	I		784CIP2E_4 784CIP2E_5	4018
1749	3535	5321	7107	784CIPZE_5	4467
1750	3536	5322	7108	784C_P2E_6	4865
1751	3537	5323	7109	784CIP2E_/ 784CIP2E 8	4916
1752	3538	5324 5325	7110	784CIP2E_8	4923
1753	3539	5325	7111	784CIP2E_9	4926
1754 1755	3540 3541	5326	7112	784CIP2E_10	4962
1756	3541	5327	7113	784CIPZE 12	4963
1757	3543	5328	7114	784CIP2E 13	4964
1758	3544	5330	7116	784CIP2E 14	4988
1759	3545	5331	7117	784CIP2B_15	5835
1760	3546	5332	7118	784CIP2E 16	7682
1761	3547	5333	7119	784CIP2E 17	7682
1762	3548	5334	7120	784CIP2E 18	7699
1763	3549	5335	7121	784CIP2E 19	7707
1764	3550	5336	7122	784CIP2E 20	7707
1765	3551	5337	7123	784CIP2E 21	7752
1766	3552	5338	7124	784CIP2E 22	8357
1767	3553	5339	7125	784CIP2E 23	9065
1768	3554	5340	7126	784CIP2E 24	9324
1769	3555	5341	7127	784CIP2F 1	2976
1770	3556	5342	7128	784CIP2F 2	3559
1771	3557	5343	7129	784CIP2F 3	4021
1772	3558	5344	7130	784CIP2F 4	4474
1773	3559	5345	7131	784CIP2F 5	4566
1774	3560	5346	7132	784CIP2F 6	4705
1775	3561	5347	71.33	784CIP2F_7	4707
1776	3562	5348	7134	784CIP2F 8	4712
1777	3563	5349	7135	784CIP2F_9	5008
1778	3564	5350	7136	784CIP2F_10	5009
1779	3565	5351	7137	784CIP2F_11	5015
1780	3566	5352	7138	784CIP2F_12	5015
1781	3567	5353	7139	784CIP2F_13	7724
1782	3568	5354	7140	784CIP2F_14	7725
1783	3569	5355	7141	784CIP2F_15	8828
1784	3570	5356	7142	784CIP2F_16	8830
1785	3571	5357	7143	784CIP2F_17	9739
1786	3572	5358	7144	784CIP2F_18	9896

TRADOCS:1416247.1(%CS701!.DOC)

TABLE 7

	BLE /		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Lcucine; M=Methionine, N=Asparagine,
1	to first	amino acid	
1	amino acid		P=Proline, Q=Glutamine, R=Arginine,
1		residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	1	\=possible nucleotide insertion)
5359	337	1131	AHLSARLSALILDEVAILPAPQNLSVLSTNMKHLLMWSPVIAPG
	1	l	ETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITA
ł	1	ì	TVPYNLRVRATLGSQTS/CLEHP/VSIPLIETQPSLPDL/RMEI
1	1		
i	1		TKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIP
ł	ł	1	VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPL
	1	}	VLALFAFVGFMLILVVVPLFVWKMGRLLQ/YLLLPRGGSSQTPW
L		ì	KITQF
5360	2	1115	PRVRSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLK
1	1	}	CVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPED
ļ	1	}	SGKYTCRVSNRAGAINATYKVDVIQRTRSKPVLTGTHPVNTTVD
	[[
I	(ļ	FGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKF
I	1	1	VVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYS
1	1		FRSAFLTVLPDPKPPGPPVASSSSATSLPWPVVIGIPAGAVFIL
1	1		GTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPSL
1	1		AALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTGHS
1			TPHTYTHPPPSCQLNSSHS
5361	3	925	HEGSISSANILLDDQFQPKLTDFAMAHFRSHLEHQSCTINMTSS
	ĺ		SSKHLWYMPEEYIRQGKLSIKTDVYSFGIVIMEVLTGCRVVLDD
1	l]	PKHIQLRDLLRELMEKRGLDSCLSFLDKKVPPCPRNFSAKLFCL
1	(AGRCAATRAKLRPSMDEVLNTLESTQASLYFAEDPPTSLKSFRC
1	l ·		PSPLFLENVPSIPVEDDESQNNNLLPSDEGLRIDRMTQKTPFEC
]			SQSEVMFLSLDKKPESKRNEEACNMPSSSCEESWFPKYIVPSQD
L			LRPYKVNIDPSSEAPGHSCRSRPVESSCSSKFSWDEYEQYKKE
5362	2	4879	SCQVEGCTRTYNSSQSIGKHMKTAHPDQYAAFKMQRKSKKGQKA
İ			NNLNTPNNGKFVYFLPSPVNSSNPFFTSQTKANGNPACSAQLQH
1	}		VSPPIFPAHLASVSTPLLSSMESVINPNITSQDKNEQGGMLCSQ
1	i '		MENLPSTALPAQMEDLTKTVLPLNIDRGSDPFLSLPAESSSIDL
{	(FPSPADSGTNSVFSQLENNTNHYSSQIEGNTNSSFLKGGNGENA
ļ	i :		VFPSQVNVANNFSSTNAQQSAPEKVKKDRGRGQTGKERKPKHNK
1			RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA
1	1 .		EIAQELLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD
1	1		PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL
1			ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH
1	[TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN
1			GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS
1			ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH
			SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT
	(VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT
1	į		
1			LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ
			NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL
1	į į		QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSZ
1	1		MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPE
1			MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT
	1		EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTEENKKESO
1 1			PALELRAETONTHSNVAVIPEKQLIEKKSPDKTESSLQVITVTS
1	j		EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKKPVSQSLEFPTRY
1 1			
1 1	l	•	SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE
; l	j		ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL
, ,			HEMTPEEIESMTASVDVGKPPCDQLECKSSFTTYLNYVVHLEAD
i i	ĺ		HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK
			HKAHLIRPRRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI
, 1			KMPKTKRKKKNNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN
] [i i		DALSECTSRFVTQYPCMIKGCTSVVTSESNIIRHYKCHKLSKAF
1 1	j		
)]]		TSQHRNLLIVFKRCCNSQVKETSEQEGAKNDVKDSDTCVSESND
1 [Į.		NSRTTATVSQKEVEKNE*DEMDELTELFITKLINEDSTSVETQA
1 (ŀ		NTSSNVSNDFQEDNLCQSERQKASNLKRVNKEKNVSQNKKRKVE
1		•	KAEPASAAELSSVRKEEETAVAIQTIEEHPASFDWSSFKPMGFE
]			VSFLKFLEESAVKQKKNTDKDHPNTGNKKGSHSNSRKNIDKTAV
L			TSGNHVCPCKESETFVQFANPSQLQCSDNVKIVLDKNLKDCTEL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	nucleotide	location	Glutamic Acid, F-Phenylalanine, G=Glycine,
NO:	· ·	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	location		L=Leucine, M=Methionine, N=Asparagine,
ì	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
\	to first	amino acid	S=Serine, T=Threonine, V=Valine,
j	amino acid	residue of	W=Tryptophan, Y=Tyrcsine, X=Unknown, *=Stop
İ	residue of	amino acid .	Walryptopnan, iarytesine, kaunkhown, wastop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
Į.	sequence		\=possible nucleotide insertion)
			VLKQLQEMKPTVSLKKLEVHSNDPDMSVMKDISIGKATGRGQY
5363	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
1 3303	1	1	PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
1		ì	RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
}	ł.	Į.	QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
	l .	1	PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
	j	1	CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
	Ę	1	CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
ŀ	1		ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
İ	İ)	1TCTSRNRCNDQDTR1SYRIGDIWSRRDRRGNDDQC1C1GHGRG
1		l .	EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
1			DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
1			GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
1	1	1	KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
ì		1	DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
1		1	DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
1		(DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
l		i	GDSWEKYVHGVRYOCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
1			TETPSOPNSHPIOWNAPOPSHISKYILEWRPKNSVGRWKEATIP
1			GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
ì	1	1	PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1	1	1	SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
1 .	j	1	VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
	1	1	POAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
ì	1	1	ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1			KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
}	ì	1	TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
l	1		TGLSPGVTYYFKVFAVSHGRESKPDIAQQITKD\DAFINDQFVN
1	i	1	ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
- (Ĭ	į	PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
1	į.	(TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
1			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
1	1		LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
1	Į.	1	HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
		Ì	PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
į		i	GRMLOSLS 1 FFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
1		· I	\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
1	1		TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
	Ì	1	SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
ł			APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
1			YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
l .	1	}	ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1	1	Į.	ISVKWLPSSSPVIGIRVIII\PANGFG\FIXIKIAGFG\TSITT EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
1		1	EGPÖRTAR I AASA I WÖMLEGESÄLTAÄTMA I MIRKET WEITHE I DA
ŀ		1	DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1	1	1	ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
1	f		QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1	1	†	SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
1	1	1	ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
1	1		DVRSYTITGLOPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
1	}	1	NT.RFLATTPNSLLVSWOPPRARITGYIIKYEKPGSPPREVVPRP
1			RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
1	1		OLUTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
l			SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
j	1		ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
ļ	1		LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
i	i	1	DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
1	1	ļ	DUSCEDELLA COMPONENTATION OF AND CONTROL CHICKETER CODE
}			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
1	1		HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
[RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
l		1	ADREDSRE
5364	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
			PRSWRROPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
			RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
L	<u> </u>		

SEQ	Predicted	Predicted end	I have and account
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	1	Glutamic Acid, F=Phenylalanine, G=Glycine,
	1	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	_mogrible musl-still delection,
 			\=possible nucleotide insertion)
1	1		QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
1	1		PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
-		l	CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
ì	1	İ	CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
J	1	į	ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
ł	1	[EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
Ì	1	i	DECLERACIONOL P PARACOLARDA AND CONTROL OF THE PROPERTY OF THE
J	1	<u>}</u>	DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
1		i	GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
· Į	1	}	DNMKWCGTTQNYDADQKFGFCPMAAHZEICTTNEGVMYRIGDQW
	ŀ		DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
1	1	İ	DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
	1		GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
1	1		TETTS OF MENT TO THE TOTAL CONTROL OF THE TOTAL CON
I			TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
l	1		GHLNSYTIKGLXPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
1	1		PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1			SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
ļ	1		VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
į)		PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
			ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1	1		KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
1	1		TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
İ			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
1	j		PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
ł	}		TELEPHONETIA TO DE CARRO
1	1		TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
1			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
i	į į		LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
}	j i		HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
1	i		PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
ľ	ł i		GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
1			\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
1			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
1	į į		SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
	į į		APAVTVRYYR I TYGETGGNS PVQEFTVPGSKSTATISGLKPGVD
1	j		YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
			TSVENT DESCRIPTION DIVISION DESCRIPTION OF THE PROPERTY OF THE
1	i i	i	ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1	l 1	i	EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
ļ	1		DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1	í	1	ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
1	1 1	j	QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
	1		SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
	1		ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIORTIKP
1	j l		DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
]	j l		NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
1	[•	RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
Ī	, ,	Ì	QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
1]	İ	SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
j .	l ·	ļ	VICOLATION DECOMMENT TO CONTRACT THE THURK HAND AND COMMENT TO CONTRACT THE THURK HAND AND COMMENT TO CONTRACT THE THURK HAND AND COMMENT TO CONTRACT THE THURK HAND AND COMMENT TO CONTRACT THE THURK HAND AND COMMENT TO CONTRACT THE THURK HAND AND COMMENT TO CONTRACT THE THURK HAND AND COMMENT TO CONTRACT THE THURK HAND AND COMMENT TO CONTRACT THE THURK HAND AND COMMENT TO CONTRACT THE THURK HAND AND COMMENT TO CONTRACT THE THURK HAND AND COMMENT THE CONTRACT THE THURK HAND AND COMMENT THE CONTRACT THE CONTR
1	[Ì	ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
1	ł ł	1	LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
]	1	DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
į		į	SSRWCHDNGVNYKIGEKWDROGENGOMMSCTCLGNGKGEFKCDP
			HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
j l		1	RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
L		1	ADREDSRE
5365	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
		_	PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
			RGDGDGLILLANT CI CTANDETCA CVCIDCA COLTECTOR
i i	1		RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
ļ <i>1</i>			QSKPGCYDNGKHYQINQQWBRTYLGNALVCTCYGGSRGFNCESK
]		j	PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
i			CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
			CKPLAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
	·		

- 550	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	(Asalanine, Cecysterne, D-Aspartic Acid, Be
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	scquence	204	\=possible nucleotide insertion)
	Bequence		ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
ŧ	1	j	EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
}	ì		DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
ì	1	į.	GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
l .	\	1	GNSNGEPCVLPFTINGRIFISCITEGRQDGnbaCGITGATEQDQ
1	Į.	ľ	KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
1	Į.]	DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
1		ł	DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
I	1	1	DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
	1	j	GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
i	1	1	TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
1	ł	4	GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
l)	}	PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
l		1	SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
1	1	1	VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
1		Į.	POAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
l	1		ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
ĺ	1		KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
1		1	TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
1			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
1			PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
ì		Į.	PERNEQPASETTVSEVALKGNQESPRATGVFTTEQFGSSTFFTN
	i		TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
	[VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
1	1 .		LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
1	1	j	HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
(Í	1	PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
1	1	1	GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
]	1	1	\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
	· ·	1	TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
1	1		SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
1	1	1	APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
1	1	1	YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
1	([ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
}	1	1	EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
1	1	1	DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
ł	1	}	ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTATPAPTDLKFT
1	1 .	i	QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1	,	1	SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
i	1	1	SVVVSGLEVATKIEVSVIADADIDISKEAQGVVIIDENVOITKA
ı		· ·	ARVIDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
j	ţ	1	DVRSYTITGLOPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
1		ļ	NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
1	1		RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
1	1	1	QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
}	j		SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
1	1	1	ALSOTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
İ			LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
.]	1	1	DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
ł			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
1			HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
1	1	1	RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
1		1	ADREDSRE
5366	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
1 2200		1	PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
1			RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
1			QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
1			PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
1			CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
1	1		CITANKCHEGGQSIKIGDINKKPHEIGGINDGVCZONGKODKI
1			CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGGGR
1	1 .		ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
l .	1		EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
		l	DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
1			GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
.NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	1	Glutamic Acid, F=Phenylalanine, G=Glycine,
l l	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
J	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	seducitie	Codon, /=possible nucleotide deletion,
<u> </u>	Taguente	 	\=possible nucleotide insertion)
ĺ	1		KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
-]	1		DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
1		'	DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
ŀ		İ	DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
ł		ł	GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
j			TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
1	1	į	GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
1		'	PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1	1		SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
}	1	j	VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
1	1	•	PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
l	1		ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1	(KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
1			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
1			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
1	1		PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
1	j l		TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
-	1		VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
			LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
1	1 1		IIADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
			PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
l l	ļ.		GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
ì	1		\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
	l i		TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLITNLTPGTEYVV SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPISLLI\SWD
1	1 1		APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
1	!		YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
1	1		ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
			EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
İ	1		DVDSIKIAWESPOGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1	1 1		ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
	[]		QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
1	1 1		SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
	i i		ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
1	1		DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
ì			NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGS?PREVVPRP
	Į į		RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
1			QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
	i i		SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGOE
1	i		ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLOFRVPGTSTSAT
1	i	i	LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNOPT
		İ	DDSCFDPYTVSHYAVGDEWERMSESGFKLLCOCLGFGSGHFRCD
	ļ		SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
, ,		į	HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGORGWRCDNCR
, 1	1		RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
5367	- 325		ADREDSRE
3307	235	3591	KKILNMLCKKNIVIEYLADILYEYLYGFCFSGIKKYLIIHVLRL
1	t		ILELWMTRLLLEKSVSLQTQYLLLIVKILSWFPGKEMRHHLOTM
1	1		EVMMRKQDS/RIVGNGSEQQLOKELADVLMDPPMDDOPGEKRIV
1 1	!	j	KRSQLDGEGDGPLSNQLSASSTINFVPLVGLOKPEMSLPVKPGO
, ,		!	GDSEASSPFTPVADEDSVVFSKLTVLGCASINIAPRSEVEALRIM !
]]		!	SILRSQCQISLDVTLSVPNVSEGIVRLLDPOTNTEIANYPIYKI
ļ [•	LFCVRGHDGTPESDCFAFTESHYNAELFRIHVFRCEIOEAVSRT
, l		Ì	LYSFATAFRRSAKQTPLSATAAPOTPDSDIFTFSVSLEIKEDDG
1 i		i	KGYFSAVPKDKDRQCFKLRQGIDKKIVIYVOOTTNKELAIERCF
[[j	GLLLSPGKDVRNSDMHLLDLESMGKSSDGKSYVITGSWNPKSPH
	1		FQVVNEETPKDKVLFMTTAVDLVITEVOEPVRFLLETKVRVCSP
1	. 1	1	NERLFWPFSKRSTTENFFLKLKQIKQRERKNNTDTLYEVVCLRS
	1	i	ESERERRKTTASPSVRLPQSGSQSSVIPSPPEDDEREDNDEPLL
	1	1	SGSGDVSKECAEKILETWGELLSKWHLNLNVRPKOLSSLVRNGV
<u> </u>			PEALRGEVWOLLAGCHNNDHLVEKYRILITKESPODSAITRDIN

			Y
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
			Codon, /=possible nucleotice deletion,
	amino acid	sequence	\=possible nucleotide insertion)
_	sequence	<u> </u>	\=possible nucleocide insertion/
			RTFPAHDYFKDTGGDGQDSLYKICKAYSVYDEEIGYCQGQSFLA
			AVLLLHMPEEQAFSVLVKIMFDYGLRELFKQNFEDLHCKFYQLE
		1	RLMQEYIPDLYNHFLDISLEAHMYASQWFLTLFTAKFPLYMVFH
	1		IIDLLLCEGISVIFNVALGLLKTSKDDLLJ.TDFEGALKFFRVQL
	l	1	PKRYRSEENAKKLMELACNMKISQKKLKKYEKEYHTMREQQAQQ
	1	1	EDPIERFERENRRLQEANMRLEQENDDLAHELVTSKIALRKDLD
		j	NAEEKADALNKELLMTKQKLIDAEEEKRRLEEESAHLKKMCRRE
	İ		LDKAESEIKKNSSIIGDYKQICSQLSERLEKQQTANKVEIEKIR
	ſ	ł	OKVDDCERCREFFNKEGRVKGISSTKEVLDEDTDEEKETLKNQL
	ţ		OKADDCEKCKELLUKEGKAKG1221 VEADED1DEFVETEVAĞD
			REMELELAQTKL\QLVEASCKIQD\LEHPF*GLPFNE\VQAA\K
	1		KTWFNRTLSSIKTATGVQGKETC
5368	573	2014	GAAAGAADPRRGSLGGRTMLDFAIFAVTFLLALVGAVLYLYPAS
	- · -		ROAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLHERYGPVVS
	j]	FWFGRRLVVSLGTVDVLKQHINPNKTLD/LF*NHAEVIIKVSIW
			WWQCE*KP\QRKKLYENGVTDSLKSNFALLLKLPEELLDKWLSY
	1		PETQH\VPLSQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHG
	ļ	į	TVWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERK
	1	Ì	
	1	ĺ	GRNFSQHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTW
		1	AIWFLTTSEEVQKKLYEEINQVFGNGPVTPEKIEQLRYCQHVLC
		1	ETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVLQDP
		i .	NTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVT
	ľ	i	TVLLSVLVKRLHLLSVEGQVIETKYELVTSSREEAWITVSKRY
5369	1	6622	PRSLCFSLWAEAAVLADGGLRRRRRLLRGTMSASFVPNGASLED
3347	†	3323	CHCNLFCLADLTGIKWKKYVWQGPTSAPILFPVTEEDPILSSFS
	Į		RCLKADVLG/VWRRDQRPERRE\L*IFWGGEDP\VLLTLFTMTY
	1	ł	QKKKMECGRMDFPMNAVLCFSKAVHNLLERCLMNRNFVRIGKWF
	1	1	VKPYEKDEKPINKSEHLSCSFTFFLHGDSNVCTSVEINQHQPVY
	1		VKPYEKWEKPINKSEHESCSFIFF ENGDSHVCISVEINGREFFI
	1		LLSEEHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK
	ì		LIGEWKQFYPISCCLKEMSEEKQEDMDWEDDSLAAVEVLVAGVR
	i		MIYPACFVLVPQSDIPTPSPVGSTHCSSSCLGVHQVPASTRDPA
	i		MSSVTLTPPTSPEEVQTVDPQSVQKWVKFSSVSDGFNSDSTSHH
	1	1	GGKIPRKLANHVVDRVWQECNMNRAQNKRKYSASSGGLCEEATA
	1	1	AKVASWDFVEATQRTNCSCLRHKNLKSRNAGQQGQAPSLGQQQQ
		1	AKVASWDFVEATQRTNCS CLRHKNLKSRNAGQQGQAPSLGQQQQ ILPKHKTNEKOEKSEKPOKRPLTPFHHRVSVSDDVGMD\ADS\A
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ
: 			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEM\NSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEM\NSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEM\NSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQMSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDLEQEFPPQPLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKODAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGFFGQESVTSVTELMVQCXK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGFFGQESVTSVTELMVQCXK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEOEIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMHGTEMANSPQ EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYROSWTVGKLELLSSGPSMPPIKEGDGSNMDQE
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPFIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFFTPRTP
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEFKIDPYAFVEGDEEF LFPDKKDRQMSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKBSKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSVYVKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPPIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEFKIDPYAFVEGDEEF LFPDKKDRQMSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKBSKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPFIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTTSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPPIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPTPRFPTPRTP RTPRTPRGAGCPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTDPDLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGGESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSTTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPFIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD IIGRNTDCGKEAEKFFEALRATSAEHVNGGLKESEKLSDDLILL
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECTYRQSWTVGKLELLSSGPSMPPIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD IIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL LODOCTNLFSPFGAADQDPFPKSGVISNWVRVEERDCCNDCYLA
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKBSKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPFIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD IIGRNTDCGKEAEKRFEALRAFSAEHVNGGLKESEKLSDDLILL LQQCTNLFSPFGAADQDPFPKSGVISNWVRVEERDCCNDCYLA LEHGROFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKBSKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPFIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNKKFGNNSGLFFEDELD IIGRNTDCGKEAEKRFEALRAFSAEHVNGGLKESEKLSDDLILL LQDQCTNLFSFFGAADQDPFPKSGVISNWVRVEERDCCNDCYLA LEHGROFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMHTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQMSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMMMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPFIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD IIGRNTDCGKEAEKRFEALFARFASEHVNGGLKESEKLSDDLILL LQDQCTNLFSPFGAADQDPFPKSGVISNWVRVEERDCCNDCYLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMILSLQPVLDDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSPPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQMSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKBSKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMMMNNKEYGSMDTTPGGTVLEGDSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPPIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSFSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD IIGRNTDCGKRAEKRFEALRATSAEHVNGGLKESEKLSDDLILL LQDQCTNLFSPFGAADQDPFPKSGVISNWVRVEERDCCNDCYLLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG TDESPEPLPITFILGYDYDYLVLSPFALPYWERLMLEPYGSQR
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKTDPYAFVEGDEEF LFPDKKDRQMSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPPIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD IIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL LQDQCTNLFSPFGAADQDPFPKSGVISNWVRVEERDCCNDCYLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMILSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG TDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR DIAYVVLCPENEALLNGAKSFFRDLTAIYESCRLGQHRPVSRLL
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMHGTEMANSPQ EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGGESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPPIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD IIGRNTDCGKRAEKFFEALRATSAEHVNGGLKESEKLSDDLILL LQDQCTNLFSPFGAADQDPFPKSGVISNWVRVEERDCCNDCYLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMILSLQPVLQDAIQKKRTVRPWGVQGPLTWQGFHKMAGRGS YG TDESPEPLPIPTFILGYDYDYLVLSPFALPYWERLMLEPYGSQR TDESPEPLPIPTFILGYDYDYLVLSFFALPYWERLMLEPYGSQR TDESPEPLPIPTFILGYDYDYLVLSFFALPYWERLMLEPYGSQR TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTDPDLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQMSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNKEYGSMDTTPGGTVLEGNSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPPIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD LIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL LQDQCTNLFSPFGAADQDPFPKSGVISNWVRVEERDCCNDCYLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQOFHKMAGRGSYG TDESPEPLPIFFILGYDYDYLVLSPFALPYWERLMLEPYGSQR DIAYVVLCPENEALLNGAKSFFRDLTAIYESCRLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKKKLYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDGVTKTPSTPQSQHFYQMPTDPDLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNKEYGSMDTTPGGTVLEGNSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPPIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD IGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL LQDQCTNLFSPFGAADQDPFPKSGVISNWVRVEERDCCNDCYLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG TDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR DIAYVVLCPENEALLNGAKSFFRDLTAIYESCKLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLTTPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKBSKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPFIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD IIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL LQDQCTNLFSTFGAADQDPFPKSGVISNWVRVEERDCCNDCYLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG DIAYVVLCPENEALINGAKSFFRDLTAIYESCRLGQHRPVSRLL TDGIMKVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQ
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKBSKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECIYRQSWTVGKLELLSSGPSMPFIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD IIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL LQDQCTNLFSTFGAADQDPFPKSGVISNWVRVEERDCCNDCYLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG DIAYVVLCPENEALINGAKSFFRDLTAIYESCRLGQHRPVSRLL TDGIMKVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQ
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMHGTEMANSPQ PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMHGTEMANSPQ EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF LFPDKKDRQNSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT PGSKRSANGSDDKASCKESKTGNLDPLSCISTADLHKMYPTPPS LEQHIMGFSPMNMNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY LPLIKLPEECTYRQSWTVGKLELLSSGPSMPPIKEGDGSNMDQE YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP RTPRTPRGAGGPASAQGSVKYENSDLYSPASTPSTCRPLNSVEP ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDCCICVCNMNIK GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD IGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL LQDQCTNLFSPFGAADQDPFPKSGVISNWVRVEERDCCNDCYLA LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG TDESPEPLPIPTLLGYDYDYLVLSPFALPYWERLMLEPYGSQR DIAYVVLCPENEALLNGAKSFFRDLTAIYESCRLGQHRPVSRLL TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nuclcotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	
1	residue of	1	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	<u> </u>	\=possible nucleotide insertion)
		1	TLPPHIKSTVSVQIIPCQYLLQPVKHEDREIYPQHLKSLAFSAF
			TQCRRPLPTSTNVKTLTGFGPGLAMETALRSPDRPECIRLYAPP
ĺ	i	1	FILAPVKDKQTELGETFGEAGQKYNVLFVGYCLSHDQRWILASC
1	•	} "	TDLYGELLETCIINIDVPNRARRKKSSARKFGLQKLWEWCLGLV
		1	QMSSLPWRVVIGRLGRIGHGELKDWSCLLSRRNLQSLSKRLKDM
j			CRMCGISAADSPSILSACLVAMEPQGSFVIMPDSVSTGSVFGRS
1	İ	•	TTLNMQTSQLNTPQDTSCTHILVFPTSASVQVASATYTTENLDL
1		}	AFNPNNDGADGMGIFDLLDTGDDLDPDIINILPASPTGSPVHSP
1			GSHYPHGGDAGKGQSTDRLLSTEPHEEVPNILQQPLALGYFVST
İ	1		
1	ĺ		AKAGPLPDWFWSACPQAQYQCPLFLKASLHLHVPSVQSDELLHS
1	1	i	KHSHPLDSNQTSDVLRFVLEQYNALSWLTCDPATQDRRSCLPIH
5370	1006		FVVLNQLYNFIMNML
33/0	1226	716	RWSRKLELRRAAQATESRPPQSQEMHPPTGKEVHALKRLRDSAN
	1	1	ANDVETVQQLLEDGADPCAADDKGRTALHFASCNGNDQIVQLLL
İ	(1	DHGADPNQRDGLGNTPLHLAACTNHVPVITTLLRGGARVDALDR
	1		AGRTPLHLAKSKLNILQEGHAQCLKAVR/HGGEADHPYAEGVSG
			APRAT*AARCSGVFPSPSRWLGSAPWSRSSCTIWSLPLHEAKCR
1	ĺ	[AVRPLSSAAQGSAPSSSSCCTVSTSLALAESLSLFRACTSLPVG
L	<u> </u>	1	GCISWL
5371	1331	167	IAAMLWKLLLRSQSCRLCSFRKMRSPPKYRPFLACFTYTTDKQS
1	[SKENTRTVEKLYKCSVDIRKIRR*KDGYF*RMKPMLKKLRI/F
1	[LQELGADETAVASILERCPEAIVCSPTAVNTQRKLWQLVCKNEE
{	((ELIKLIEQFPESFFTIKDQENQKLNVQFFQELGLKNVVISRLLT
[ĺ		AAPNVFHNPVEKNKQMVRILQESYLDVGGSEANMKVWLLKLLSQ
1	ļ		NPFILLNSPTAIKETLEFLQEQGFTSFEILQLLSKLKGFLFQLC
	1	{	PRSIQNSISFSKNAFKCTDHDLKQLVLKCPALLYYSVPVLEERM
Ì		[QGLLREGISIAQIRETPMVLELTPQIVQYRIRKLNSSGYRIKDG
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5372	51	857	HLANLNGSKKEFEANFGKIQAKKVRPLFNPVAPLNVEE
33.2	j 21	05/	SPGAQFLWAAPDMPDPLFSAVQGKDEILHKALCFCPWLGKGGME
Ì	'		PLRLLILLFVTELSGAHNTTVFQGVAGQSLQVSCPYDSMKHWGR
il i			RKAWCRQLGEKGPCQRVVSTHNLWLLSFLRRWNGSTAITDDTLG
} .			GTLTITLRNLQPHDAGLYQCQSLHGSEADTLRKVLVEVLADPLD
			HRDAGDLWFPG\DLRASRMPMWSTASPGASWKEKSPSHPLPSFS
1 1		ŀ	SWPASFSSRF*QPAPSGLQPGMDRSQGHIHPVNWTVAMTQGISS
			KLCQG
5373	2814	346	VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY
1			QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG
			TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE
1			ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD
1			KTSTTGSILNLNLDRSKAEMDLKBLSESVOQQSTPVPLISPKRO
j į			IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS
}			DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP
1			TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDFSGKAKPS
į i	į		PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE
1			GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAO
į į			TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP
1			
į į	' l		AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTQSSPLVTSSGSM
			STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI
, 1			YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQQEL\SBMKHN
] [(LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAVDETKKKQWC
į ;	į.		AMPKKEAI FYCCWNTSYCDYPCQ\QAHWPEH\MKSCTQSATAPQ
j)			\QEADAE\VNTETLNKSSQGSSSSTQSAPSETASA\SKEKETSA
[]	l		EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS
<u> </u>			DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK
5374	2814	346	VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPFRTPYTPNSQY
1	ĺ		QMLLDPTNPSAGTAKIDKQEKVKLNPDMTASPKILMSKPVLSGG
			TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASE
		{	ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAFITTKTD
] [ĺ	KTSTTGSILNLNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ
1 1			IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS
	1	5	
1 1	i	j	DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
_	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
			Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDFSGKAKPS
	1	Ì	PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE
	i	j	PHPIKDKLKGKDETDSPTVALGDDSDSE (NEDVIDLGEDRSGKE
	Į.	1	GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ
l	1	i	TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP
	Ì	1	AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTQSSPLVTSSGSM
	1	1	STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI
	Į.	1	YNDLSKN\TTWKAQLAEDSQGLRIEIEKLQWLHQQEL\SEMKHN
İ		ì	LELTMAEMROSWEOERDRLIAEVKKQLELEKQQAVDETKKKQWC
ĺ		1	ANFKKEAIFYCCWNTSYCDYPCQ\QAHWPEH\MKSCTQSATAPQ
	Ì	ì	\QEADAE\VNTETLNKSSQGSSSSTQSAPSETASA\SKEKETSA
Į .	l .	1	EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS
Ì	1		DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK
 _	l	<u> </u>	DEKRGS TRESHIN TPS TOHGRESHIP GRESKAGT FE GOTSK HIFLAEEEPMLERRCRGPLAMGPAQPRLLSGPSQESPQTLGKES
5375	2907	1116	HIFLAREEPMLERKCKGPLANGPAQPKLLDGGGGGAY I DOKES
1	1		RGLRQQGTSVA\QSGAQAPGRAHRCAHCRRHFPGWVA\LWLHTR
1	1	1	RCQA/RGLPLPCPECGRRFRHAPFLALHRQVHAAATPDWGFACH
1	1	į.	LCGQSFRGWVALVLHLRAHSAAKAGPFACPKMARDAFWRRKAAS
1	1		SSILRRCHPSRPRGPRPFICGNCGRSILPTWDQ/LKVAHKRVHV
Į	1	i	SRRP*ERGPPAKVFWGPRPRGPPTGDTPPGPGGDAVDRPF\QCA
]	ì	1	CCGKRFRHK\PNLIRSHAACISGERPHQ/CSRECG\KRFTNKPY
ļ		Į.	LTS\HRRITHTAROPYPCKECGRRFRHKPNLLSHSKIHKRSEGS
1	1	1	AOAAPGPGSPOLPAGPQESAAEPTPAVPLKPAQEPPPGAPPEHP
ł	j	1	QDP1EAPPSLYSCDDCGRSFRLERFLRAHQRQHTGERPFTCAEC
1	l	1	GKNFGKKTHLVAHSRVHSGERPFRLARKCGRRFLPRASQSGGRN
Į	1	1	SAEPNAPRFGPFVCPDCGKAFRHKPYLAAHRPIATPAEKPYVCP
}	1		DCRKAFSQKSNL\VSHRRIHTGERPYACPDCDRSFSQKSNLITH
	ł		RKSHIRDGAFCCAICGQTFDDEERLLAHQKKHDV
			VSTFSLCLWPAGGGGRGVSNMAQSKRHVYSRTPSGSRMSAEAS
5376	4504	591	ARPLRVGSRVEVIGKGHRGTVAYVGATLFATGKNVGVILDEAKG
1		ŀ	KNDGTVQGRKYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDS
1			KNDGTVQGRKYFTCDEGAGIFVAQQQIQVABDGADIIGIBIIDO
1		ł .	SASKVLKREGTDTTAKTSKLRGLKPKKAPTARKTTTRRPKPTRP
Į.	- {	1	ASTGVAGASSSLGPSGSASAGELSSSEPSTPAQTPLAAPIIPTP
1		{	VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA
}	1	i	KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKEAKEAL
1	l l	1	EAKERYMEEMADTADAIEMATLDKEMAEERAESLQQEVEALKER
i .	ì	1	VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV
1	1	1	RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ
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	Į.	1	DIEAMNEMNDBLOENARETELELREQLDMAGARVREAQKRVEAA
1			DLEAMNEMNDBLOENARETELELREQLDMAGARVREAQKRVEAA
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA OFTVADYOOTIKKYROLTAHLODVNRELTNQQEASVERQQQPPP
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SELREGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEOLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKYGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYOHIYSIHLAEOPEDCTMOLADHIKFTQSALDCMSVEVG
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG BLEAFIOGSGRATDIALLLRDLETSCS\DIRQFCKKIRRRMPGT
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPOVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLIMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRNMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI ADLAENEGILVAALEELAFKASEOIYGTPSSSPYECLRQSCNIL
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTINQQEASVERQQQPPP ETFDFKIKFAEKKHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL TSTMNK\LVTAMOEGBYDAERPPSKPPP\VELRAAALRAEITDA
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAFGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGBYDAERPPSKPPP\VELRAAALRAEITDA
			DLEAMNEMNDBLQENARETELELREQLDMAGARVERAÇKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK/LVTAMQEGBYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVOTRLEETQALLRKKEKEFEETMDALQADIDQL
			DLEAMNEMNDBLQENARETELELREQLDMAGARVERAÇKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKORLNSOSKRTIEGLRGPPPSGIATLVSGIAGEEQQR
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALBELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGBYDAERPPSKPPP\VELRAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGOAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALBELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGBYDAERPPSKPPP\VELRAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGOAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGBYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAOMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RFGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRRMPGT DAPGIPAALAPGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTINQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAITGQAPGSVPGGPGLVKDSPLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG
			DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTANQEGBYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGORHRLVLTOEOLHOLHSRLIS
5377	762	1106	DLEAMNEMNDBLQENARETELELREQLDMAGARVERAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAFGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAQQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLAQSCNIL ISTMNK\LVTAMQEGBYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKBLKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS DVPCKRVLPAEAOEKGOLTLSCGESGEEG\F*YHEVRQAEGES*
5377	762	1106	DLEAMNEMNDBLQENARETELELRBQLDMAGARVERAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAFGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGBYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTX
5377	762	1106	DLEAMNEMNDBLQENARETELELREQLDMAGARVERAQKRVERA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSORPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTX SS*WPGYDGWWGGOVIFIFRGMRWEEQP
5377	762 2009	1106	DLEAMNEMNDBLQENARETELELREQLDMAGARVREAQKRVEAA QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRRMPGT DAPGIPAALAPGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALBELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGBYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGFGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS DVPCKRVLPPAEAQEKGGLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTX SS*WPGYDGWWGQQYIFIFRGMRWEEQP OBSGTTLRPLPDLPOLKRREATSRNRALKPRGRLVLMTSCLPAL
			DLEAMNEMNDBLQENARETELELREQLDMAGARVERAQKRVERA QETVADYQQTIKKYRQLTAHLQDVNRELITNQQEASVERQQQPPP ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT KAIKYYQHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG RLRAFLQGGQEATDIALLLRDLETSCS\DIRQFCKKIRRMPGT DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL ISTMNK\LVTAMQEGEYDAERPPSKPPP\VELRAAALRAEITDA EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL KDEVLKETVSORPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG KVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES* /WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTX SS*WPGYDGWWGGOVIFIFRGMRWEEQP

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
I	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
1	l		SFSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD
İ	1		VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH
]	ł	}	KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP
	5	ĺ,	QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV
1		ľ	EELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
1	İ	1	HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
J]	ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
1	[PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ
5379	2009	CCA	VNPIFSEAC
1 .	1	664	QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL
1	1		RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSRSEVDLTR
1		1	SFSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH
1		1	VPQMGCVFITTALFILANKMIBLSVILIPASILVAEKFSLFTAVH KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP
1	ļ	1	QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV
1			EELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
I			HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
			ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
			PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ
			VNPIFSEAC
5380	2	2050	PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
(SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME
1			SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSOARPHL
1			SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPOSSP
1			RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA
1			YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIOP
1			RGPI/EQVYQEIA/ILKKLDHPNVV/KLVEVL/DDPNEDHLYMV
)			F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII
1			H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
1			FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM
1 1			CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI
1			KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV
			ILVKTMIRKRSFGNPFEGSRRBERSLSAPGNLLTKKPTRECESL
1 1			SELKT*KISPLPACCKVT*EPPHPSGCRPSCWQPPFLHTHSQPR *PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL
1 .]	ļ		PDLVGAPGSHFCFLNIALLRYNSHTM
5381	2	2050	PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
1	ļ		SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME
1 .1			SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL
1 1			SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP
1	j		RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA
1 1			YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP
1 1			RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV
1 1			F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYOKII
, ,			H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
j 1	•		FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM
ļ 1	İ		CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI
1 1	j		KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV
]]			ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL
] [ſ		SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR
(!	į.		*PEPPRIDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWI.
5382	1525		PDLVGAPGSHFCFLNIALLRYNSHTM.
3384	1536	203	GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS
İ	İ		VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE
1	i	Ì	LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG
1	ļ		YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD
			DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH
)			RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL
			KKYTKFLFVRDPFVRLISAFRSKFBLENEEF/*PQVRRAHAAAV
	j	j	ROPHOPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH
		<u></u> <u>_</u>	WRQVYRLCHPCQIDYDFVGKLETLDEDAAQLLQLLQVDLAAPLP

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	
ar	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalarine, G=Glycine,
1 1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ j	amino acid	sequence	Codon, /=possible nucleotide deletion,
1		sequence	\=possible nucleotide insertion)
L	sequence		PELPGTGPPSSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKP
1 1	1	}	
	1		ENLLRD
5383	45	5250	VERLLGCRNSKRTWRMLISKNMPWRRLQGISFGMYSAEELKKLS
			VKSITNPRYLDSLGNPSANGLYDLALGPADSKEVCSTCVQDFSN
] .		Į	CSGHLGHIELPLTVYNPLLFDKLYLLLRGSCLNCHMLTCPRAVI
) j	J		HLLLCQLRVLEVGALQAVYELERILSRFLEENADPSASEIREEL
	i	I	EQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHMNAKRC
]	}	l.	PHCKTGRSVVRKEHNSKLTITFPAMVHRTAGQKDSEPLGIEEAQ
1	Į.		
1 1	-	1	IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSGMDDDGMESRFN
[1		PSVFFLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVMKDVVL
1		ļ	IRKLLALMAQEQKLPEEVATPTTDEEKDSLIAIDRSPLSTLPGQ
1	(1	SLIDKLYNIWIRLQSHVNIVFDSEMDKLMMDKYPGIRQILEKKE
1 1	1	1	GLFRKHMMGKRVDYAARSVICPDMYINTNEIGIPMVFATKLTYP
Į į	}	1	QPVTPWNVQELRQAVINGPNVHPGASMVINEDGSRTALSAVDMT
1	1		OREAVAKOLLTPATGAPKPQGTKIVCRHVKNGDILLLNRQPTLH
1	ì	,	RPSIQAHRARILPEEKVLRLHYANCKAYNADFDGDEMNAHFPQS
j .		[
[l		ELGRAEAYVLACTDQQYLVPKDGQPLAGLIQDHMVSGASMTTRG
1	1	1	CFFTREHYMELVYRGLTDKVGRVKLLSPSILKPFPLWTGKQVVS
	1		TLLINIIPEDHIPLNLSGKAKITGKAWVKETPRSVPGFNPDSMC
Í	Į.	1	ESQVIIREGELLCGVLDKAHYGSSAYGLVHCCYEIYGGETSGKV
	İ		LTCLARLFTAYLQLYRGFTLGVEDILVKPKADVKRQRIIEESTH
1	1	ł	CGPOAVRAALNLPEAASYDEVRGKWQDAHLGKDQRDFNMIDLKF
	\$		KEEVNHYSNEINKACMPFGLHRQFPENTLQLMVQSGAKGSTVNT
1		}	MOISCHLGOIELEGRSTPLMASGKSLPCFEPYEFTPRAGGFVTG
1	ł		RFLTGIKPPEFFFHCMAGREGLVDTAVKTSRSGYLQRCIIKHLE
1	1	ļ	
ĺ			GLVVQYDLTVRDSDGSVVQFLYGEDGLDIPKTQFLQPKQFPFLA
		Ï	SNYEVIMKSQHLHEVLSRADPKKALHHFRAIKKWQSKHPNTLLR
	1	1	RGAFLSYSQKIQEAVKALKLESENRNGR/RPWDS/G/RMLRMWY
1	l	1	ELDEESRRKYQKKAAACPDPSLSVWRPDIYPASVSETFETKVDD
1	{	t	YSOEWAAQTEKSYEKSELSLDRLRTLLQL\KWQRSLCEPGEAVG
J		1	LLAAQSIGEPSTQMTLNTFHFAGRGEMNVTLGIPRLREILMVAS
	1	ļ	ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ
1	i	Ì	ESFCMEEKONKFQVYQLRFQFLPHAYYQQEKCLRPEDILRFMET
}		1	•
1	}	} '	RFFKLLMESIKKKNNKASAFRNVNTRRATQRDLDNAGELGRSRG
{	· ·	ţ	EQEGDEEEEGHIVDAEAEEGDADASDAKRKEKQEEEVDYESEEE
1	l		EEREGEENDDEDMQEERNPHREGARKTQEQDEEVGL/GH*GGPV
1	1 .	1	PSRPPDAAPETHPQPGAPGA\EAMERRVQAVREIHPFIDDYQYD
		1	TEESLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC
}		1	LINETTNNKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH
1		1	AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCF
1		1	EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDBLR
		1	
L	<u> </u>		SPSACLVVGKVVRGGTGLFELKQPLR
5384	196	886	QSCGQRLPTVL*L*GPPGSCPCILSLF\PGRPHALPEIRPYINI
1	1	1	TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG
1	1	1	APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT
ŀ	1	j	GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS
1	}	1	ERSIMOSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF
1	1	1	SGHLIKAEDD
	 	 	
5385	326	799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM
1	1	1	SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A
1	1		VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ
I	1	1	SDGERKAYVRLAPDYDALVVATKIGIT
		799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM
5386	326		
5386	326	1	
5386	326	133	SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A
5386	326	133	SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ
5386	326	133	SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT
5386	326	2117	SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ
			SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT
			SPTFRRPKTL*LRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY
			SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL
			SPTFRRPKTL*LRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ SDGERKAYVRLAPDYDALVVATKIGIT FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY

SEQ	Predicted	Predicted end	I min and a second
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
I	amino acid	residue of	S=Serine, T=Threonine, V=Valine
- !	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
i		Ì	SVWETRIKLLCCCIGKDDHTRVAFSSTAFLFSTYFSDTDLVPSD
1	1	}	IAAGLALLHQQQDNIRNNQEPAOVVCHAPGSSOEADIDAELKNC
1			HHYMQFAAAAYGWPLYIYRNPLTGLCRIGGDCCRSKNPQTMT/M
j	}		VGGDQLQL/CTSAPILHTHRAAVQGLHPRQLPWTRFTELPFLVA
1			LDHRKESVVVAVRGTMSLQDVLTDLSAESEVLDVECEVQDRLAH
			KGISQAARYVYQRLINDGILSQAFSIAPBYRLVIVGHSLGGGAA
1 .	ì		ALLATMVRAAYPQVRCYAFSPPRGLWSKALQBYSQSFIVSLVLG KDVIPRLSVTNLEDLKRRILRVVAHCNKPKYKILLHGLWYELFG
ļ		· ·	GNPNNLPTELDGGDQEVLTQPLLGEQSLLTRWSPAYSFSSDSPL
j	j		DSSPKYPPLYPPGRIIHLQEEGASGRFGCCSAAHYSAKWSHEAE
l l			FSKILIGPKMLTDHMPDILMRALDSVVSDRAACVSCPAQGVSSV
		1	DVA
5388	1569	753	TADGGAGGGRRQAGVRRHYLYPFTGGYRRRAACQAERPAARS
1		1	KDTDLAAYQKGNLGVQLRNMAQETNHSOVPMLCSTGCGFYGNPP
1		1	TNGMCSVCYKEHLQRQNSSNGRISPPVOCTDGSVPEAOSALDST
ļ	1	}	SSSMQPSPVSNQSLLSESVASSOLDSTSVDKAVPETEDVOASVS
	1		DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
			TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHOOLLEYK
5389	1569	753	ILEHLQTKN
	1303	/53	TADGGAGGGGRQAGVRRHYLYPFTGGYRRRAACQAERPAARS
1			KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
1	į		TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST
l l			SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
			TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
			ILEHLQTKN
5390	217	1332	EDPRKLMEDKMWSECEGPEMSLVCLTDFQAHAREQLSKSTRDFI
			EGGADDSITRDDNIAAFKRIRLRPRYLRDVSEVDTRTTIOGERI
1			SAPICIAPTGPHCLVWPDGEMSTARAAOAA\GICYITSTFASCS
}			LEDIVIAAPEGLRWFQLYVHPDLOLNKOLIORVESLGFKALVIT
			LDTPVCGNRRHDIRNQLRRNLTLTDLOSPKKGNAIPYFOMTETS
1			TSLCWNDLSWFQSITRLPIILKGILTKEDAELAVKHNVQGIIVS
1		•	NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK
1			ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEFHTSMA\ LTGCRSVAEINRNLVQFSRL
5391	1	1292	VKKAAGRSRGPPTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF
1 1			QPPVCNKLMHQEQLKVMFVGGPNTRKDYHIEEGEEVFYQLEGDM
	•		VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER
1 1	ļ		RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQEFFS
1.	1	• .	SEQYRTGKPIPDQLLKEPPFPLSTRSIMEPMSLDAWLDSHHPEL.
	1	•	QAGTPLSLFGDTYETQVIAYGOGSSEGLRONVDVNI.WOLEGGGV
	}		VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTOGSVALSVT\O
]]	ļ		DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV
] [1	i	YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWOTOPTAI.
5392	1	1623	PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS
	-	1043	IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR
			CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAAEWIRKGS
1 1			FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFMT RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA
]		Ì	GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD
[[YVAYVAKDPINGRACHILECCEGL\AQSIISTVGQAFELRFKQY
1	1		LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL
[]	1		GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP
1	1		PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR
) i	j		PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ
1	ſ	i	LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGOYVLTGMH
j i	1		AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE
F303			SELHLRGVVSREP
5393	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
<u> </u>			PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
ю:	nucleotide	location corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	location	to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	to first	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of		Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence	<u> </u>	\NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV
)		LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK
	1	j	SOKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
	1		OVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
	}		STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
	}		RAPTDDDKNIYLTLPPNDHVNSNN
			GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
5394	2	982	PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG
	}	ł	\NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV
	Ì	l .	LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK
			SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
	}	i .	QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
	1	1	QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVABIICKKKKISAV
	(STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
	1		RAPTDDDKNIYLTLPPNDHVNSNN
5395	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLS_QASDFDGAS
			SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
			KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
	1		RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
	1]	RKTLPLTTAPEAGEVTPSDSGGQEDSPARGES V ROST DISEDIO
	1	1	SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
	}	i	PRSPAEPNDIPIAKGTYTFDIDAWDDPNFNFSSISKAQUSTKO
			POOSYNFDPDTCDESVDPFKTSSK1FSSF3KBFASTEITADAMB ANGVDGDGLNKPAKKKKTPLXTDTFRVKKSPKRSPLSDPPSQDP
	1	1	ANGVDGDGLNKPAKKKTPLXTDTFKVKKSPAKSFBSDFFSQDF TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
			YPOPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD
	1		DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
			DDAPKKQALYLMFDTSQESPVKSSPVKMSESPTFCSGSSFBBTS ALVNTAAKNQHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP
			ALVNTAAKNOHPVPRGLAPNOESHLQVPEASSQREBEAMAGTE SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
}	1		PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
	ì		PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
(i		PDLDSALQIARAETTIKEREVSEWRDKTEESKKEVILLEKKTYND YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
	1		\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
ļ		1	YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
1			CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
			RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
5396	3135	531	SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
1	1		SSGNPEAVALAPDAYSTGSSSASSTHARTARAFTOLINGGETTE KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
	1	1	KPTETPPVKETQQEPDEESLVPSGENIASEIXIESAKIESISIA LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
	İ	ì	LIEETPLEPAAGPKAACPLDSESVEGVVPFASGGGKVQUSTIVO
	1	1	RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
	1		SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
{	1	1	PROPAREDIDIANGTYTED DKWDDDWANDESSISKWCSERD PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
	1	į.	POOSYNFDPDTCDESVDPERTSSKTPSSPSRSEASFELFASAME
	1	1	TOPOCO IN THE PROPERTY AND MEDITAL ACTION OF THE PROPERTY AND THE PROPERTY
·	1	}	ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
1		}	ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
i			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD VPOPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD
1			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKOALYLMFDTSOESPVKSSPVRMSESPTPCSGSSFEETE
1			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE ALUNTAAKNOHPVPRGLAPNOESHLQVPEKSSQKELEAMGLGTP
		,	ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFRETE ALVNTAAKNQHPVPRGLAFNQESHLQVPEKSSQKELEAMGLGTP SPAIRITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFRETE ALVNTAAKNQHPVPRGLAFNQESHLQVPEKSSQKELEAMGLGTP SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN DDLEAOKLOPEAAHPTDYSISKTALYSRIGTAEVEKPAGLLFQQ
			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE ALVNTAAKNQHPVPRGLAFNQESHLQVPEKSSQKELEAMGLGTP SEAIBITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ DDLDSALOIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE ALVNTAAKNQHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP SEAIBITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLABKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE ALVNTAAKNQHPVPRGLAFNQESHLQVPEKSSQKELEAMGLGTP SEAIBITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLABKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFBETE ALVNTAAKNQHPVPRGLAFNQESHLQVPEKSSQKELEAMGLGTP SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKERBVSEWKDKYEESREVMEMKIVAE YEKTIAQMIEDEQREKSVS\NQTVQQLVLEKEQA\LADLNSVEK \SLADLFRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR YOALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
			ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFRETE ALVNTAAKNQHPVPRGLAFNQESHLQVPEKSSQKELEAMGLGTP SEAIBITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK \SLADLFRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS CPV\DALKRTLEOKNKEIEBLTKICDELIAKMGKS
5397	3135	531	ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFRETE ALVNTAAKNQHPVPRGLAFNQESHLQVPEKSSQKELEAMGLGTP SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLABKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5397	3135	531	ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFRETE ALVNTAAKNQHPVPRGLAFNQESHLQVPEKSSQKELEAMGLGTP SEAIBITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR YQALKVHA\EEKLDRANAE IAQVRGKAQQEQAAHQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
5397	3135	531	ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFRETE ALVNTAAKNQHPVPRGLAFNQESHLQVPEKSSQKELEAMGLGTP SEAIBITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLABKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS CRV\DALERTLEQKNKEIELTKICDELIAKMGKS SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
5397	3135	531	ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFRETE ALVNTAAKNQHPVPRGLAFNQESHLQVPEKSSQKELEAMGLGTP SEAIBITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
5397	3135	531	ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFBETE ALVNTAAKNQHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKERBVSEWKDKYEESREVMEMRKIVAE YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK \SLADLFRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVONSPPVG
5397	3135	531	ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFRETE ALVNTAAKNQHPVPRGLAFNQESHLQVPEKSSQKELEAMGLGTP SEAIBITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK \SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA

SEQ	Predicted	Predicted end	Desire
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	1	\=possible nucleotide insertion)
- 1			PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
1		}	ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
			TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
		ł	YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD
- 1			DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
1			ALVNTAAKNQHPVPRGLAPNQESHLOVPEKSSOKELEAMGLGTD
ľ			SEATETTAPEGSFASADALLSRLAHPVSLCGALDVI.FDDI.AFZN
}	1		PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLIFOO
	ì		PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMDKIVAR
f			YEKTIAQMIEDEQREKSVS\HOTVOOLVLEKEOA\LADLNSVEK
1			\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAORVLGBVKKEEOB
1			YQALKVHA\EEKLDRANAE\IAOVRGKAOOEOAAHOAST.AERCC
5398	56	5426	CRV\DALERTLEQKNKEIBELTKICDELIAKMGKS
		3420	SGEVCRMESNFNQEGVPRPSYVFSADPIARPSEINFDGIKLDLS
	}		HEFSLVAPNTEANSFESKDYLQVCLRIRPFTQSEKELESEGCVH
			ILDSQTVVLKEPQCILGRLSEKSSG\QM\AQKFSFPPGFLGPAT
			TQKEFFQGCIMHP\VKDLLKGQSRLIFTYGLTNSGKTYTFQGTE ENIRILPRTLNVLFDSLQERLYTKMNLKPHRSRBYLRLSSEQEK
1 1			EEIASKSALLRQIKEVTVHNDSDDTLYGSLTNSLNISEFEESIK
			DYEQANLNMANSIKFSVWVSFFEIYNEYIYDLFVPVSSKFQKRK
i 1			MLRLSQDVKGYSFIKDLQWIQVSDSKBAYRLLKLGIKHQSVAFT
1 1			KLNNASSRSHSIPTVKILOIEDSEMSRVIRVSFISLCDLAGER
))			TMKTQNEGERLRETGNINTSLLTLGKCINVLKNSEKSKEOOUVD
1		(FRESKLTHYF/QSFFNGKGKICMIVNISOCYLAYDETINGTURE
1 1			ALAQKVCVPDTLNSSQEKLFGPVKSSODVSI.DSNSNSKTI.MIVD
1 1			ATISWENSLEDLMEDEDLVEELENAEETED/VGETKLIDEDLDV
1			TLEENKAFISHEEKRKLLDLIEDLKKKLINEKKEKITLEEKIDD
1 (Ì	i	EVTQEFTQYWAQREADFKETLLQEREILEENAERRLAIFKDLVG
1 1	1		KCDTREEAAKDICATKVETEEATACLELKFNQIKAELAKTKGEL
1 1	ì		IKTKEELKKRENESDSLIQELETSNKKIITQNQRIKELINIIDQ
1 1			KEDTINEFQNLKSHMENTFKCNDKADTSSLIINNKLICNETVEV PKDSKSKICSERKRVNENELQQDEPPAKKGSIHVSSAITEDQKK
1 1	1		SEEVRPNIAE IEDIRVLQENNEGLRAFILTIENELKNEKEEKAE
]]			LNKQIVHFQQELSLSEKKNLTLSKEVQQIQSNYDIAIAELHVQK
1 1		ĺ	SKNQEQEEKIMKLSNEIETATRSITNNVSQIKLMHTKIDELRTL
1 1			DSVSQISNIDLLNLRDLSNGSEEDNLPNTQLDLLGNDYLVSKQV
1 1		1	KEIKIQEPNRENSFHSSIEAIWEECKEIVKASSKKSUOTURI RO
			QIEKLQAEVKGYKDENNRLKEKEHKNODDIJLKEKETI. TOOLKEE
1 1	İ	Ĭ	LQEKNVTLDVQIQHVVEGKRALSELTOGVTCVKAKIKPI.PTTT P
1 1	l l	i	TQKVERSHSAKLEODILEKESIILKI.ERNI.KEEOEUI.ODGUMM
]		I.	KULNVKELKLKEEITQLTNNLODMKHIJOLKEEEEETNDOPTDV
1 1	[1	LKEELSASSARTQN\LNADLORKEEDYADI.KEKT.TDAKKOTKOU
1 1		1	QKEVSVMRDEDKLLRIKINELEKKKNQCSQELDMKQR\TIQQLK
1 1	j		EQLINQKVEEAIQQYERACKDLNVKEKIIEDMRMTLBEQEQTQV
1		[.	EQDQVL\EAKLEEVERLATELDRWRVKCNDLETKNNQRSNKEHE
1 1		1	NNTDVLGKLTNLQDELQESEQKYNADRKKWLEEKMMLITQAKEA
1 1			ENIRNKEMKKYAEDRERFFKQQNEMEILTAQLTEKDSDLQKWRE ERDQLVAALEIQLKALISSNVQKDNEIEQLKRIISETSKIETQI
1		i i	MDIKPKRISSADPDKLQTEPLSTSFEISRNKIEDGSVVLDSCEV
1	[1:	STENDQSTRFPKPELEIQFTPLQPNKMAVKHPGCTTPVTVKIPK
!!	1	! ;	ARKRKSNEMEEDLVKCENKKNATPRTNLKFPISDDRNSSVKKEQ
1 1		1	KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS
	1	[]	PSILQSKAKKIIETMSSSKLSNVBASKENVSQPKRAKRKLYTSE
5399			ISSPIDISGQVILMDQKMKESDHOIIKRRLRTKTAK
3399	705	230 (GPRMAKFLSQDQINEYKECFSLYDKOORGKIKATDIMVAMPCIC
1	1	#	ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMOTKOEDDKKE
		1 -	LLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLERE
5400	931	`	\ADIEPNGKVKYDEFIHKITSYLDGTY
_ }		248	SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQXVK
1		∤ ⊊	QASMEDIPGRGHKYRLKFAVEEIIOKOVKVNCTAEVLYPSTGOE
	<u></u>	L	TAPEVNFTFEGETGKNPDBEDNTFYQRLKSMKEPLEAQNI\PDN

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	Amalanine C=Cvsteine, D=Aspartic Acid, E=
ID	beginning nucleotide	location	Glutamic Acid. F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	In-Leucine Mamethionine, NaAsparagine,
		amino acid	p-proline, O=Glutamine, R=Arginine,
	to first amino acid	residue of	c-cerine TaThreonine, V=Valine,
	residue of	amino acid	N-Trantophan Y=Tyrosine X=Unknown, *=Stop
	I		Codon /=possible nucleotide deletion,
	amino acid	sequence	_possible nucleotide insertion)
	sequence		FGMVSDEMTLVLHLAWVACGYIIWONSTEDTWYKMVKIQTVKQV
			QRNDDFIELDYTILLHNIASQEIIPWQMQVLWHPQYGTKVKHNS
		1	RLPKEVQLE
	l		TGWSYGPTTSLAFLAPRDFPFPPKLLIHPQAVVRLSCGAGSMGS
5401	3	1360	QAAAEWRNWASWEGSSSLSGCSMGCFKDDRIVFWTWMFSTYFME
		1	KWAPRODDMLFYVRRKLAYSGSESGADGRKAAEPEVEVEVYRRD
		1	SKKLPGLGDPDIDWEESVCLNLILQKLDYMVTCAVCTRADGGDI
		İ	HIHKKKSQQVFASPSKHPMDSKGEESKISYPNIFFMIDSF\EE\
	i .		VFSDMTVGKGEMVCVELVASDKTNTFQGVIFQGSIRYEALKKVY
	1		DNRVSVAARMAQK\MSFGFSKYSNMEF\VR\MKGPQGKGHAEMA
	4		VSRVSTGDTSPCGTEEDSSPASPMHERVTSFSTPPTPERNNRPA
	1	1	VSRVSTGDTSPCGTEEDSSFASFINERVISISTET FFSPSLKRKVPRNRIAEMKKSHSANDSEEFFREDDGGADLHNAT
		1	PFSPSLKRKVPRNKTAEMKKSHSANDSEEFFKEEDSGABERKHT NLRSRSLSGTGRSLVGSWLKLNRADGNFLLYAHLTYVTLPLHRI
			LTDILEVRQKPILMT
5402	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV
		1	PGADILNSYAGLACVEEPNDMITESSLDVAEEEIIDDDDDDITL
		1	TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS
			PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ
)	1	PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL
			ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D
	į		MNYEPMGRALRYYYORGILAKVEGORLVYOFKEMPKDLIYINDE
			DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK
		\	PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ
İ		1	PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP
			RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP
ſ	}	1	MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT
1	ļ.		VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ
			ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS
}			QVAMKQNELLEPNSF
5403	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV
3103	i		PGADILNSYAGLACVEEPNDMITESSLDVABEEIIDDDDDDITL
ł	1	į.	TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS
1	1		PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ
ł		1	PKRKKGRKTKPPRFDSPATTPNISVKKKNKDGKGNTIYLWEFLL
}	1	1	ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D
			MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE
ì			DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK
1		1	PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ
1		(PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP
1	1		RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP
			MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT
ļ	1	i	VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ
Ì	•		ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS
1		ŀ	OVANKONELLEDNSF
	187	1111	LDUTT TEAKMETI OSTI LLLLVPLIKPAPPTQQDSRI IYDYGT
5404	10/		DARRESTESONVENKYLDGKNIKEKETVIIPNEKSLQLQKDEAL
1	1		THE PREVENDEMOTCLL CVCLSGSVYCEEVDIDAVPPLPKESAY
1	1		LUADDNETERI.T\ AKDFADIPNLRRLDFTGNLIEDIEDGTFSKL
1	1	I	CTUEBLELARNOLIKI.PVI.PPKLTLFNAKYNKIKSRGIKANAFK
			KINNITTELVI DHNALESVPLNLPESLRVIHLQFNNIASITDDIF
1	Ī		CVANDTSVIRDRIEEIRLEGNPIVLGKHPNSFICLKRLPIGSIF
			ONCOCHADONOHOSCSSLVVIOOPSLDSRPRLDYEREIQPTA
5405	2199	1220	TI CLDOTKA TRESNEYTEGPSVVKRPAPRTAPRQEKHERTHELL
1			PINVNNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS
1)		NSSASSEQGLLGRSPPTRPVPGHRSERAIRTQPKQLIVDDLKGS
1	1	•	NSSASSEQGLLGRSPPTRPVPGHRSERATRTQTACKRQCLCSAE LKEDLTQHKFICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE
1			LKEDLTQHKFICEQCGKCKCGECTAPRI LPSCHACKRQCBCSCS SMVEYGTCMCL\VKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR
1	Ì		YLCMGAMSLFLPCLLCYPPAKGCLKLCRCYDWIHRPGCRCKNS
1	1		
1	1		NTVYCKLESCPSRGQGKPS
5406	5 279	2732	RWRTYNVEGPLTFMDVAIEFCLEEWQCLDTAQQNLYRNVMLENY

SEQ	Predicted	Dradiated - 3	
ar a	beginning	Predicted end nucleotide	
NO:	nucleotide	location	M=Alanine, C=Cysteine, D=Aspartic Acid E_
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
I	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ł	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
}	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
		 	RNIVELG(IIAVCANDI TEGE FORWERS
j	l		RNLVFLG/IIAVSKPDLITCLEQEKEPWEPMRRHEMVAKPPVMC SHFTQDFWPEQHIKDPFQKATLRRYKNCEHKNVHLKKDHKSVDE
ł	1	1	CKVHRGGYNGFNQCLPATQSKIFLFDKCVKAFHKFSNSNRHKIS
1	1		HTEKKLFKCKECGKSFCMLSHLAQHKIIHTRVNFCKCEKCGKAF
1	1		NCPSIITKHKRINTGEKPYTCEECGKVFNWSSRLTTHKKNYTRY
	İ	İ	KLYKCEECGKAFNKSSILTTHKIIRTGEKFYKCKECAKAFNQSS
Ī	1	į	NI.TEHKKIHPGEKPYKCEECGKAFNWPSTLTKHKRIHTGEKPYT
- 1	i	}	CEECGKAFNQFSNLTTHKRIHTA\EKFYKCTECGEAFSRS\SNL
1			TKHKEIHTEKKPYKCEECGKAFKWSSKLTEHKLTHTGEKPYKCE
1	ļ	1	KCGKAFNCPSIITKHNRINTGEKPYTCEECGKVFNWSSRLTTHK
ŀ	j		KNYTRYKLYKCEECGKAFNKSSILTTHKKIHIEKKFYKCEECGK
			AFKWSSKLTEHKITHTGEK?YKCEECGKAFNHFSTLTKHKDTUT
		1	GEKPYKCEECGKAFTOSSNLTTHKKIHTGEKFYKCEFCGVAFTO
1	İ		SSNLTTHKKIHTGGKPYKCEECGKAFNOFSTLTKHKITHTERVE
1	4	1	I KCEECGKAFKWSSTLTKHKIIHTGEKPYKCRECG\KDEKLCCT
	1		LSTHKIIHTGEKPYKCEKCGKAFNRPSNLTEHKKTHTGEGPYKG
1	j		EECGKAFNYSSHLNTHKRIHTKEOPYKCKECGKAFNOVSNLTTU
5407	3		NKIHIGEKLYKPEDVIVILTTPOTFSNIK
		659	RPRRRQSSCCTGWLAGWLLRAAPRFCRRTETDMEQGKGLAVLIL
1	}		ALLLUGTLAQSIKGNHLVKVYDYOEDGSVLLTCDARAKNITTHE
ł	1	}	KDGKMIGFLTEDKKKWNLGSNAKDPRGMYQCKGSQNKSKPLQVY
1			YRMCQNCIELNAATISGFLFAEIVSIFDLAVGVYFIAGTGMEFR
5408	2745	6128	QS\RASDKQTLLP\NDPAPTQPLKDPRKMTQYSHLQGN\QLRRN
	}		QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP
	1		HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF
1			STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP
ĺ	1		RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE
1	1		VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM
ł	1		NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD
ļ	1		LVQKLWSGTQKNVAPLKLRWTIAKYAPRFNGFOOODSOELLAFI
) [LIGHEDLNRVHEKPYVELKDSDGRPDWEVAAFAWDNHI.ppnpc
i			IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSI.DI.DMDSVMHI
1			ETTVIKLDGTTPVRYGLRLNMDEKYTGLKKOLSDLCGLNSBOTI
İ	1		LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFFIPVPVSDTSAGD
1	1		TOTOPSSSPSTNEMFTLTTNGDLPRPIFIPNGMPNTNAPCCTEX
	1		NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR
1	1 1		PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH
ŀ	1 1		AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE
ł			DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR
	1		LPPILIIHLKRPQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP
1]	}	ALCOHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS
1	1	ł	PSSLSANI ISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS
1			KGRLRLPQIGSKNKLSSSKENLDASKENGAGOICELADALSDGU
1]	j	VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG
1	1		NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHVUTVAVA
			PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEOGGIDVAGELDV
5409	3745		TDGKKMADTSSMDEDFESDY\EKYCVI.O
5.05	2745	6128	QGSKGTCHPQAQQPWDEGVWOEAPSOSRPWGOSOEPPTMPORT D
<u> </u>	i i	i	HARQHTPLPLGSADYRRVVSVRPOGPHRDPKDSRDAAKPPOGET
i l		ŀ	APRPVPASRGGKTLCKGYROAPPGPPAOFORPICSASPPWASRE
1 1	1	1	STPCPGGAVREDTYPVGTOGVPSLALAOGGPOGSWRFI.EWKSMP
	ļ	1	REPTDEDIGGPWFPHYDFERSCWVRAISOEDOLATCWOAFHCGF
	į	i	VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGISNIGNUCEM
[1	1	NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCVGD
	ſ	1.	LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL
		} .	LDGL:HEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDPPNFLSLPLPMDSYMHL
		3	A V V P P P P P P P P P P P P P P P P P
	ĺ	1.	PITTITUT DOMINITATE TO THE BOLL DE THE BOLL DE LA PROPERTIE DE
		Į.	EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
[amine acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	}	\=possible nucleotide insertion)
· · · · · ·			TOTDFSSSPSTNEMFTLTTNGDLPRPIFIPNGMPNTVVPCGTEK
İ		1	NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR
i	1		PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH
	}	ł	AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE
}	l	ļ.	DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ
i		1	VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR
	j	l .	LPPILITHLKRFQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP
{	{	4	ALCOHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS
1			PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS
	1		KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH
1		l .	VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG
ł	!	i	NHSBEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN
1		1	PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK
l		Į.	TDGKKMADTSSMDEDFESDY\EKYCVLQ
<u> </u>		710	LRPPGQARHVWLAARMQAPHKEHLYKLLVIGDLGVGKTSIIKRY
5410	2	1 /10	VHONFSSHYRATIGVDFALKVLHWDPETVVRLQLNDIAGQERFG
1			VHONFSSHIRATIGUDFADKULMINDE TVVILLED VALLED
}	ļ		KPVSVVLLANKCDQGKDVLMNNGLKMDQFCKEHGFVGWFETSAK
1		1	ENINIDEASRCLVKHILANECDLMESIEPDVVKPHLTSTKVASC
	i		SG\CAKILVGTFAGVW
	<u> </u>		TGPAAAGRRKALGSFGKPSPVTGLRAARRRTRPSAPAAPSVGC
5411	1302	289	GKRRESDAGAGGERASVRTGSGRRGGRTMAGDSEQTLQNHQQ?N
	1		GGEFFLIGVSGGTASGKSSVCAKIVQLLGQNEVDYRQKQVVILS
ì		j	QDSFYRVLTSEQKAKALKGQFNFDHPDAFDNELILKTLKEITEG
1 .	1	1	KTVQIPVYDFVSHSRKEETVTVYPADVVLFEGILAFYSQER/IR
1	1	1	DLFQMKLFVDTDADTRLSRRVLKDISERGRDLEQILSSSTLRFV
	1	}	Kby/Leelchbk/Kandalibk/Gydn/KabinFinghio/Di
}	1	1	LNGGPS\NRQTNGCLNGYTPSRKRQASESSSRPH
L			QGISNFFHKEANFWFEVSGYLISPLRSPFVDPALEWSLMASPWN
5412	3180	313	CGISNFFHKEANFWFEVSGILISFIKSFFVDFABBUGGETED IN KMEGESSRFEIHTPVSDKKKKKCSIHKERPQKHSHEIFRDSSLV
1	1	1	NEQSQITRRKKRKKDFQHLISSPLKKSRICDETANATSTLKKRK
1	1	1	KRRYSALEVDEBAGVTVVLVDKENINTPKHFRKDVDVVCVDMS
1	1	l l	IEQKLPRK\PKTDKFQVLAKSH\AHKSEALHSKVREKKNKKHQR
1	ì	•	KAASWESQRA\RDTLPQSEFPTQEESWLSVGPGGEITELP\ASA
Į.	1	1	HKNKSKKKKKKSSNREYET\LAMPEGSQAGREAGTDMQESQPTV
1	ļ		GLDDETPQLLGPTHKKKSKKKKKKKKNHQEFESLAMPEGSQVGS
1	1		EVGADMQES\RPAVGLHGETAGIPAPAYKNKSKKKKKKSNHQEF
1			EVGADMQES\RPAVGLHGETAG1FAFA1RNRSKKKKKKSNNQEF EAVAMPESLESAYPEGSQVGSEVGTVEGSTALKGFKESNSTKKK
1	1		EAVAMPESLESAYPEGSQVGSEVGTVEGSTALKGFRESKSTARK SKKRKLTSVKRARVSGDDFSVPSKNSESTLFDSVEGDGAMMEEG
ł	}	1	SKKRKLTSVKRARVSGDDFSVPSKNSEST LFDSVEGDGARMELG VKSRPRQKKTQACLASKHVQEAPRLEPANEEHNVETAEDSBIRY
-			VKSRPRQKKTQACLASKHVQEAPRLEPAREEHNVETAEDSEIRT LSADSGDADDSDADLGSAVKOLOEFIPNIKDRATSTIKRMYRDD
1		1	LSADSGDADDSDADLGSAVKQLQEFIPHIRDRAISII KRHIRDD LERFKEFKAQGVAIKFGKFSVKENKQLEKNVEDFLALTGIESAD
1	[LERFKEFKAQGVAIKFGKFSVKENKQLEKNVEDFLADIGIESAD KLLYTDRYPEEKSVITNLKRRYSFRLHIG\RNIARPWKLIYYRA
1	1		KLLYTDRYPEEKSVITNLKRRYSFRLAIG\RNIARPWADIIIKA KKMFDVNNYKGRYSEGDTEKLKMYHSLLGNDWKTIGEMVARRSL
1	1		KKMFDVNNYKGRYSEGDTEKLKMYHSLLGNDWKIIGEMVARKSI SVALKFSQISSQRNRGAWSKSETRKLIKAVEEVILKKMSPQELK
) ·	1		SVALKESQISSQRNKGAWSKSETKKLIKAVEEVILIKAMSEQBEK
1			EVDSKLQENPESCLSIVREKLYKGISWVEVEAKVQTRNWMQCKS
1	1		KWTEILTKRMTNGRRIYYGMNALRAKVSLIERLYEINVEDTNEI
1			DWEDLASAIGDVPPSYVQTKFSRLKAVYVPFWQKKTFPEIIDYL
1			YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPPRDIFYYEDD
	_1		SEGGGHRKRKRRPRRHAWFTPVIPVLWEAKAGWII
5413	3753	1304	RFPAGVAPRRAMANVSKKVSWSGRDRDDEEAAPLLRRTARPGGG
1	1	1	TPLLNGAGPGAARQSPRSALFRVGHMSSVKLDDELLEP\DMDPP
Į.		1	HPFPKEIPHNEKLLSLKYESLDYDNSENQLFLEEERRINHTAFR
1		1	TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKGNID
1	1	1	KFTEKGGLSFSLLLWATLNAAFVLVGSVIVAFIEPVAAGSGIPQ
ł		1	IKCFLNGVKIPHVVRLKTLVIKVSGVILSVVGGLAVGKEGPMIH
1		1	SGSVIAAGISQGRSTSLKRDFKIFEYLRRDTEKRDFVSAGAAAG
1		1	VSAAFGAPVGGVLPSLEEGASFWNQFLTWRIFFASMISTFTLNF
1		1	VLSTYHGNMWDLSSPGLINFGRFDSEKMAYTIHEIPVFIAMGVV
1		1	GGVLGAVFNALNYWLTMFRIRYIHRPCLQVIEAVLVAAVTATVA
ł	1	1	FVLIYSSRDCQPLQGGSMSYPLQLFCADGEYNSMAAAFFNTPEK

SEQ	Predicted	15.31.	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide	(A=Alanine, C=Cvsteine, D=Aspartic Acid R-
""	location	location	Giutamic Acid, F=Phenvlalanine G-Glyging
1		corresponding	H=H1Stidine, I=Isoleucine, K=Tygine
1	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine
- 1		amino acid	P=Proline, Q=Glutamine, R=Arginine
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			SVVSLFHDPPGSYNPLTLGLFTLVYFFLACWTYGLTVSAGVFIP
ł			SLLIGAAWGRLFGISLSYLTGAAIWADPGKYALMGAAAQLGGIV
1	-	1	RMTLSLTVIMMEATSNVTYGFPIMLVLMTAKIVGDVFIEGLYDM
1	j	1	HIOLOGYDRI LWED DYMOUGY TO DEVELOP THE CONTROL OF T
1		1	HIQLQSVPFLHWEAPVTSHSLTAREVMSTPVTCLRRREKVGVIV
ļ	ļ	ł	DVLSDTASNHNGFPVVEHADDTQPARLQGLILRSQLIVLLKHKV
1	1]	FVERSNLGLVQRRLRLKDFRDAYPRFPPIQSIHVSQDERECTMD
ļ	1		LSEFMNPSPYTVPQEASLPRVPKLFRALGLRHLVVVDNRNQVVG
5414	2130		LVTRKDLARYRLGKRGLEELSLAQT
	1 2230	390	GVASAWDRALPSPLLSPTSRVFRTSPPRCVSTETGRRDRARVPS
1	1		QWCSVLQGKLPVSGRTSLACVRSILLSPASSPRKVGTVGGTCAP
ı	1		AGAAPRDHGRVRHRRPSSARRMTRTTGOCLAPRGCOGDDGTDGD
İ	1	}	RSPRSRTRRGCSASPACLP/CRSALIVAVLCYINIJ.NYMDRFTV
1	i	l .	AGVLPDIEQFFNIGDSSSGLIOTVFISSYMVLAPVFGVLGDDVM
- }			RKYLMCGGIAFWSLVTLGSSFIPGEHFWLLLLTRGLVGVGEASY
			STIAPTLIADLFVADQRSRMLSIFYFAIPVGSGLGYIAGSKVKD
1		ł	MAGDWHWALRVTPGLGVVAVLLLFLVVREPPRGAVERHSDLPPL
l l			NPTSWWADLRALARNPSFVLSSLGFTAVAFVTGSLALWAPAFLL
ŀ	1		RSRVVLGETPPCLPGDSCSSSDSLIFGLITCLTGVLGVGLGVEI
1	1	{	SRRLRHSNPRADPLVCATGLLGSAPFLFLSLACARGSIVATYIF
	ľ		IFIGETLLSMNWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGD
1	1		AGSPYLIGLISDRLRRNWPPSFLSEFRALQFSLMLCAFVGALGG
			AAFLGTAHLH
5415	693	2986	
1	1		IPPKTKLELQKH\LTTLT\NQEQATIFEEVQKLRPRNEQRENEL
1]		IISPLRCLFEBKQKEHIHIGEMKQTSQMAAENIGSELPPSATRF
1	i		RLDMLKNKAKRSLTESLESILSRGNKARGLQBHSISVDLDSSLS
1	1 1		STLSNTSKEPSVCEKRALPISESSFKLLGSSEDLSSDSESHLPE
1	1		EPAPLSPQQAFRRRANTLSHFPIECQEPPQPARGSPGVSQRKLM
-			RYHSVSTETPHERKDFESKANHLGDSGGTPVKTRRHSWRQQIFL
1	· · · · · · · · · · · · · · · · · · ·		RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCECGPFGPPPE
1	l I		EKKRTSRELRELWQKAILQQILLLRMEKENQKLQASENDLLNKR
}	1		LKLDYEEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGO
İ			GVP\RHHRGEIWKFLAEQFHLKHQPPSKQQPKDVPYKELLKQLT
	1		SQQHALLIDLGRTFPTHPYFSAOLGAGOLSLYNILKAVSLIDGE
1	1		VGYCQGLSFVAGILLLHMSEEEAFKMLKFLMFDMGLRKOVPDDM
ł	ł [•	ILLQIQMYQLSRLLHDYHRDLYNHLEEHEIGPSI.YAADWET.TWE
1	[ASQFPLGFVARVFDMIFLOGTEVIFKVALSLIGSHKDITLOUEN
1	1 1		LETIVDFIKSTLPNLGLVOMEKTINOVFEMDIAKOLOAVEVEVU
i	1		VLQEELIDSSPLSDNQRMDKLEKTNSSLRKONI.DLI.FOLOVANG
] !		RIQSLEATIEKLLSSESKLKQAMLTLELERSALLQTVEELRRRS
-			AKPSDREPECTOPEPTGD
5416	27	4074	KSQLFCFWGGKAGDILSGDODKEOKDPYFVETDYGYOLDIDELY
]		•	YVDDIQKGNTIKRLNIQKRRKPSVPCPEPRITSGQQGIWTSTES
1 1			LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP
1			ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEF
1	}		RRPRLASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYG
1 1			SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM
1 1	.		ATALKEL FEOURET DU OUVIOUR OFFICE AND MANAGEMENT DE LA CONTRACTION DEL CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION DE LA CONTRACTION D
1 1	· .	ļ	AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME
1	i		TUPOSTOPI VERDOL / TO THE TOTAL TO THE TOTAL TOT
, ,			TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC
1 1	i	i	RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE
į i	j	ì	AMIGUMTEADKEIELQQQTIESLKEKIYRLEVQLRETTHDREMT
) 1		ł	KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH
		İ	MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER
[1	VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESUNDITIESUND
<i> </i>	1	İ	NLNLKEVRS IGCGDCSVDVTVCSPKECASRGVNTEAVSOVEADV
		i	MAVPRTADQDTSTDLEQVHOFTNTETATLIESCTNTCLSTLDKO
	1	ſ	TSTQTVETRTVAVGEGRVKDINSSTKTRSTGVGTLLSGUSGEDB
	l l	1	PSAVKTKESGVGQININDNYLVGLKMRTIACGPPOLTVGLTASP
1	1	İ	RSVGVGDDPVGESLENPQPQAPLGMMTGLDHY1ERIQKLLAEQQ
1	ſ	i	TLLAENYSELAEAFGEPHSOMGSINSOLTSTLSSTNSIMVER CT
<u> </u>		ļ	EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE

Predicted Display Di				
Incation Corresponding C	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Corresponding	ID			(A=Alanine, C=Cysteine, b=Aspartit Actu, s=
Cotresponding to first amino acid amino acid cand acid cand acid cand acid cand acid cand acid sequence companies to the companies of the cand acid sequence companies to the companies of the co	NO:	nucleotide	location	Giutamic Adid, Ferhenyiatanine, Oscajomo,
to first anino acid anino acid residue of anino acid sequence seq			corresponding	H=HISCIGINE, I=ISOIEUCINE, N=Asparagine,
amino acid residue of amino acid sequence Sequence Sequence Codon, /=possible nuclectide deletion, ->possible nuclectide insertion) Settiks: sinkkcomkonskonakkking/volkoviterissbossible nuclectide insertion) Settiks: sinkkcomkonskonakkking/volkoviterissbossible nuclectide insertion) Settiks: sinkkcomkonskonakkking/volkoviterissbossible populery Settiks: sinkkcomkonskonakkking/volkoviterissbossible populery Settiks: sinkkcomkonskonakkking/volkoviterissbossible populery Settiks: sinkkcomkonskonakkking/volkoviterissbossible populery Settiks: sinkkcomkonskonakkking/volkoviterissbossible populery Settiks: sinkkcomkonskonakkking/volkoviterissbossible populery Settik				n neeling O-Clutemine ReArginine.
main acid sequence mino acid sequence mino acid sequence Apossible nuclectide insertion				p=proline, Q=Glucamine, N=Majine,
meino acid sequence Codon, /=possible nuclectide deletion, -possible nuclectide insertion Settus inkxEconthosnakkniqovinogyErrisposses Settus inkxEconthosnakkniqo				Saserine, lainteonine, value, value, vastop
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ENROLPPSTOLPKHNILHUTKTLHETRRILEGERATMONTICES REPRILASE EGGMCTTSS LEPSTUSGENHACHLOGNGYGONODY SYAPAPTTSSMGS I RHSPLSGISTPYINNSPHICHITREOM ALALKERLEEDOWTI PULQWITSULGEKROLYGOLKONGRAA SQINVCGYRKESYAGNASOLBOLGRARRSGGELYIDYEBEEME TVEGSTORIKEFROLYTA-MQALBOLGOSCRASEBLERGEC RSVAWGABEMMODIVYHRGSRSCCDAVGTLVBWRNCGVSVTK KINGELGAAGSKKVDVACATMAQPLIVERNOCGVSVTK AMLGWITEADKEILLQQCTIESLKEKIYRLEVQLRETTHDREMT KIKGSLQAAGSKKVDVACATMAQPLIVERNOCGVSVTK WILDVOTCVGTSVETNSVGISCQPECKNKVVQPELPMNWNIVKER VEMBDRCAGRSVEMOLGKSVEVSVSVCGTGSRTEESVNDLTLLKK NILLKEVRSIGGGCSVDVTVCSPECASROWITCAVGOVBAV MAVPRADODTSTDLEGVHOFTNITETALLESCTNTCLSTLDKO TSTQTVETRTVAVGEGRVKDUSPTSTLSGENGSGFDR PSAVKTKESGVGOININDYLVSLUKRTIAGPPOITVOLATASK RSVGVGDDPVGESLEBNQPQAPLGMMTGLDHYLERIOKLAGG TELARNYSELARAGSPHSQMSSLNSOLISTLSSINSVMKSAST EELRRIPDEOKTSLCKITGSSLGSTCKGGGLGSGFLSSGTSOGPE QBVGTSEGKFISSLDAPPTOGGTLSFOWLITDQIAAGLYACTINN ESTIKSINKKKOGNKONGAKKHLOPUNGGYETTSSDBSSD ESSSSSDDECUVIEYPLEEBEEBEDDTROMAGGHAVNIEGL KSANVEDBEOQVGECEPEKVSITERFYLSEKHLAGACHLLKINTIND PRALTSKOMR FCLNTLORGEMFRYSSGKSAIPANVGYIAAFBAI KSANVEDBEOQVGECEPEKVSITERFYLSEKHLAGACHLLKINTIND PRALTSKOMR FCLNTLORGEMFRYSSGKSAIPANVGYIAAFBAI SPDVLRYVINLADGNGWATALHYSVENETVUKLLIDADVGNU HQNKAGYTPIMAALAAVABKUMRIVELLFOCGUVAARASGAG QTALMLAVSHGRIDWYKSLLACGADVNIQDDEGSTALMCASEIG HVBIVKLILLAQPGCNGHLEDNOGSTALSIALKAGHKUTAVLLYA HVWFAKAQSPGTPRIGRKTSSGTHRGSSD VPRAGGGMETGAABLIVOALLGICHVONVODPLRVLFGFLYR CROPENVALLAQPGCNGHLEDNOGSTALSIALKAGHKUTAVLLYA HVWFAKAQSPGTPRIGRKTSSGTHRGSSD GROUPMINISTGRAVENSAMATAUGHTENTACHTWRODYTLLEVRUPVEHVVK GKQVSVALLARGERGRAVVGAAABEVBRIPBISTTEL DGRQVEKVQPPQPVERMAHGSGRARAPGRAVAGAABEVBRIPBISTEL BCGQCVLVALLSKYGEYWNNALLEGEEPTOIDKRKRESNATYDD EGGVTUAVALSSSIRVAMGEBGSGTGGGRAKKHWRHPERADA KOPASLPQC/LGP/DCVRRAPGSSTGGGGGRAKHKWMKHPERADA KOPASLPQC/LGP/DCVRRAPGSSTGGGGGGRAKHKWMKHPERADA KOPASLPQC/LGP/DCVRRAPGSSTGGGGGGGRAKHKWMKHPERADA KOPASLPQC/LGP/DCVRRAPGSSTGGGGGGGCHURDWRGKT PGREGORGERGVARAGGGAAGAUGAGACOCCHURDPGKT VALKHMERCYAKYESGTGFSGMYNTALGEMERGFRUFAMTAV VALKHMERCYAKYESGTGFSGMYNTALGERGERPLGWWVLGG VALKHMERCYAKYESGTGFSGMYNTALGERGERPLGWWV		1		YVDDIQKGNIIAKBNIQKKKAPSVFCFBIKTIDGQGGUTTID
REPELAS FGGMGTTS SLDS FYUSGONHAPAKHOLOKYCKNODYO SYADAD TIS SMSS I RHSPLSSGISTYNNSPHHICH TROM ALALKRIKELEEOVRTI PULQWISVLQEKRQUNGLKUNGRAA SQINVCGVIKKEYSAGNAS CLBOLSRARRSGGELYIDYEBEME TVEQSTOR IKEFROL YA MQALEQKI QDS SCEASSELRENGEC RSVAVGAREMMIDI VYYHRISSS CODANGTI VEMRINGGVSUTE AMIGWITEADKEI ELQQTIESLKKIY RILEVQLEETHDREMT KLKQELQAAGSRKKUNKATMAQPLYFSKVVEAVVURDOWNGSH MDLVDTCVGTSVETNS WIS ISCQDECKNIVVGPELPMINN IVKER VEMHORCAGRS VEMCDKS VS VSS VCCTGSNTEESUNDLITLLKT NILMKEVRS IGCGDC SVUDTVCS PRECASROWTEANS VERAN MAVPRIADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSTKTRS IGVGTLISGRISGFDR PSAVIKKESGYGOLIN HONNIVUSLIKMRI IACGPQI TVGLTASK RSVGVDDDPVGESLENPQDQADIGMMTALHYITERIQKILAEQQ TLLLAENYSESLABRAGGPHSOMGSLMMTALHAYVERICKSFDR PSAVIKKESGYGOLIN HONNIVUSLIKMRI IACGPQI TVGLTASK RSVGVDDPVGESLENPQDQADIGMMTALHAYVERICKSFDR PSAVIKKESGYGOLIN HONNIVUSLIKMRI IACGPQI TVGLTASK RSVGVDDPVGESLENPQDQADIGMMTALHAYVERICKSFDR PSAVIKKESGYGOLIN HONNIVUSLIKMRI IACGPQI TVGLTASK RSVGVDDPVGESLENPQDQADIGMMTALHAYVERICK STAGNIVATAN ESTLKSIMKKONKONKONNIGNKKNILOPVGINGGYETTSSDSSSD ESSSSSDDDCDVIEY PLEBEBEEEDDTGCMAGGHAVANI ISGL KSARVEDDEMQVQSCEPRINSLANGHAVI IEGL KSARVEDDEMQVQSCEPRINSLANGHAVI IEGL KSARVEDDMYQGSCHEPRINSSGSA I PANVGYI IACHTAN PKALTSKOMR FCLATILGBEMFRVSSGSA I PANVGYI IACHTAN PKALTSKOMR FCLATILGBEMFRVSSGSA I PANVGYI IACHTAN PKALTSKOMR FCLATILGBEMFRVSSGSA I PANVGYI IACHTAN PKALTSKOMR FCLATILGBEMFRVSSGSA I PANVGYI IACHTAN PKALTSKOMR FCLATILGBEMFRVSSGA I PANVGYI IACHTAN PKALTSKOMR FCLATILGBEMFRVSSGA I PANVGYI IACHTAN PKALTSKOMR FCLATILGBEMFRVSSGA I PANVGYI IACHTAN PKALTSKOMR FCLATILGBEMFRVSSGA I PANVGYI IACHTAN PKALTSKOMR FCLATILGBEMFRVSSGA I PANVGYI IACHTAN PKALTSKOMR FCLATILGBEMFRVSSGA I PANVGYI IACHTAN PKALTSKOMR FCLATILGBEMFRVSSGA I PANVGYI IACHTAN PKALTSKOMR FCLATILGBEMFRVSSGA I PANVGYI IACHTAN PKALTSKAM PKALTSKAM PKALTSKAM I PANVAL PKALTSKAM PKALTSKAM PKALTSKAM PKALTSKAM PKALTSKAM PKALTSKAM PKALTSKAM PKALTSKAM PKALTSKAM PKALTSKAM PKALTSKAM PKALTSKAM PKALTSKAM PKALTSKAM PKALTSKAM PKALTSKAM PKALTSKAM PKALTSKAM PKALTSKAM PKALTSK				LSSSMSUUMAQUENT LIAAGQVISITTIOATTICET
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ALALKRLELEGOVRTIPULOVKISULOEKROUVSCLKORAA SQINVCGYRKSYSHARNSGCELYIDYEEEME TVEQSTQRIKEFROL\TADMOALEOKIODSSCRASSILERNGEC RSVAVGAEENNNDIVVYHRGRSCKDAAVGTLVENNRGSVOTE ANLGWYTERDKEIELQCOTIESLKEKIYRLEVOLRETTHDREMT KIKQELQAAGSRKKVDKATWAQPLVYSKVVEAVVQTRODMVGSH MDLVDTCVGTSVETNSVGISCQPECKKKVVGFELEMWWHIVKER VEMEDRCAGRSVEMCDKSVSVEVSVCCTGSNTEESVENDLITLIKT NILKKEVSIGGGDCSUDVTVGSECARGWYTEAVGYVEAAV MAVPRTADODTSTDLEQVHOFTNTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGEVVDTVTGSTKTSIGVGTLISGHSGFDR PSAVKTKESGVGOININDNYLVGLKMRTIACGPGITTGLITASK RSVGVDDDPVGESLENPQPQAPLGMMTGLDHYIERIQKILABGQ TSTQTVESTETVAVGEGEPHSQMGSLINGLISTLSSINSWKSAST EELRNPDFQKKTSIGKITGSYLGYTCKCGGLGGSSPLSSGTSQPE QSVGTSEGKPISSLDAPFTQEGTLSPVNLTDDQLAAGIYACTNN ESTLKSIMKKKDGNKDSNGAKKNLQFYGINGGGSTELSSGTSQPE GSSSSSBDECDVIEPPLEEEEEEDDTGMAEGHAVNIEGI KSARVEDEMQVQBCEPEKYTRERYELSERMLSACNLLKNTIND PKALTSKOMRFCLNTLIGHENFRVSSQXSAIPAWGGYTASDDSSD ESSSSSBDECDVIEPLLEEEEEEDDTGMAEGHAVNIEGI KSARVEDEMQVQBCEPEKYTRERYELSERMLSACNLLKNTIND PKALTSKOMRFCLNTLIGHENFRVSSQXSAIPAWGGYIAFFAI SPULEVYUNLADGGNGNTALHYSVSHNFFIVKLLLDADVCNUD HONKAGYTPIMLAALAAVBERDDRIVGDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHUDIAVLLYA HUNFAKAQSFGTPRLGRKTSGPDTHGGGDUNAKASQAG GTAMLANSHGRIDHWKGLLACGAUVHIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHUDIAVLLYA HUNFAKAQSFGTPRLGRKTSGPDTHGSFD GRAVLUFLTRDDVGKKINGSPTAGAEKSPOPVPQEIEIDSTTEL DGHGEVEKVQPPGPVKEMAHGSGAZAPAGAASVPR\BPPI LPRIQEGFOKNPDSYNGAVERNYHSGDYTLLEXVPLYPKHVKK GKQVSVALSSSIRVAMLEENGERVLMSGLTHKINTESLUSL BEGKCYLVNLSKVGEVWWMAILEGEEPTDIDKINKERSMATVDE EGGKVLVNLSKVGEVWWMAILEGEEPTDIDKINKERSMATVDE EGGKVLVNLSKVGEVWWMAILEGEEPTDIDKINKERSMATVDE EGGKVLVNLSKVGEVWWMAILEGEEPTDIDKINKERSMATVDE EGGKVLVNLSKVGEVWWMAILEGEEPTDIDKINKERSMATVDE EGGKVLDVINLSKVGEVWWMAILEGEEPTDIDKINKERSMATVDE EGGRUPAMFNISGAVGF GREDPAMFNISGAVGF GREDPAMFNISGAVGF FORLOPSKYGGGBENFRYBYBLITGDFCRLPK BLEAIILRARQQAVREDESNBGDSDDTDLDIFCYGGGBFINFRE BLEAIILRARQQAVREDESNBGDSDDTDLDIFCYGGGBFINFRE BLEAIILRARQQAVREDESNBGDSDDADTDLDIFCYGGGBFINFRE VARRWRCYAKVESCLRAREVUSKLLDEFFEGRINVFTAHVN RAGLLAMLHOTTOHDPLITTBRSADR			1	RRPRLASFGGMGTTSSEPSFVGSGMMFFMGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
SQINVCGVRKEYSAGNASQLEQLSRARSGETYIPYELEME THOSTORI KERFOLI TADMOALDEQKIQDSSCEASSIERNGEC RSVAVGAEENMNDIVVYHRGSSCKDAAVGTLVENRNGGVSVTE ANLGVWTEADKEIELQQCTIESLKEKIYYLEVQLEETHDREMT KKOELQAAGSRKKWDKATMAQELVTSKVVEAVVQTRODMVGSH MOLVDTCVGTSVETNSVGISCQPECKNKVVQEEDMWMIVKER VEMPDRCAGRSVEMCKSVSVEVSVCSTGSNTESSVADLTLLKXT NIALKSVRSIGGEDCSVDVTVCSPKECASRGVNTEAVSQVEAAV MAVPRTADQDTSTDLLEQVMOPTHATLIESCTNTCLSTLDKK TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKKESGVGOININDNYLVGKMRTALLESCTNTCLSTLDKK RSVGVCODDPVGESLENPQQAPLGMMTGLDHTIERIQKLLAEQQ TLLAENYSELABAFGEPHSQMGSLNSQLISTGLISTISSINSVMKSAST EELENDFPGKTSIGKITTSVLGTYCKCGGLQGSGELSSGTSQPE QEVGTSGCKPISCHLTGVLGVGYFTMATCLAGHSGFDR RSVGVCODDPVGESLENPQQAPLGMMTGLDHTIERIQKLLAEQQ TLLAENYSELABAFGEPHSQMGSLNSQLISTGSITSSINSVMKSAST EELENDFPGKTSIGKITTSVLGTYCKCGGLQGSGSLSSGTSQPO QEVGTSGCKPISCHLTGVLGTTSVLGTYCKCGGLGGSGSLSSGTSQNT ESTLKSIMKKKDONKDSNGAKKNLOFVCKGGGLGGSGSLSSGTSQNT ESTLKSIMKKKCONKDSNGAKKNLOFVCKGGGLGGSGSLSSGTSQNT ESTLKSIMKKKCONKDSNGAKKNLOFVCLNGGYGTTSSDDSSSG GEVGTSGKRITTGLEWFRYSSSATPANVGGYIAAFBAI KSARVEDEMQVGCCEPEKVSIRERYELSEMMLSACKLLKNTIND PKALTSKOMRFCLNTLQUEWFRYSSATPANVGGYIAAFBAI KSARVEDEMQVGCCEPEKVSIRERYELSEMMLSACKLLKNTIND HONKAGYTPIMLAALAAVBARKONRIVELEFLGCGDVNAKASQAG QTALMILAVSHGRIDMOSTALHYSVSHSNFEIVULLLDADVCNVD HONKAGYTPIMLAALAAVBARKONRIVELEFLGCGDVNAKASQAG QTALMILAVSHGRIDMOSTALHYSVSHSNFEIVULLLDADVCNVD HONKAGYTPIMLAALAAVBARKONRIVELVELFLGGGDVNAKASQAG QTALMILAVSHGRIDMOSTALICHSTFULLELDADVCNVD HONKAGYTPIMLAALAAVBARKONRIVELVELFLGGDVNAKASQAG QTALLAHLARAQOROTRICKTSGPTHGSFD LEFTIQEGFGCNPDSYNGADALULQVFKTPIMARQDDEKR RQLLEKIRRKEEERAKTVSAAAARSKEPVPVQETELISTTEL DGAGEVEKVVQPPGVVKEMAHGSQEBAPGAVGGASVPR\EPSIL DGAGEVEKVVVNLSKVGEWWMAILLGEGEPTDIDKINKRESNATTUB EEGAVLUNLSKVGEWWMAILLGEGEPTDIDKINKRESNATTUB EEGAVLUNLSKVGEWWMAILLGEGEPTDIDKINKRESNATTUB EEGAVLUNLSKVGEWWMAILLGEGEPTDIDKINKRESNATTUB EEGAVLDRLTPDYHOKIGGCPGSKYCSDDCGMKLAANRIYELI PQRIQOMQOSPCIAEERGKRUNKHDERGDFCGGBLFVHFERDAD KORASCHOPKKGGBGROTABERGKLUBGTTLGFCRLFKTL PQRIQOMQOSPCIAEERGKTGSTGSNYPTRIEGATRLCOWAPRELL PQRIQOMQOSPCIAEERGFTGSNYPTELGGATRLFCDVFRERDE PL	1	[1	SYAPAAP ITSSEGSSTRESPESSOES TO EKROLVSOLKNORAA
TVEOSTORIKEFROLIVADAGALEQKIODSSEASSELRSEKERSEK RSYAVGABERNMANDIVHRGSRSCKDAAVGTLVEWRNCGVSVTE ANLGUWTEADURIELQQOTIESLKEKIYRLEVOLRETTHDREMT KIKQELQAAGSRKKUDKATWAQPLVERVUORTDOMVGSH MDLVDTCVGTSVETRISVUSISCQPECKNKVVGPELDMAWHIVKER VEMEDRCAGRSVEMCDKSVSVEVSVEVETSSTRESVINDLTLLKK INLIKKEVRSIGGGDCSUNDTVCSPKECASRGVNTEAVSQVEARV MAVPRTADQDTSTDLEQVHOFTNTETATLESCTNTCLSTLDKQ TSTQTVTETTVAVGEGRVKDINSTRESGVENTLGSHSCHDE PSAVKTKESGVGOININDNYLVGLKMRTIACGPOITTGLTASK RSVGVGDDPVGESLENPQDQAPLGKMTLSSINSVMKSAST EELRNPDFQKTSLGKTTGSYLGYTCKGGLGSGSPLSSQTSQPE QSVSTSEGKFISSLDAFPTQEGTLSFVNLITDQIAAGLYACTINN ESTLKSIMKKKDGNKDSNGAKKNLQFYGINGGYETTSSDDSSD ESSSSSEDDECDVIEVEFLEEEEEDBDTGGAEGHHAVNIEGL KSARVEDEMQVGCEPEKVEIRFYELSEKMLSACRLLKNTIND PKALITSKOMRFCLNTLOHEBWFUSASAIPANWGYIAFFAI SPDVLKYVINLADGNENTALHYSVSHSNFEIVKLLDADVCNVD HQNKAGYTFINLAALAAVSAEKDHRIVEELFGGDVNAKASQAG QTAMLAVSHGRIDWKGLLACGADVNIQDBGSTALMCASEHG HVBIVKLLLAQPGCNGHLEDNDGSTALSIALRAGHKDIAVLLYA HUNFAKAQSFGTFRLGKTSSGDFTHGSGFD SVFRAGGDMETGAAELYDQALGIIQHGWODFLKVLLYA HUNFAKAQSFGTFRLGKTSSGDFTHGSFD SVFRAGGDMETGAAELYDQALGIIQHGWODFLKVLLFGFLYR CGUSVALLSSSIRVAMLEENCERVLMSGKTHKINTESSLWSL DGHQEVEKVQPFQPVKEMAHGSGARAGABEVPRLPPI LPRIGEFOKNPDSYKMGAVERYTHSGDYTDLEVRYPVKHAVK GKQVSVALSSSIRVAMLEENCERVLMSGKKHAGAAASHKVPLPPI LPRIGEFOKNPDSYKMGAVERYTHSGDYTDLEVRYPVKHAVK GKQVSVALSSSIRVAMLEENCERVLMSGKKHAGAAASEKSPR GGRIDFAMFRISGRAQF GGRIDFAMFRISGRAQF GGRIDFAMFRISGRAQF SSSRCERFGRKSEEEGRRSDTSGFGRSKHKVNMKHERADA NDPASLPC/LGF DCVTRAPGSSKYCSDDCMKLAANRIYELL DGHQEVEKVQPFQPVEEMAHGSGARAGAREVPR EEQAVLDRLTFDYHQKLOGKPQSHELKVHEMLKKGNDAEGSPF GGRIDFAMFRISGRAQF GGRIDFAMFRISGRAQF TYCKGLOVLCCHESSBCDSDDDDTOLIGFGCYGGHIFF BLEAIILRAKQQAVREDEESNBGDSDDTDLDIFGCSGHIFF BLEAIILRAKQQAVREDEESNBGDSDDTDLDIFGCSGHIFF BLEAIILRAKQQAVREDEESNBGDSDDTDLDIFGCSGHIFF FORLOWGUSPCLABERGKEERFFTLGEATRLFCDDYSPGSKT YCKRIQVLCCHERSRDFKCFTAMFW RAGLLAAMLHOTIGHDPLITTDLFSSADR RAGLLAAMLHOTIGHDPLITTDLFSSADR]	Į	Ì	ATABARDAEDEEQUATITY DE VALUE DE LA CALIFICATION DE
RSVAVGAEENMBDIVVYIRGSRSCKDAAVGTLVBMINCUSVYIR ANLGWMTRADKEI ELQQOTIE ELQQOTIE ELGGOTIE ELGGOTIE ELGQOTIE ELGGOTI	{	1		SQINVCGVRRRS ISAGRADQUAGED HOLDS SCEASSELRENGEC
AMLGWATEADAKEIELQQQTIESLKEKIYRLEVQLRETTHREATI KLKQELQAAGSRKKUDKATMAQUYSKUVBAVVQTEDQWQGSK MDLVDTCVGTSVETNSVGISCQPECKNKVVQFEDQMVGSK MDLVDTCVGTSVETNSVGISCQPECKNKVVQFEDPMWMIVKER VEMERCAGRSVEMCDKSVSVEVSVCTGSNTEESVNDLTLLKY NINLKEVRSIGCGDCSVDTVVGSPKECASRGVNTEAVSQVEAV MAVPRTADQDTSTDLEQVNQFTNTETATLIESCTNTCLSTLDKQ TSTQTVGTETRTVAVGGERVKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQITUGITASK RSVGVDDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAEMYSELARAFGEPHSQMSGLNSQLISTLSSINSVMKSAST EELRNDEPGKTSIGKTTGSYLGYTCKCGGLQSGSPLSSQTGOPE QEVGTSGKPISJADAPTYDETLSPVNLTDDQLAAGLYACTNN ESTLKSIMKKKDGNKDSNGAKKNLQPVGINGGYETTSSDDSSD ESSSSSDDDECDVIEPYLEPEEEEEDEDTTRGMAEGHHAVNIEGL KSARVEDEMQVQSCEPEKVSIRERTYSLSKMMSACNLLKNTIND PKALTSKDMRFCLNTLQHEMFRVSSQXSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNGNTALHYSKISNEFIVKLLLDADVCNVD HQNRAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVAGLLACADVNIQDEGSTALMCASSHG UTSTLLLARAGGCONGHLENDDGSTALSIALEAGHKDLAVLLYA HVNPAKAQSGTTPLGRKTSPGFTHRSSD SVFRAGGDMETGAAELTODALLGILONVGNVODFLRVLFGFTYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTPDIMARQDDEKR RQLEEKIRKEEEEAKTVSAAAAEKFPDVPVQCEIELDSTTEL DGHQGVKVLQVPGGVKEMAIGSQBAEAPGAVAGAAEVRN\EPPI LPRIQGOPGNPDSYNGAVRENTWSQDYTDLEVRYPVKHVVK GKQVSVALSSSSIRVAMLEERGRYLMGGKLTHKINTESSLWSL EEGAVLDRLIFDTYHQKLQGKPQSHBLKVHEMLKKSWDAEGSPFR GGREPPAMFITISFGAVQF EGGAVLDRLIFDTYHQKLQGKPQSHBLKVHEMLKKSWDAEGSPFR GGREPPAMFITISFGAVQF GGREPPAMFITISFGAVQF SESBRCERFGRKSEEEGRRSDTGFGRSKHKVNNKHPERADA KDPASLQC/LGP/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PORIQOMQGSPCIABEHKKLLERIRERQOSARTELQCMERRFFH ELEAILRAKQGAVREDEESREGGSDDTDLQICVSCGHFINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPFHSRDPKVPADEVCGCPLVRDVPLITGDFGRLK RCCHCHYCWELRRRAEVULERRREVULERGGRENGLTVAGGERPLGWERRFFH FLEAILRAKGGAARGRAGDFRAERGRENDTDLQICVSCGHFINPR VCKRLQVLCPFHSRDPKVPADEVCGCPLVRDVPLITGDFGRLK RCCHCRYCWERLRRAEVULERRREVULERGGRENGLFGRLEREFR PGRACHCPWCGGAGGGDFILTSRSADB	i	1	1	TVEQSTQRIREFROM (IADAQAEDQRIVEMENCGVSVTE
KIROBLOAAGSRKKUDKATMAQPLUFSKVDAVQTROWINDWITUKER MDLVDTCVOTSVETTNSVGISCOPECKNKVUOPELPHNWMITUKER VMMDRCAGRSVEMCDKSVSVEVSVCETGSNTEBSVADLITLIKT NIMIKEVRSIGCODCSVDVTVCSPIEGASRQNTEAVSQVEAAV MAVPFRADQDTSTDLEQVNQFTNTETATLIBSCTNTCLSTLDKQ MAVPFRADQDTSTDLEQVNQFTNTETATLIBSCTNTCLSTLDKQ TSTQTVETETVANGEGRVKDINSSYKTRSIGGGTLLSGHSGFDR PSAVKTKESGVGOININDMYLLVARTIACEPPOINTGLTASK RSVGVCDDDFVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAEMYSSLARAFGEPHSQMSLNSQLISTILSINSVKASAT EELRNPDFQKTSLGKTTGSYLGYTCKCGGLQSGSPLSSQTTQPE QEVGTSEGKPISSLDAPPTQEGTLSFVNLIDTDQLAAGLYACTINN ESTLKSIMKKKCNKLSNGAKKNLQFVGINGGYETTSSDDSSSD ESSSSSDDDEDVIEYPLEEEEEEEDBDTRGMAEGHHAVNIEGL KSARVEDEMQVQSCEPEKVSIRRYYSLSSKMLSACNLLKNTIND PKALTSKDMRFCLNTLQHEMFRYSQSKAIPAWODYIAAFEAI SPDVLRYVINLADGNGNTALHYSVSHSNPEIVKLLLDADVCNVD HQNKAGYTFIMLAALAAVEAEKDMRIVELFGCGDVNAKASQAG CTALMLAVSHGRITDMVKGLLACADVNIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLENNDGSTALSTALEASEHG HVBIVKLLLAQPGCNGHLENNDGSTALSTALEASEHG HVBIVKLLLAQPGCNGHLENNDGSTALSTALEASEHG HVBIVKLLLAQPGCNGHLENNDGSTALSTALEASEHG HVBIVKLLLAQPGCNGHLENNDGSTALSTALEASEHG HVBIVKLLLAQPGCNGHLENNDGSTALSTALEASEHG HVBIVKLLLAQPGCNGHLENNDGSTALSTALEASEHG HVBIVKLLLAQPGCNGHLENNDGSTALSTALEASEHG HVBIVKLLLAQPGCNGHLENNDGSTALSTALEASEHG HVBIVKLLLAQPGCNGHLENNGSQLAGAGAVVPQLEELDSTTEL DGHQEVEKVQPPGPVKEMAHGSQLALGTLVYKOPLETTSL GKUSVALSSSSIRVAMLEERGREVLMEGKLTHKINTESSLWSL GKUSVALSSSSIRVAMLEERGREVLMEGKLTHKINTESSLWSL GKUSVALSSSSIRVAMLEERGREVLMEGKLTHKINTESSLWSL GKUSVALSSSSIRVAMLEERGREVLMEGKLTHKINTESSLWSL GKOVSVALSSSSIRVAMLEERGREVLMEGKLTHKINTESSLWSL GKOVSVALSSSSIRVAMLERGREVLMEGKLTHKINTESSLWSL GKOVSVALSSSSIRVAMLERGREVLMEGKLTHKINTESSLWSL GKOVSVALSSSSIRVAMLERGREVLMEGKLTHKINTESSLWSL GKOVSVALSSSSIRVAMLERGREVLMEGKLTHKINTESSLWSL GKOVSVALSSSSIRVAMLERGREVLMEGKLTHKINTESSLWSL GKOVSVALSSSSIRVAMLERGREVLMEGKLTHKINTESSLWSL GKOVSVALSSSSIRVAMLERGREVLTHEGKULHKKRUPAGA KDABABLOC/LGP/CDP/CVCRAQPSKYCSDDCMKLAANRIYEIL PGRIQOMQGSCIABEHGKKLLERIRREGOSATRILGEMERFFH URLATLIRAKGQOAVREDEESSEDTSGGGGSGRIKVNNKHPERADA VARHMERCYAKYSSOTSFGSMYFTRIGGATRIKFCDVYNQGSCT YARHMERCYAKYSSOTSFGSMYFTRIGGATRIKFCDVYNPQSKT YCKLQVUCCHH	1	1		RSVAVGAEENINDI VVIAROSROSISSI VRLEVOLRETTHDREMT
MDLVDTCVGTSVETNSVGISCQECKRKVGPELENNWHIVLEK VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT NILMIKEVRSIGCDCSVDVTVCSPKECASRGVTEAVSQVEAAV NAVPRTADQDTSTDLEGVHOFTNTETATLIESCTNTCLSTLDKO TSTQTVETRTVAVGEGVEKUNINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGOININDTLVGLKMETIACGPPGITVGLTASR RVGVGDDPVGESLENPQPOAPLCMMTGLDHYTERIGKLLAEQQ TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSISINSVMKSAST EELRNDPDGKTSLGKITGSYLGYTCKGGGLQSGPLSSQTSQFE GVVSTSGKPISSLDAPFDGGTLSPVNLTDDQTAAGLYACTNN ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSDDSSSD ESSSSBDDECDVIEYPLEBEEEEDBDTGGMASGHIAVIEGL KSARVEDEMQVQCCEPEKVSIRERYELSERMLSACNLLKNTIND PKALTSKOMRFCLNTLGHEWFKVSSGXSATPAWVGDIAAFAL SPDVLRVINLADGNGNTALHYSVSHSNFETVKLLLDADVCNVD HQNKAGYTPIMLAALAAVGARKDNRIVEELEGCGDVANKASQAG QTALMLAVSHGRIDMYKGLLACGADVNIQDDEGSTALKASEHG HVBIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNPAKAQSPGTPPLIGRTSSGDPTHGSFD SVPRAGGMMETGAABELTVOALLGITQHFWFVDGEIELDSTEL DCHGGVEKVQPFGVKEMAHGSQRAEAFCAVAGABEVPR\EPPI LPRIQEGFQKNPDSSNGAVRENYTMSGDYTDLEVVFVPKHVVK GKQVSVALSSSIRVAMLEGNERVLMSGKLTHKINTESSLWSL EEGKULVNLSKVGEYWWNAILEGEEPIDIJKINKERSMATVGE EEGAVLDRLTTDYHGKLGGKPQSHBLKVHEMLKKGWDAEGSPF GCRPPAMFINISPGAVQF GCRPPAMFINISPGAVQF GCRPPAMFINISPGAVQF GCRPPAMFINISPGRAGE SESBACBAFGRRKSEEGGRRSDTSGFGRSRKKVWNKHPERADA KDPASLPGC/LGP/CCVRPAQPSSKYCSDDCGMKLAANRIYEIL PGRQWQOSPGIAEEHGKKLLERIRREQGSARTBLQEMERFIH BLEATILRAKQQOVREDEESEMGBDSDDTOLDIFCVSCGHPINFR VALRHMERCYAKYESQTSFGSNYPTHIEGATRLGCHERPLRY VALRHMERCYAKYESQTSFGSNYPTHIEGATRLFCDVINPQSKT YCKRLQVLCPEHSRDDKYPADEVGCPLVRDVPBLTUDFCRLJK RQCLALMHLHOTTGHOPLTTDLRSSADR		Ī		MI WORL OF ACCEPTATIONATMACHINESKYVEAVVOTRDOMVGSH
VEMERICAGRS VEMCDKS VSTUSVECKTGSNTESSNDLTLLLAT. NIANKEVRS IGCGDGS VDTVTGS KACASROWNTEAVS OVERAV MAYPERTADODTSTDLEQ VHQFTNTETATL IESCTNTCLSTLDKQ TSTQTVETRIVAVGEGEVKDINSSTKRS IGVGTLLSGHSG FDR PSAVKTKESGVGOTNINDNIAVGKMETI ACGPPQI.TVGLTASH RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMSAST EELRDEPGKTSLGKITGSYLGYTCKGGGLQSGSPLSSOTSQPE QEVGTSEGKPISSLDAPFTOEGTLSPVALTDQLAAGLYACTINN ESTLKSIMKKEVGNKDENGAKKNLQFVGINGGYETTSSDDSSD ESSSSEDDECDVIEYPLEEEEEEEDBTGRGMASCHHAVNIEGL KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLOHEMVSSQKSASIPAMVGDVIAAFEAI SPDVLRXVINLADGNGNTALHYSVSHSMFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVEAEKDMRIVEELECGEDVAKASQAG QTALMLAVSHGRIDMVKSLLACGADVNIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLEDNGSTALSIALEAGHKDIAVLLYA HVNPAKAQSPOTPPLIGRISPGFTRGSFD SVPRAGGDMETGAAELYDQALLGILQHVGNVQDFFRVLFGFIJK KIDETYRLLRHESDRMGFPPGAAQALVQDFKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAREKEPVPVVQEIELDSTTEL DGHQEVEKVQPPGPVKEMAHGSQRAEAPGAVAGAAEVPR\EPPI LPRIQEGFQRNPDSYNGAVERNYTMSQDYTDLEVRVPVPKHVK GKQVSVALSSSIRVAMLEENGERVLMSGKLTHKINTESSLWSL EPGKCVLVNLSKVGEFWMAILEGEEPIDINKINKERSMATVDE EQGVLDRLIFDYHQKLQCKGPGSDTEESPFLGPRAAEEG GCRPDPAMFNISPGAVQF SESACRAFGRRSSEEGGRRSDTSGFGRSKKKUMKKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCMKLAANRIYEIL PORIQMQSPCILABEHGKKLLERIRREQQSARTRLQEMERRH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCHPIMPR VALRHMERCYARYESGTSGSMYPTRIEGATRLFCDVANPQSKT YCKRLQVLCPEHSRDPKVPADEVGCPLVEVPUFUELDFURPL VALRHMERCYARYESGTSGSMYPTRIEGATRLFCDVANPQSKT YCKRLQVLCPEHSRDPKVPADEVGCPLVEVPUFUELEDFURPL VALRHMERCYARYESGTSGSMYPTRIEGATRLFCDVANPQSKT YCKRLQVLCPEHSRDPKVPADEVGCPLVEVPUFUELEDFURPL VALRHMERCYARYESGTSGSMYPTRIEGATRLFCDVANPQSKT YCKRLQVLCPEHSRDPKVPADEVGCPLVEVPUFUELGFCRLPK VALRHMERCYARYESGTSGSMYPTRIEGATRLFCDVANPGSKT YCKRLQVLCPEHSRDPKVPADEVGCPLVEVPUFUELGFCRLPK VALRHMERCYARYESGTSGSADR	ł	1		NEW WEIGHT STREET STORE CHIKVYGPELPMNWWIVKER
NIMLKEVRSIGGGDCSVDVTVCSPRCASRGVNTEAVSQVEAV MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNICLSILDKG TSTQTVETRTVAVGEGRYKDINSSTKTRSIGVGTLLSGHSGFDR PSAVKTKESGVGQININDNYLUGLKMRTIACGPPQITVGLTASK RSVGVGDDPVGESLENPQDQAPLGMMTGLDHYIERTQKLLAEQQ TLLAEMYSELAEAFGEPHSQMGSLNSOLISTLSSINSVMKSAST EELRNDDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE QEVGTSEGKEY ISSLDAFPTQGGTLSPVNLTDDQIAAGLYACTNN ESTLKSIMKKKDGNKDSNGAKKNLQPVGINGGVETTSSDDSSD ESSSSESDDECDLYEYPLEEEEEEEDEDTRGMAEGHHAVAIGGL KSARVEDEMQVQBCCPERVGIRGYELSEKMLSACVLLKNTIND PKALTSKDMRFCLNTLOHEWFRVSSQXSAIPANVGDYIAAFEAI SPDVLRYVINLADGNGNTALHYSVSISNFEIVKLLDADVCNVD HQNKAGYTPIMLAALAAVEREKDMRIVEELFGCGDVNAKASQAG CTALMLAVSHGRIDMVKGLLACGADVNIQDEGSTALMCASEHG HVEIVKLLLAQPGCNSHLENDGSTALSIALEAGHKDIAVLLYA HVNPAKAQSPGTTPLGRKTSPGPTHRGSFD VALTENGAMPPPP GAAQALVLQVFKTPHMARQDDEKR RQLEEEKIRRKEEEEAKTVSAAAAEKEPVDVPVQEIEIDSTTEL DCHQEVEKVQPPGPVKEMAHGSQBAPGAVAGAAEVPNEPPI LPRTIGGPGKNPDSYNGAVRENTYMSQDYTDLEVRVPVHHVK GKQVSVALSSSIRVAMLEENGBRUMGGKLTHKINTESSLWSL EPGKCVLUNLSKVGEWWMAILEGGEPPIDIDKINKERSMATVDE EGGAVLDRLITPDYHQKLQGKPQSHELKVHEMLKKGNDAEGSFFR GQRPDPAMFNISPGAVQF GKPVSRVLSRSSIRVAMLEENGBRUMGGKLTHKINTESSLWSL EPGKCVLIVNLSKVGEWWMAILEGGEPPIDIDKINKERSMATVDE EGGAVLDRLITPDYHQKLQGKPQSHELKVHEMLKKGNDAEGSFFR GQRPDPAMFNISPGAVQF THPLDDDLVSRTSVQGFLMTMACPGMSDTEESPFLGFRAAEG GKPSPAMFNISPGAVQF GTHPLDDDLVSRTSVQGFLMTMACPGMSDTEESPFLGFRAAEG GKPSVLDRLIFPYHQKLQGKPCSHELKVHEMLKKGNDAEGSFFR GREAPLAFGRKSEEEGRSDTSGFGRSRHKVNMKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYSIL PQRIQQQQSPCIAEEHGKKLLERIRREQQSARTRLOGMERPH VALRHMERCYAKYESQTSFGSMYPTRIGATRLFCDVXNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGPLURDFEILTGFCRLPK RQCNHYCWEKLERAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLALMLHQTTQHDPLTTILSRSADR	ł	1	i	WEMUDECAGE SVEMCDKSVSVEVSVCETGSNTEESVNDLTLLKT
MAYPETADQDTSTDLEQVHQFTINTETATLIESCTNTCLSTLDKQ TSTQTVETRTVAVGEGRVKDINSSTKTRSIGVGTLLSGRSGFDR PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQITVGLTASR RSVGVGDDPVGESLENPQPQAPLGMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGGEPBISQMGSLNSQLISTLSSINSVMKSAST EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSGYTSQPE QRVGTSEGKPISSIDAFFTQEGTLSPVNLTDDQIAAGLYACTINN ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSD ESSSSESDDECDVIEYPLEEEBEEDEDTRGMAEGHHAVNIEGL KSARVEDEMQVQECEPEKVSIRRFYELSEKMLSGAVLKNTIND PKALITSKOMRFCLNTLQHEWFRVSSQKSAIPANVGDYIAAFEAI SPDVLRXVINLADGRGNTALHYSVSISNFEIVLLLDADVCNVD HQNRAGYTPINLAALAAVERKOMRIVEELFGCGDVMAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLEDNOGSTALSIALEAGHKDIAVLLYA HVNRAKAQSFGTPRLGSKEXTSPGFTHRGSFD SVPRAGGDMETGAAELYDQALLGILOHVGNVOPFLRVLFGFLYR KTDFYRLLRHESDRMGFPFBAAQALVLQVFKTPHMARQDDEKR RQHEEKIRKREEEEAKTVSAAAAEKEPVVPVQCIEIDSTTEL DGHQEVEKVQPFGPVKEMAHGSQBAEAPGAVAGABEVPR\BPPI LPRIQEQFQKNPDSYNGAVRENTWSGDYTDLERVYPVFWHVKW GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EFGKCVLVNLSKVGEWWNNALLEGEFPIDINKRERSMATVDE EQQAVLDRLIFDYHQKLOGKPQSHELKVHEMLKKSWDAEGSFFR GCRFDPAMFNISPGAVQF SESACEAFGRRKSEEERGRSDTGGFGRSRKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCGDDCGMKLAANRIVEIL PQRIQOWQOSPCIABEHGKKLLERIRREQGSARTRLQEMERFH BLEAIILRAKQQAVREDEGESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYARVESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPABEVCGASGDTDTLGIFCVSCGHPINPR VALRHMERCYARVESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPABEVCGASGTURDFETGFGFCRIFK RQCNNHYCWEKLERAEVDLERVRWYKLDELFFEQERNVTAMTN RAGLLALMLHQTTQHDPLTTTLRSSADR	İ	•)	NI NI VEUD CIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV
TSTQTVETRITVAVGEGRIVADINSSTRISIGGISTERS PSAVKTKESGVGOININDNYLVGLKMRITACGPPOITVGLTASH RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLLAEQQ TLLAENYSELAEAFGEPHSQMGSLINGQLISTLSSINSVMKSAST EELRNPDFQKTSLGKITGSYLGYTCKCGGIGGGSPLSSQTSQPE QEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTINN ESTLKSIMKKKDGNKDSNGAKKNLOPVGINGGYETTSSDDSSSD ESSSESDBEDECDVIEFY LEEEBEEEDEDTRGMAEGHHAVMIEGL KSARVEDEMQVQECEPEKVSIRERYELSEMALSACVLLKNTIND PKALTSKDMRFCLNTLQENFRVSGKSAIPANVGDYIAAFEAI SPDVLRYVINLADGRGNTALHYSVSSINFFIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVEREKDMRIVEELFGCGDVMAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVBIVKLLLAAPGCNCHLEDNDCSTALSIALEAGHKDIAVLLYA HVNPAKAQSPGTPRLGRKTSPGFTHRGSFD SVPRAGGDMETGAAELTYDQALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHESDRMGFPFGAAQALVLQVFKTFDHMRQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKBPVDVPVQEIEIDSTTEL DGHGEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\RPPI LPRTQCOPQKNPDSYMGAVRENTTWSQDYTDLEVRVPVPKHVK GKQVSVALSSSIRVAMLEENGERVLMGGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWKNAILEGGEFPIDDKINKERSMATVDE EQGAVDDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GGRFDPAMFNISFGAVQF SESSACEAFGRKSEEEGRRSDTSGFGRSRKHKVNWKHPERADA KOPASLPQC/LGF/DCVRPAQPSSKYCSDOGMKLAANRIVEIL PQRIQQWQQSPCIAEBHGKKLLERIRRSQGARTHLODWNPOSKT VLKRIMGRCYAKYESQTSFGSMYSTRIGGATRLFCDVNPOSKT YCKRLQVLCPEHSRDPXPAPADEVGCGLURDFELTGGFTCRIPK RQCNEHYCWEKLRRAEVDLERVRWYKLDELFEQERNVTAMTN RAGLLALMLHQTTQHDPLTTILRSSADR	1.			MANDETADODTSTDLEOVHOFTNTETATLIESCTNTCLSTLDKQ
PSAVKTKESGYGOININDNYLVGEKMRTIAGFPGITVGLITASK RSYGYGDDPVGESLENPQPQAPLGMMTGLDHYIERIQKLIAEQQ TILAENYSELAEAFGEPHSQMGSLNSQLISTLSSINSVMKSAST EELRNPDFQKTSLGKTTGSVLGYTCKCGGLQSGSELSSGTSQFE QRVSTSEGKPISSLDAFPTQBGTLSPVMLTDDQIAAGLYACTNN ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSDD ESSSSESDDECDVIEVPLEEEBEEDEDTRGMAEGHHAVNIEGL KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACHLKNTIND PKALTSKOMRFCLNTLQHEWFRVSSQKSAIPANVGDYIAAFEAI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVBAEKDMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD SYPRAGGOMETGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTPDHAARQDDEKR RQLEEEKLRRKEEEEAKTVSAAAAEKEPVPVPQEIEIDSTTEL DGHQSVEKVQPPGPVKEMAHGSQEAEAPGAVGAGAEVPR\EPPI LPRIQEQFQKNDPSYNGAVRENYTNSODYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EBGKCVLVMLSKVGGYWNNAILEGEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHBLKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF SESBACEAFGRRKSEEEGRRSDTSGFGRBRKHKVNWKHPERADA KOPASLPQCY/LGF/DCVPRAGPSSKYCSDDCGMKLAANRIYEIL PQRIQQMQSPCIAEGHCKKLLERIRREQQSARTRLCEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRIMBERCYAKYESQTSFGSNYPTRIEGATRLFCDVYNPQSKT YCKRLGVLCPEHSRDPKVPADEVCGCFLVRDVFELVPNPQSKT YCKRLGVLCPEHSRDPKVPADEVCGCFLVRDVFSLTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTTQHDPLTTDLRSSADR	Į.	į		MAYER TADOD IS TO THE TOTAL VICEGRUKDINSSTKTRS IGVGTLLSGHSGFDR
RSUGVEDDPVGESLENPQPQAPLGMMTGLDHYTERIQKLAECQ TLLAENYSELAEAFGEPHSQMGSLINGUISTISS INSVMSAST EERRNPPFQKTSLGKLTGSVLGYTCKCGGLQSGSPLSGTSQPE QEVGTSEGKFISSLDAPFTQGETLSPVALITDQLAAGIAACTINN ESTLKSIMKKKGDKNSDRGAKKNLQFVGINGGYETTSSDDSSSD ESSSSESDDECDVIEYPLEEEEEEEDDTRGMAEGHHAVNIEGL KSARVEDEMQVQSCEPEKVSITRENYELSEKMLSACKLLKNTIND PKALTSKDMRFCLNTLQHEMFRVSSGXSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNGNATALHYSVSHSNFEIVKLLLDADVCNVD HONKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVGALLACGADVNIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTFRLGKKTSFGPTHRGSST SVFRAGGDMETGAAEI,TOQALIGILOHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFFPGAAQALVLQVFKTPDHMARQDDEKR RQBLEEKIRRKEEEEAKTVSAAAAEKEFVPVVQEIEIDSTTEL DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEGFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMSGKLTHKINTESSLWSL EFGKCVLVMLSKVGEYWMNAILGEEPFDIDKINKERSMATVDE ECQAVLDRLTFDYHQKLQGKPQSHBLKVHEMLKKGWDAEGSPFR GGRFPPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQFLMTMACPGMSDTEESFFLGFRAAEEG SESBACEAFGRRKSEEEGRRSDTSGFGRSRKHKVNMKHPERADA KOPASLPQC/LGF/DCVURPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLCEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPIMPR VALRIMBERCYAKVESQTSFGSNYPTILEGATRIFCDVYNPQSKT YCKRLQVLCPEHSRDFKVPADEVGCFLVRDVFSLTGDFCRLFK RQCNRHYCKEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLALMLHQTTGHDPLTIDLRSSADR	Ì	1 .	1	DEALETTE GUGOTNINDNYLVGLKMRTIACGPPQLTVGLTASR
TILAENYSELARAFGEPHSQMSLNSQLISTLSSINSWKSATS EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSGTSQPE QBVSTSEGKPISSLDAFPTQEGTLSFVNLTDQLAAGLYACTNN ESTLKSIMKKKDCNKDSNGAKKNLQFVGINGGYETTSSDDSSD ESSSSEDDBCDVIEYPLEEEEEEDBDTRGMAEGHHAVNIEGL KSARVEDEMQVQSCEPERVEIRERYSLSEKKLSACNLLKNTIND PKALTSKDMRFCLNTLGHEWFRYSSQKSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVEAEKUMRIVEELEGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNPAKAQSPGTPRLGRKTSPGFTHRGSFD KTDFYRLLRHPSDRMGFFPGAAQALVLQVFKTFDHMARQDDEKR RQHLEEKIRRKEEEEAKTVSAAAAEKEPVDVPVQEIEIDSTTEL DCHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAASVPR\BPJ LPRIQEQFQKNPDSYNGAVRENTTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMSGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWMAILEGEEPIDIDKINKERSMATVDE EQQAVLDRLTFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF 5419 1395 259 GTHPLDPDLVSKTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRKSEEGGRRSDTSGFGRSRKHKVNNKHPERADA KDPASLDAVGCAGAGAAVYE ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFLTCHPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLALMILHQTIQHDPLTTDLRSSADR	1	l l	Ì	PSYCHOLD PAGES LENPOPOAPLGMMTGLDHYIERIQKLLAEQQ
EELRNPDFQKTSLGKTTGSYLGYTCKCGGLQSGSPLSSGTSQFE QRVGTSEGKPISSLDAPPTQEGTLSPVNLTDDQLAAGLYACTNN ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSSD ESSSESDDECDVIEYPLEEEEEEDBDTRGMAEGHHAVNIEGL KSARVEDEMQVQECEPEKVIERRYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLGHEWFRVSSQXSAIPANVGDYIAAFEAI SPDVLRTVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HQNRAGYTPIMLAALAAVEABKDMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLEDNGSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTPRLGRKTSPGFTHRGSFD SVPRAGGMBTGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLHRHPSDRMGFFPGAAQALVLQVFKTFDIMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVDVPVQEIEIDSTTEL DGHQEVEKVQPPGFVKEMAHGSQBAEAPGAVAGAEVPR\EPPI LPRIQEGFQKNPDSYNGAVRENTWSODYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVALSKVGEYWWMAILEGEEPIDIDKINKRESMATVDE EEQAVLDRLIFDYHQKLQGKPQSHELKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF SESEACEAFGRKSEEEGRSDTSGFGRSKHKKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIVEIL PQRIQQWQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH BLEAIILRAKQQAVREDEESNEGBDDDTDLQIFCVSGHPINMS VALRIMERCYAKYESQTSFGSMYPTRIEGATRLFCDVNPQSKT VCKRLQVLCPEHSRDFKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLALMILHQTIQHDPLTTDLRSSADR		ŀ	· I	TILDENVERIARARGEPHSOMGSLNSOLISTLSSINSVMKSAST
QEVGTSEGKPISSLDAFPTQEGTLSPVALITDDQIAAGLYACTINN ESTLKSIMKKKDONKDSNGAKKNLQFVGINGGYETTSSDDSSDD ESSSESDDECDVIEYPLEEEEEEDEDTRGMAEGHHAVNIEGL KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLENDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSFGTPRLGRKTSPGPTHRGSFD 5418 24 1133 SVPRAGGDMETGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAAEKEPVPVPVQEIEIDSTTEL DGHQEVEKVQPPGPVXEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEGFGNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEERGERVLMEGKLTHKLINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTPDYHQKLQGKPQSHBLKVHEMLKKGWDABGSPFR GQRFDPAMFAISPGAVQF GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG GRFDPAMFAISPGAVQF 5419 1395 259 GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAEEG SESEACEAFGRRKSEEEGRRSDTSGFGRSRKHKWWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PORIQQWQQSFCIAEEHGKKLLERIREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLOIFCVSCGHPINPR VALRHMERCVAKYESQTISFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RRGLLALMLHGTIQHDPLITDLRSSADR	[ł	}	FELDNDDFOKTSLGKTTGSYLGYTCKCGGLOSGSPLSSQTSQPE
ESTLKSIMKKKDGNKDSNGAKKNLQFYGINGGYETTSSDDSSSD ESSSESDDECDVIEYPLEEEEEEDEDTRGMAEGHHAVNIEGL KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKNTIND PKALTSKDMRFCLNTLQHEWFRVSQXSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNCHTALHYSVSHSHFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVEIVKLLLAQPGCNGHLEDNDGSTALSIALBAGHKDIAVLLYA HVNRAKAQSFGTPRLGRKTSPGPTHRGSFD SVPRAGGDMETGAAELVDOALLGILOHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRKEEEEAKTVSAAAAEKEEVPVQCEIELDSTTEL DCHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPR\EPPI LPRIQEGFQRNPDSYNGAVRENTYWSQDYTDLEVRVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMSGKLTHKINTESSLWSL EPGKCYLVNLSKVGEYWNNAILEGEEPIDLIKKINKERSMATVDE EEQAVLDRLTFDYHQKLOGKPQSHELKVHEMLKKGWDAEGSFFR GQRFDPAMFRISPGAVQF GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESFFLGPRAAEEG GCRFDPAMFRISPGAVQF SESBACEAFGRRKSEEEGRRSDTSGFGRSKKHKVNWKHPERADA KDPASLPQC/LOF/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAILLRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPBHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RRGLLALMLHQTIQHDPLTTDLRSSADR	1			OPUGTSECKDISSLDAFPTOEGTLSPVNLTDDQIAAGLYACTNN
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KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACILLKNTIND PKALTSKOMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAI SPDVLRYVINLADGNGNTALHYSVSHSNFEIVKLLLDADVCNVD HQNKAGYTPIMLAALAAVEAEKDMRIVEELFGCGDVNAKASQAG QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG HVBIVKLLLAQPGCNGHLEDNDGSTALSIALEAGHKDIAVLLYA HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD SVPRAGGDMETGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDEKR RQELEEKIRRKEEEEAKTVSAAAEKEPVPVPVGLIELDSTTEL DGHQEVEKVQPPGPVKEMAHGSQEAEAPGAVAGAAEVPN\EPPI LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVVPVPKHVVK GKQVSVALSSSIRVAMLEENGERVLMEGKLTHKINTESSLWSL EPGKCVLVNLSKVGEYWWNAILEGEEPIDIDKINKERSMATVDE EEQAVLDRLTFDYHQKLQGKPQSHBLKVHEMLKKGWDAEGSPFR GQRFDPAMFNISPGAVQF SSESACEAFGRRKSEEEGRRSDTSGFGRSKKHKVNWKHPERADA KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL PQRIQQWQQSPCIAEEHGKKLLERIRREQQSARTRLQEMERRFH ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIGGATRJFCDVYMPQSKT YCKRQVLLOPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDLTTDLRSSADR	1	1)	FEGGERSDDECDVIEVPLEEEEEEDEDTRGMAEGHHAVNIEGL
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ELEAIILRAKQQAVREDEESNEGDSDDTDLQIFCVSCGHPINPR VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKT YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR	ì	1	•	POPTOONOOS POTA ERHIGKKI JERTRREOOSARTRLOEMERREH
VALRHMERCYAKYESQTSFGSMYPTRIEGATRLFCDVYNPQSKI- YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR NPAGACOPPKGGASGRIYLSPRIDRVSVAGCEERPLGWVWVLGG)	}		PURIQUEQUE CIMEDIO AND DE CONCONTRO OTROVS CHPINPR
YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK RQCNRHYCWEKLRRAEVDLERVRWYKLDELFEQERNVRTAMTN RAGLLALMLHQTTQHDPLTTDLRSSADR NPAGACPPKGGASGPLYLSPRLPRVSVAGCEERPLGWVWVLGG			,	ELEATILE AND AND EDGE ENGLISHED TO BE THE TRUNCH OF THE TRUCK OF THE TRUNCH OF THE TRUNCH OF THE TRUNCH OF THE TRUNCH OF THE TRUNCH OF THE TRUNCH OF THE TRUNCH OF THE TRUCK OF THE TRUNCH OF THE TRUCK OF THE TRUCK OF THE TRUNCH OF THE TRUCK OF THE T
RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN RAGLLALMLHQTIQHDPLTTDLRSSADR NENGGACDEKGGASGRIYLSPRLPRVSVAGCEERPLGWVWVLGG	Į.			VALRHMERCIAKIESQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKIESATKUI COTTREQUISTOSMITIKI COTTREATICAL COTTREQUISTOSMITIKI COTTREQUISTOSMITIKI COTTREATICAL COTTREATIC
RAGLIALMLHQTIQHDPLTTDLRSSADR NENGACDEKGGASGRIVISPRLPRVSVAGCEERPLGWVWVLGG		}	į	YCKRLQVLCPEHSKDPKVPADEVCGCPHVRDVFHHEIGDFCKMTK
NENGGACPEKGGASGRI, VI.SPRI, PRVSVAGCEER PLGWVWV LGG				ROCKET AT MY HOSTOUDDLE STOPP DECADE
5420 117 1733 NEAGGACPFRGGASGRLILDFRDFRUSVAGGBERT BOWN AGGELPHERIK GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR	}			KAGLLALMUNGTIQMUPTITULKSSADA
GGFLPAKPPKAQKILIGI SIYALQSIYLIKE 212 VIG VIG Q21	542	0 117	1733	NEAGGAUPERGGASGREEDSPREARVOVASCEEMED SON THE S
		<u> </u>		GGREFAKALKWÖKUTGL SUWEÖSHEWE DI BATGALTE

	SEO	Predicted	1 5-232-4-3	
	ID	beginning	Predicted end	
	NO:	nucleotide	nucleotide	I wentuitie, CECVSCOING N-Accepted Acts of
	}	location	location	Glucamic Acid, F=Phenvialanine C_Cl
	1	corresponding	corresponding	A=HISCICINE, I=Isoleucine V-Typine
	İ	to first	to first	L=Leucine, M=Methionine N=Asparagine
	1	amino acid	amino acid	P=Proline, O=Glutamine, P-Arginine
	ļ		residue of	S=Serine, T=Threonine, V=Valine
	1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown + G==
	Í	amino acid	sequence	[Codon, /=possible nucleoride delories
	ļ	sequence		\=possible nucleotide insertion)
	l			ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/
	1	1	1	LLELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGS
		1	1	LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLGRV
			1	YETVVMIMILTILLE CMUREDON TURNOUT TO THE SEGFAGSREGULGRV
			1	YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP
		1		YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE
				QLYCSAFEEAALTRICNPTSCWLPLDMELLHRQVLALQTQRVL
		}		LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID
- 1		1		EAAMPRGMQGTSLGQVSFSXLGSFGAVIQVVLIFYLMVSSVVGF
- 1		1		YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL
- 1		1	1	TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV
1	5421	117	1733	RAELIRAFGERE
- 1		1	1/33	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG
- (1		GOF DPARPPRAQRHLGFSHAEOSMEADDVEVI.GVDBOT BUDD TD
-			}	ECIISTLLEATLYILCHIFLTRFKKPAFFTT\CMMVMDDcmpr /
- [LEGGIF TUATALGAVLLLPFSIISNEVIT, ST. DDNVVTONI NOS
-			ĺ	LINGLWALVELESNLSLIFLMPFAYFFTESEGFACEDVOUS
-]		YETVVMLMLLTLLVLGMVWVASAIVDKNKANDESI,VDEWEVVI D
-1		}		YLYSCISFLGVLLLLLVCTPLGLARMFSVTGKLLVKDDLLEDLED
- }		1		QLYCSAFEEAALTRRICNPTSCWLPLDMELLHROYLALOTOPYT
-				LEKKRKASAWQRNLGYPLAMLCLLVLTGI.SVI.TVATUTI ELL TO
П		!		BAAMPRGMQGTSLGQVSFSKLGSFGAVTOVVT.TEVI.MUSCUNGE
ı				ISSPERSERPRWHDTAMTOLIGNCYCLLAT.GGALDURGDWG Gr
				TREDLEGDEGRENWLGNEYIVELYNAAFAGLTTLCIJKTETAAN
H	5422			RABBIRAFGERE
1	3122	3	1263	SCGESLPTWLAGASRPGIGRKGGAWGGRGGSSPAQVLLSPGPVF
1				MAGCHWWHLSKDQAGVORCDLGSSOPPDIGFKPFSCIST Decking
1				I INDIVICES MEADLSGFNIDAPRWDORTELCDVEUE NITTORS (
1	ĺ			TVFVSERELDWAKVMVEKSRMGVVPPGTOVEOLLVAKKI VDCAR
1				APDIGERMOVIGEMSFOLPGGMIITGFMLOFVDTMDAVITEMONT
1				NQSFNALVNYINRNAASPTSVROMALSVETATTTTAVATAVOLANA
J	1	i		LIKKAPPLIVGRWVPFAAVAAANCVNI DMMDOORI TVCTCUVDDA
	,	· f		ENEIGHSKRAAAIGITOVVISRITMSAPGMTI.DUTMPDI PUTT
		1		FMQKVKVL/SAPLQVMLSGCFLIFMVPVACGI.FDOVCPT.DVGVT
⊬	5423		·	EPKLQDTIKAKYGELEPYVYFNKGL
1	3423	3186	905	GVSMALGEEKAEAEASEDTKAQSYGRGSCRERELDIPGPMSGEQ
	Í			PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD
1	1	1		ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE
	ł			EXPOILS DERITICS GHDADTEDDES LADI. POAT. DI COOPUCCO
1	1	1		LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQERAEPRG
1	j	1	i	GSLARVSSSLEPVVPOEPSSVVGLGPRPOWSPOPVESCOPACT
	- 1	J		GRRRLSFQABYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT
	1	!		YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP
1	i		1	TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW
		1	ł	SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL
		1	Ì	RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY
1	1	J		LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
			ł	PASFPSSSQSQLPPGAALQGSGDPEGQNPCFLRS FVRAHDSAG
	1	<u> </u>	Ì	EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
	1		}	GGEQGKESLVQC\VKTFC\CQLEBLICWLYNV\ADVTDHGTPAR
		1	-	SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE
	ļ	ļ	1	MTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP
_			1	DKKPMAAMEHPCEGV
	5424	3186		
	1		=	GVSMALGEEKAEABASEDTKAQSYGRGSCRERELDIPGPMSGBQ
	l		1	PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD
	1	ĺ	1	ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE
	1			EFPOTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG
	J		į.	LSCLSQWKSVLSPGSAAOPSSCSISASSTGSSLOCHOFDAFDDC
	ł	1	1.3	GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL
	- 1	l l	1,	GRRRLSFQAEYWACVLPDSLPPSPDRHSPI.WNPNWRYPDI.I DUT
		ĺ	<u> </u>	IPLKPGPQLPKHLDSRVPADPVLODSGVDI.DSFSVSDA CTI.USD
_				TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ľ	i e		Codon, /=possible nucleotide deletion,
ļ	amino acid	sequence	\=possible nucleotide insertion)
i	sequence	L	\=possible nucleocide insercion/
	I]	SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL
1	1	Ì	RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY
1	}	ì	LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
1	(PASFPSSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG
1	ł	ł.	EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
1	ì	l	GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
1	1	Į.	SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE
Į.	1	1	NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP
l		1	DKKPMAAMEHPCEGV
			GFCPSPSLGHQPPRVLHPTMSMAVETFGFFMATVGLLMLGVTLP
5425	1086	115	
1	1	Į.	NSYWRVSTVHGNVITTNTIFENLWFSCATDSLGVYNCWEFPSML
[ALSGYIQACRALMITAILLGFLGLLLGIAGLRCTNIGGLELSRK
{	1	1	AKLAATAGAPH\ILPGICGMVAI\SWYAFNITR\DFSDPLYPGT
1			KYELGPALYLGWSASLISILGGLCLCSACCCGSDEDPAASARRP
İ	1	}	YQAPVSVMPVATSDQEGDSSFGKYGRNALRVAALCRGPRCLPTA
}			PKKRGPGRGPFPYSNLRGRPRPVPVAPPRPRPRVLHSHGPSQAK
1		J.	NCSWEVAYLPSEAGSLIF
5426	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
1	i	1	PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA
1		}	GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL
1		1	TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK
l	l.	1	LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRI IGVKVHPGQR
1	j	1	KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL
1	Ì		EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD
1	([TMINDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
1	i .	1	LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN
]]	1	POMGETAEAMAHEAAGAETEAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA
	1	1	POWGELIEAMAHEAAGGETEAEALDWDADADADADADAGGA
1	1		LQASVLDDWFPLQGGQGQVHLRLEWISLLSDAEKLEQVLQWNWG
	1	į	VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
ì	ţ		MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV
1	1	•	KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
ļ	}	1	KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR
1	1	l l	PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
1	1	į	VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF
}	1		DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL
Į.		1	ERLTPRPTAABLEEVLQVNSLIQTQKSAELAAALLSIYMERAED
1			LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
1	· I		RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL
1]	1	SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS
[1	GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE
1			ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ
}			KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
1	1	1	LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
			TOWARD TOTOR ON TOTOR OF THE TO
5427	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
1		İ	PAAHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA
1			GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL
J	1	1	TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK
1		1	LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR
i		1	KEOILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL
1	1		EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD
1]	TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
1		İ	LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN
1		1	PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV
1		1	LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG
1		1	VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
ı		1	ASSKIDA LUDIMOEDAN INDUMENTALIA TORDITET ADVICOMINENTALIA
1	1	1	MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV
1			KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
1	Į.		KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR
1		1	PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
1	1	}	VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF
1	1	1	DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL
1		1	<u> </u>

SEQ	1000		
ID	Predicted beginning	Predicted end	The state of the containing commit well and the state of
NO:	nucleotide	nucleotide	Maraidnine, CaCvsteine, Dalamartic Acid n
1	location	location	Grundmic Acid, F=Phenylalaning C_Cl
1	corresponding	corresponding to first	n=nistidine, I=Isoleucine, Kulycine
1	to first	amino acid	Debeucine, MeMethicnine, Nelsparagies
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
<u> </u>	sequence		Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			ERLTPRPTAAELEEVLQVNSLIQTQKSAELAAALLSIYMERAED
1	1		LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
ļ	}		RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL
			SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS
	ĺ	1	GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE
1		Į	ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ
1	j		ARKIDSPEENERFEWELPLDEAORRKLDVSVKSNSSEMEDEDET
5428	3		LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
1 3420	1 3	1839	SSRSERLSACATAPPWLVSSRPARPAOLORPGKMVFDGAFRLED
-			LVHFSVSELPSRGYGVMEEIRROGKLCDVTLKIGDHKFGAHDIV
1			LAASIPYFHAMFTNDMMECKODEIVMOGMDPSALEALINEAVNC
1		1	NLAIDQQNVQSLLMGASFLOLOSIKDACCTFLPFPI.UDVNGLGIV
i	•	İ	ROFAETMMCAVLYDAANSFIHOHFVEVSMSEFFIALDI EDVI DI
- }	1		VSRDELNVKSEEQVFEAALAWVRYDREQRGTFL\RNLQSNIRLL
Ì	· J		FCRPQFLSDRVQQDDLVRCCHKCRDLVDEAKDYLLMPERRPHLP
1		1	AFRTRPRCCTSIAGLIYAVGGLNSAGDSLNVVEVFDPIANCWER
Ì		İ	CRPMTTARSRVGVAVVNGLLYAIGGYDGQLRLSTVQAYNTETDT
)	j		WTRVGSMNSKRSAMGTVVLDGQIYVCGGYDGNSSLSSVETYSPE TDKWTVVTSMSSNRSAA\GVTVFEGRIYVSGGHDGLQIFSSVEH
l			YNHHTATWHPAAGMLNKRCRHGAASLGSKMFVCGGYDGSGFLSI
			AEMYSSV\ADQWCLIVPM\HTRR\SRVSLGGPAVGRLYAVWGVT
	1		TGQSNL\SSVGDVLTPETDCWTFM\APMACHEGGVGVGCIPLLT
5429			1 *
3123	828	202	RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPF
i			AQRERFHRFQPTYPYLOHEIDLPPTISTSDGFFPDDVOCDCTG
ł	1		LEDPEQQUELNRESVRAPPNRTIFDSD_MDSARIGGPCDBCCNC
			GISAICIGSGGRMEGPPP\TYSEVIGHVPGSSEOUOOGCGPPGr
5430	441	1507	DEGTRUHHTHIAPLESAAIWSKEKDKOKCHDI.
		1307	QKRRKRRKKIMKTIQPKMHNSISWAIFTGLAALC_FQGVPVRS
1	1		GDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYA
1	1		GNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDN HPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEP
1	1		TVTWRHISPKAVGFVSEDBYLEIQGITREQSGDYECSASNDV\A
f	1		APV\VRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSA
Í	i i		EFOWYKDDKRL1/EGKKGVKVENRPFLSKL1FFNVSEHDYGNYT
1		[CVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVL
5431	 		RIGHE
1 2431	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
1 .	Į l		LPGITINP\TIAEGPSP\TSEGASEANIJIDIOVVI EEL EL PROS
]	[ARKIEAFLTQKAKVGELKDDDFERTSELGAGNGGUUTVUOLIDDG
		İ	GLIPHARALIMUEI RPAIRNOI IRELOVI, HECNEDVIVOEVON DV
		ļ	SUGEIST CMEHINDGGSLDOVLKEAKRIDEETI.GKVCTAVIDGIN 1
1 1]	İ	YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS
, · ,	[[FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP DAKELFAIFCRDUNGCHSCHDWAYSCHLAVGRYPIPPP
1 1		l	DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP
			AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV
5432	2	1312	AAAAPGSRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
[1	. 1	LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ
[]			KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS
!		ļ	GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY
		į	SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA
1	1	1	YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS
1	Į.	;	FVGTRSYMAPERLQGTHYSVQSDIWSMGLSIVELAVGPVDTDDD
1	ļ	į.	DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGUGMDCPD
1	i	1.4	AMAIFELLDYIVNEPPPKLPNGVFTPDFOEFVNKCIIKNDARDA
5433	360		DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNOPGTPTRTAV
	300	1885	SVQEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLJECLGEDGY
- 1		1 -	DEGMPSEVEVEKNEDYFKDLCGPDAGPIGNATGOADCKAODERE
		!	SLIFTLGSFMNNFMTFPTGYIFDRFKTTVARLIAIFFYTTATLI

	_		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
מז	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
[corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ .	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ		<i>2</i>	Codon, /=possible nucleotide deletion,
l .	amino acid	sequence	\=possible nucleotide insertion)
<u> </u>	sequence	<u> </u>	IAFTSAGSAVLLFLAMPMLTIGGILFLITNLQIGNLFGQHRSTI
		1	ITLYNGAFDSSSAVFLIKLLYEKGISLR/VLLHLHLCLQYLAC
{		1	ITLYNGAPDSSAVFLIREDIERGISHR/VBBRUHECDGIGAC
j	1	1	STHFPPDAPGAHPIPTAPQLQLWPVPWEWHHKGREG/QQLSMKT
	1		GSYSQRSSFQRRKRPQGQGRSRNSAPSGATL/CSRRFAWHLVWL
ì	1	§	SVIQLWHYLFIGTLNSLLTNMAGGDMARVSTYTNAFAFTQFGVL
ì	l .	ì	CAPWNGLLMDRLKQKYQKEARKTGSSTLAVALCSTVPSLALTSL
1	[İ	LCLGFALCASVPILPLQYLTFILQVISRSFLYGSNAAFLTLAFP
1		1	SEHFGKLFGLVMALSAVVSLLQFPIFTLIKGSLQNDPFYVNVMF
i		1	MLAILLTFFHPFLVYRECRTWKESPSAIA
1	l		RYAALIISLIQHKLLWRNQHCSRCVIMSPAQSAGLNWLF/GSGK
5434	66	652	RYAALITSLIQHKLLWRNQHCSKCVIMSPAQSAGIMHDF/GSGK
ì		ì	HGPFLGCSQYPACDYVRPLKSSADGHIVKVLEGQVCPACGANLV
1	1	1	LRQGRFGMFIGCINYPECEHTELIDKPDETAITCPQCRTGHLVQ
	1		RRSRYGKTFHSCDRYPECQFAINFKPIAGECPECHYPLLIEKKT
Į	1	1	AQGVKHFCASKQCGKPVSAE
5435	4704	1597	PGDSSQRLAEMSNAKERKHAKKMRNQPTNVTLSSGFVADRGVKH
3733	1 7/03	1	HSGGEKPFOAOKOEPHPGTSRQRQTRVNPHSLPDPEVNEQSSSK
]			GMFRKKGGWKAGPEGTSQEIPKYITASTFAQARAAEISAMLKAV
1	1	1	TOKSSNSLVFOTLPRHMRRRAMSHNVKRLPRRLQEIAQKEAEKA
1	1		VHQKKEHSKNKCHKARRCHMNRTLEFNRRQKKNIWLETHIWHAK
1	1		RFHMVKKWGYCLGERPTVKSHRACYRAMTNRCLLQDLSYYCCLE
	1	1	REHMVKKWGICLGERPIVKSHKACIKAHINKCHBQDEDIICEBS
l .	į		LKGKEEEILKALSGMCNIDTGLTFAAVHCLSGKRQGSLVLYRVN
1	(Į.	KYPREMLGPVTFIWKSQRTPGDPSESRQLWIWLHPTLKQDILEE
1		1	IKAACQCVEPIKSAVCIADPLPTPSQEKSQTELPDEKIGKKRKR
[1	KDDGENAKPIKKIIGDGTRDPCLPYSWISPTTGIIISDLTMEMN
1		ļ	RFRLIGPLSHSILTEAIKAASVHTVGEDTEETPHRWWIETCKKP
1	l l	i	DSVSLHCROEAIFELLGGITSPAEIPAGTILGLTVGDPRINLPQ
1	ſ	!	KKSKALPNPEKCQDNEKVRQLLLEGVPVECTHSFIWNQDICKSV
	4	l .	TENKISDQDLNRMRSELLVPGSQLILGPHESKIPILLIQQPGKV
,	1	1	TGEDRLGWGSGWDVLLPKGWGMAFWIPFIYRGVRVGGLKESAVH
1	1	1	SQYKRSPNVPGDFPDCPAGMLFAEEQAKNLLEKYKRRPPAKRPN
Į.	1	1	YVKLGTLAPFCCPWEQLTQDWESRVQAYEEPSVASSPNGKESDL
I	į.	4	YVKLGTLAPICCPWEQLIQDWESKVQAIBEESVINDICCOFEAC
i	1	•	RRSEVPCAPMPKKTHQPSDEVGTSIEHPREAEEVMDAGCQESAG
1	1	1	PERITDQEASENHVAATGSHLCVLRSRKLLKQLSAWCGPSSEDS
1	ł	{	RGGRRAPGRGQQGLTREACLSILGHFPRALVWVSLSLLSKGSPE
1	1	l .	PHTMICVPAKEDFLQLHEDWHYCGPQESKHSDPFRSKILKQKEK
1	•	ľ	KKREKRQKP\GRASSDGPAGEEPVAGQEALTLGLWSGPLPRVTL
1		§	HCSRTLLGFVTQGDFSMAVGCGEALGFVSLTGLLDMLSSQPAAQ
1			RGLVLLRPPASLQYRFARIAIEV
<u> </u>	 	635	ASDS I PWSEARTTRKLAQRGCQWSLPERMPLVVFCGLPYSGKSR
5436	1781	625	RABELRVALAAEGRAVYVVDDAAVLGAEDPAVYGDSAREKALRG
1	1		ALRASVERRLSRHDVVILDSLNYIKGFRYELY\CLARAARTPLC
1			WINNO A ENCHORUDA A LEDOCHAL TROUBLE L'ON TOUR LE DOCUMENT DE L'ON TOUR LE DOCUMENT DE L'ON TOUR LE DOCUMENT DE L'ON TOUR LE DE L'ON TOUR LE DOCUMENT DE L'ON TOUR LE DOCUMENT DE L'ON TOUR L'ON TOU
		1	LVYCVRPGGPIAGPQVAGANENPGRNVSVSWRPRAEEDGRAQAA
1		1	GSSVLRELHTADSVVNGSAQADVPKELEREESGAAESPALVTPD
1			SEKSAKHGSGAFYSPELLEALTLRFEAPDSRNRWDRPLFTLVGL
1 .	1		EEPLPLAGIRSALFENRAPPPHQSTQSQPLASGSFLHQLDQVTS
1	1	ļ	OVLAGLMEAQKSAVPGDLLTLPGTTEHLRFTRPLTMAELSRLRR
(1		ORISYTKMHPNNENLPOLANMFLQYLSQSLH
	730	1672	CQEAASEFGGPLHTPAMFLRRLGGWLPRPWGRRKPMRPDPPYPE
5437	739	10/2	PRRVDSSSENSGSDWDSAPETMEDVGHPKTKDSGALRVSRAASE
- }	1	l	PSKEEPQVEQLGSKRMDSLKWDQPISSTQESGRLEAGGASPKLR
1	1	1	WDHVDSGGTRRPGVSPEGGL\GVPGPGAPLEKPGRREKLLGWLR
1	[WUNVUSGETRREGYSEGGU GVEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
1	1	1	GEPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR
- 1	\	1	AALDTLGLRGPLGLWLHGLLSFLAALHGLHAVLSLLTAHPLHFA
1	1	i i	CLFGLLQALVLAVSLREPNGDEAATDWESEGLEREGEEQRGDPG
1	į.	Ì	KGI,
5438	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
"""	2332]	LAPPSLRRPMMCOSEAROGPBLRAAKWLHFPQLALRRRLGQLSC
ſ	i		MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
ļ	1	1	VPTRLLSRAWGRLNQVELPHWLRRPVYSLY:WTFGVNMKEAAVE
	I	1	VE TRUBBLE THE TANK THE TRUBBLE THE TRUBBLE TO THE COURT
1	1		I DI DUNDONI GEREROKI KOMARDVI AITHEVIELOUKI IMPGOVA
		·	DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT

SEO	Predicted	T	
ID	beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cvsteine, D=Aspartic Acid E
	location	location	Glucamic Acid, F=Phenylalanine G-Glucino
- 1	1	corresponding	H=H1St1dine, I=Isoleucine, K=Jusine
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP
ı	1		GMARWIKELECHNERUM TODWYGDROL TOWN
	1		GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY
1	1	ļ	FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/OS
5439	2443	1152	FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALGSL
ì	1	1132	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
1	1	1	LAPPSLRRPMMCQSEARQGPELRAAKWLHFPQLALRRRLGQLSC
ì	İ		MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
		1 .	VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE
l l	}	1	DLHHYRNLSEFFRRKLKPOARPVCGLHSVISPSDGRILNEGOVK
		1	NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNOLUT
1	ľ	ł	REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSIMSVND
i	i		GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\ NWCSIDIV
		[FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALDGEHLG/OS
5440			FNLGSTIVLIFEAPKDFNFOLKTGOKIRFGEALGSI.
3440	693	253	EPIPVTPDHRLVTMTHIV\QTFSPVNS\GOPPNYEMLKEFOEVA
1	1	i	MLGAPHNPAPPMSTVIHIRSETSVPDHVVWSLFNTLFMNTCCLG
1	Ì		FIAFAYSVKSRDRKMVGDVTGAQAYASTAKCLNIWALILGIFMT
<u> </u>			ILLIIIPVLVVQAQR
5441	2	2054	CRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFFSFIN
	l .		NSDLWVANIETGEERRLTFCHQGLSNVLDDPKSAGVATFVIQEE
]			FDRFTGYWWCPTASWEGSEGLKTLRILYEEVDESEVEVIHVPSP
1	ļ		ALEERKTDSYRYPRTGSKNPKIALKLAEFQTDSQGKIVSTQEKE
			LVQPFSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVLL
1			PPALPIPSTENEEQ\RLASARAVPRNVQPYVVYEEVTNVWINVH
1			DIFYPFPQSEGEDELCFLRANECKTGFCHLYKVTAVLKSQGYDW
			SEPFSPGEGEQSLTNAIWVNEETKLVYFQGTKDTPLEHHLYVVS
1 1			VEAAGETVDI.TTDGEGUGGGMGOVTDVTVGTKDTPLEHHLYVVS
1	1		YEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHYSSVSTPPCVHVY
			KLSGPDDDPLHKQPRFWASMMEAAKIFHFHTRSDVRLYGMIYKP
1 1			HALQPGKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGY
			AVVVIDGRGSCQRGLRFEGALKNQMGQVEIEDQVEGLQFVAEKY
1 1	}		GFIDLSRVAIHGWSYGGFLSLMGLIHKPQVFKVAIAGAPVTVWM
]			AYDTGYTERYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLILH
1 1	ţ	ſ	GFLDENVHFFHTNFLVSQLIRAGKPYQLQVALPPVSPQIYPNER
5442	1	3474	HSIRCPESGEHYEVTLLHFLQEYL
1 1		34,4	CGORSRRSPDMPEAKPAAKKAPKGKDAPKGAPKEAPPKEAPAE
1 1	- 1		APKEAPPEDQSPTAEEPTGVFLKKPDSVSVETGKDAVVVAKVNG
1	1		KELPDKPTIKWFKGKWLEIGSKSGARFSFKESHNSASNVYTVEL
l i		1	HIGKVVLGDRGYYRLEVKAKDTCDSCGFNIDVEAPRQDASGQSL
1 1	ļ	1	ESFKRTSEKKSDTAGELDFSGLLKKREVVEEEKKKKKKDDDDLG
1 1		}	IPPEIWELLKGAKKSEYEKIAFQYGITDLRGMLKRLKKAKVEVK
1 1		1	KSAAFTKKLDPAYQVDRGNKIKLMVEISDPDLTLKWPKNGQEIK
1 1	1		PSSKYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCETELEV
1	1	ĺ	KEPPVLIVTPLEDQQVFVGDRVEMAVEVSEEGAQVMWMKDGVEL
1	ł	1	TREDSFKARYRFKKDGKRHILIFSDVVOEDRGRYOVITNGGOCE
1 1			AELIVEEKQLEVLQDIADLTVKASEOAVFKCEVSDEKVTCKWVK
1 (. 1	NGVEVRPSKRITISHVGRFHKLVIDDVRPEDEGDYTFVPDGVAL
1		1	GSLSAKLNFLEIKVEYVPKO\EPPKIPIGFASGGKTSFNAD /TU
1 1	[VVAGNKLRLDV\SITGEAPSPFAT\WLKG\DEVETTTEGPTPTE
1	1		KRVDCSSFVIESAQREDEGRYTIKVTNPIGEDVASTFI.OVVDVD
[]	1	1	DPPEAVRITSVGEDWAILVWEPPMYDGGKPVTGYLVERKKKGSO
	-	!	RWMKLNFEVFTETTYESTKMIEGILYEMRVFAVNAIGVSQPSMN
1		1	TKPFMPIAPTSEPLHLIVEDVTDTTTTLKWRPPNRIGAGGIDGY
}		i	LVEYCLEGSEEWVPANTEPVERCGFTVKNLPTGARILFRVVGVN
1		-	IAGRSEPATLAQPVTIREIAEPPKIRLPRHLRQTYIRKVGEQLN
j		<u> </u>	LVVPFQGKPRPQVVWTKGGAPLDTSRVHVRTSDFDTVFFVRQAA
1	[RSDSGEVELSUOTEMWINDS DED
	1	J ;	RSDSGEYELSVQIENMKDTATIRIRVVEKAGPPINVMVKEVWGT
1	1	1:	NALVEWQAPKDDGNSEIMGYFVQKADKKTMEWFNVYERNRHTSC
	1	1	TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK
	İ		PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV
1			VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV
			NELGEALABCKLEVRVPQ

g signal peptide partic Acid, B= ne, G=Glycine, =Lysine, sparagine, ginine, ine,
ne, G=Glycine, =Lysine, sparagine, ginine, ine,
=Lysine, sparagine, ginine, ine,
sparagine, ginine, ine,
ginine, ine,
ine,
Unknown, *=Stop
deletion,
ion)
SSSSPRRSRSAAEPA
GESIGNCPFSQRLFMI
THPPFITFNSEVKTDV
AGMDIFAKFSAYIKNS
DEIDENSMEDIKFSTR
YRNFDIPKEMTGIWRY AKRLHQVKSRLLKEVS
AKKENOVKSKEBKETE
QPPTPDYTESDILRAY
SKNPGDAKYGSPKHRL
LDPFDAQPHPAPPDDG
QDPETADGPPSGQKPR
PAFAVQFDSPEWERTPG
PWFHGPLNRADAESLL
GFLHLKFARTRENQVV
YEHLYTLYBAALGIB*Ö
AAAHPGLHRERHPEGLP
LQEPRRCQVWFSQAPAH
TWARRRWRETRSRREPT
SEPYPSQLLKPIPEYSP
SSGDFSQAHSTLKLANH
PGLGKAFPSGCSAVSEP
QLSAASPDTGHDSDKSD
AGLDLPTIDTGYDSQPQ
RSREFPQFEPQRYPACA
PYGHDYPRAAYQQVIQP
PWDQEERPAQRDCSFPG
ELRPQVPQPPSPAAVPR
SMDTAMEVVKFVNFLLV
RDKTVMIIVAISPKYKQ EFIKQGSMNFRFIPVLF
LLRLLREEEYVAPPRGP
DEREBREEST VIII I NOT
RAATKLTEEKYELKEGO
MPKTLACTERPSKNSHP
DSGLYQCVIYQPPKEPH
VYKIPPTTTKALCPLYT
VTDIIRVPVFNIVILLA
PTRMSSDFQPHPSGSCA
GSFNATGOOKDTSGVAR
DPGGYRLPLAQLGRSDR
SLWTSHVPASHMPLAAA
Olgssłókkkcedcaaba
PAGRAPAPLYVGPGVSEF
PVNTIQWCPVLSKSHML
ITEAVRAARWAPCGRRIL
RITTLKFHPKDHNIFLCG
TLDILFLREGSEFLSSTD
FHERFTCPSLALHPREPV
YEGHKVEGYSVGCECSPG
LQGHTQACVGTTYHPVLP
AIGDLAPARGYSGPGRSL
<u>QLPALSK</u>
SVEQREIKGLRNKPKKTA
TSLTTKGIVRVVFFPFFF
ISLTTKGIVRVVFFPFFF VLFCSTSSPHSIPLTEVI
isltikgivrvvffpfff Vlfcstssphsipltevi Stggkrrrklrkaahlev
ISLTTKGIVRVVFFPFFF VLFCSTSSPHSIPLTEVI

SEO	Predicted	Predicted end	T
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	1	[A=Alanine, C=Cvsteine, D=Aspartic Acid p
	location	location	Glutamic Acid, F=Phenvlalanine G-Clusina
- 1	corresponding	corresponding	H=H1Stidine, I=Isoleucine, K=Iarsine
j	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
	residue of	residue of	S-Serine, T-Threonine, V-Valine
(amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *~Ston
1	sequence	sequence	Codon, /=possible nucleotide deletion
}	sequence	<u> </u>	\=possible nucleotide insertion)
		ľ	IRPEETAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGYSL
1			RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSGTSCSSPCSSS
1	1		QUSESARPESETEDVLWEDLLHCAECHSSCTSRTDVENHOTNDC
	ŀ		VKKEYRDDPFHQSHLPWLHSSHPGLEKISATVWEGNDCKKADMC
- [1	VLEISGMIMNRVNSHIPGIGYOIFGNAVSLILGI.TDRUFPLEON
1	1		TDLEQLTAHSASELYVIAFGSNEDVIVISMVIISTVADVELIMIT
	1		FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYDNRDADV
	1	1	SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT
		Ì	SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI
	İ		VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI
	1	1	LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV
5449	194	1833	IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
		1033	MASKVTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA
1	-}		HVKPDLIDVDLVRGSAFAKAXPESPWTSLTTKGIVRVVFPPFFF
İ			RWWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI
			GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRRKLRKAAHLEV HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS
			GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCET
ł	1		IRPEETAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGYSL
ŀ	1		RRHVDRTSEGVLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSSSR
			QDSESARPESETEDVLWEDLLHCARCHSSCTSETDVENHQINPC
	(VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS
1	1 1		VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA
1	}		TDLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVURVSIANT
		ļ	FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDADK
1	1		SGTSCSSRCSSSRQDSESARPESETEDVLWEDLIHCAECHSSCT
1 .	1		SETDVENHQINPCVKKEYRDDPFHOSHLPWLHSSHPGLEKISAI
			VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYOIFGNAVSLT
]	l i		LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDUTVLSMV
5450	8136	1242	IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
1	0130	1242	GQQFASFFG*NHPEVTVAMALTDIDLQLQFSMSQPEALLLLAAG
1	j	j	PADHLLLQLYSGHLQVRLVLGQEELRLQTPAETLLSDSIPHTVV
1 .]	İ	LTVVEGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGLP
	1	1	YLRGTSRPLRGCLHAATLNGRSLLRPLTPDVHEGCAEEFSASDD
1 1	1		VALGFSGPHSLAAFPAWGTQDEGTLEFTLTTQSRQAPLAFQAGG
1 1	j	ļ	RRGDPIYVDIFEGHLRAVVEKGQGTVLLHNSVFVADGQPHEVSV HINAHRLEISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEASR
1 1	Į.		HLQEHRLGLTPEATNASLLGCMEDLSVNGQRRGLREALLTRNMA
1		ļ	AGCRLEEEEYEDDAYGHYEAFSTLAPBAWPAMELPEPCVPEPGL
1 1			PPVFANFTQLLTISPLVVAEGGTAWLEWRHVQPTLDLMEAELRX
1 1	I		SQVLPSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIHD
1 1	i	}	GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDPP
1 1	İ	į.	HIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGITFOVICT
1 (i	į	SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAODI.TEP
1 1	1	j	VSDGLQASPPATLKVVAIRPAIOIHRSTGLRLAOGSAMDTLDAN
1]		LSVETNAVGQDVSVLFRVTGALQFGELOKHSTGGVEGAEWWATO
1			AFHQRDVEQGRVRYLSTDPOHHAYDTVENI.ALEVOVGORTI.SNI
1 1	į.	į	SFPVTIQRATVWMLRLEPLHTONTOOETLTTAHLEATLEEAGDS
1 1	1	1	PPTFHYEVVQAPRKGNLQLQGTRLSDGOGFTODDTOAGRUTYGA
1 1	į		TARASEAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTNV
1 1	1	1 :	LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWRG
1 1			TODKITMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQGE
}		ļ	SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRLL
		1 :	TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYRF
		13	TOEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASEP
1		1:	YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHVT
1		1:	AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMAF
1		[]	SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI
 		(;	RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS
		1 ;	LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE GVLVELEVLPAAIPLEAQNFSVPEGGSLTLAPPLLRVSGPYFPT
			THE THE THE THE TAR TH

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			LLGLSLQVLEPPQHGPLQKEDGPQARTLSAFSWRMVEEQLIRYV
		l .	HDGSETLTDSFVLMANASEMDRQSHPVAFTVTVLPVNDQPPILT
	\	1	TNTGLQMWEGATAPIPAEALRSTDGDSGSEDLVYTIEQPSNGRV
		ì	VLRGAPGTEVRSFTQAQLDGGLVLFSHRGTLDGGFPFRLSDGEH
		1	TSPGHFFRVTAQKQVLLSLKGSQTLTVCPGSVQPLSSQTLRASS
		1 .	SAGTDPQLLLYRVVRGPQLGRLFHAQQDSTGEALVNFTQAEVYA
	į.		GNILYEHEMPPEPFWEAHDTLELQLSSPPARDVAATLAVAVSFE
	j	1	AACPQRPSHLWKNKGLWVPEGQRARITVAALDASNLLASVPSPQ
	}	1	RSEHDVLFQVTQFPSRGQLLVSEEPLHAGQPHFLQSQLAAGQLV
	1	•	YAHGGGGTQQDGFHFRAHLQGPAGASVAGPQTSEAFAITVRDVN
	1)	ERPPQPQASVPLRLTRGSRAPISRAQLSVVDPDSAPGEIEYEVQ
	1		RAPHNGFLSLVGGGLGPVTRFTOADVDSGRLAFVANGSSVAGIF
	1		QLSMSDGASPPLPMSLAVDILPSAIEVQLRAPLEVPQALGRSSL
			SQQQLRVVSDREEPEAAYRLIQGPQYGHLLVGGRPTSAFSQFQI
	1		DQGEVVFAFTNFSSSHDHFRVLALARGVNASAVVNVTVRALLHV
		ł	WAGGPWPQGATLRLDPTVLDAGELANRTGSVPRFRLLEGPRHGR
		[VVRVPRARTEPGGSQLVEQFTQQDLEDGRLGLEVGRPEGRAPGP
		Ì	AGDSLTLELWAQGVPPAVASLDFATEPYNAARPYSVALLSVPEA
		}	ARTEAGKPESSTPTGEPGPMASSPEPAVAKGGFLSFLEANMFSV
		ļ	IIPMCLVLLLALILPLLFYLRKRNKTGKHDVQVLTAKPRNGLA
	į	{	GDTETFRKVEPGQAIPLTAVPGQGPPPGGQPDPELLQFCRTPNP
	ļ	1	ALKNGQYWV
5451	1	2274	RDSSEQGRTGDTLGRPSACMDALKPPCLWRNHERGKKDRDSCGR
	1	1	KNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFNFLFSPLP
	j	1	TPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARK
			GVSQKNNDLTSCCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQ
	1	\	PYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQFVGTFAQNRPEW
		}	IISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQ
			KALVLIGNVEKGFTPSLKVIILMDPFDDDLKQRGEKSGIEILSL
		ļ	YDAENLGKEHFRKPVPPSPEDLSVICFTSGTTGDPKGAMITHQN
		ì	IVSNAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQAVVYS
			CGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNE
		Į.	AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFWDKLIFAKIQDSL
		\ ·	GGRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGQTECTGGCT
l		1	FTLPGDWTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKG
		.1	TNVFKGYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRK
		1	KNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVHGESLRSSLVGV
	1	1	VVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKIGKE
	İ	1	SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYFRTQ
			IDSLYEHIQD
5452	1833	1138	SRVPSLCLSLSLSPSREPVAGAPGCGTAGPPAMATLWGGLLR
		1	LGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENSG
	[i i	HIYNKNISQKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSS
			VTIKVTIIIYLSILGLLLLYMVYLTLVEPILKRRLFGHAQLIQS
	\		DDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ
1			RKSVFDRHVVLS
5453	111	1520	PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV
ļ		l	AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE
i		1	
			PQEERSQQQDDIEELETKAVGMSNLGRFLKFDLEIGRGSFKIV
			PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI
			KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVI
			KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVI RSWCROILKGLOFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGI
			KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVI RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGI LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCI
			KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVI RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGI LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCI LEMATSEYPYSECONAAOIYRRVTSGVKPASFDKVAIPEVKEI
			KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVI RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGI LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCN LEMATSEYPYSECQNAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRONKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIA
			KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVI RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGI LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCN LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIAI KLMLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESC
			KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVI RSWCRQILKGLQFLHTRTPPIHRDLKCDNIFITGPTGSVKIGI LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIAI KLWLRIEDIKKLKGKYKDNEALEFSFDLERNVPEDVAQEMVESC YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
5454	111	1520	KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVI RSWCRQILKGLQFLHTRTPPIHRDLKCDNIFITGPTGSVKIGI LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCN LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQESTGVRVELAEEDDGEKIAI KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESC YVCEGDHKTMAKAIKDRVSLIKRKREQRQL* PSIPAAVPOSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV
5454	111	1520	KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVI RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGI LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCN LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIAI KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESC YVCEGDHKTMAKAIKDRVSLIKRKREQRQL* PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKI
5454	111	1520	KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVI RSWCRQILKGLQFLHTRTPPIHRDLKCDNIFITGPTGSVKIGI LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCN LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLNHAFFQESTGVRVELAEEDDGEKIAI KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESC YVCEGDHKTMAKAIKDRVSLIKRKREQRQL* PSIPAAVPOSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV

SEQ	Predicted	D====================================	
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cvsteine, D=Aspartic Acid P-
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
Ì	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
- 1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
- 1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
I	sequence	bequence	Codon, /=possible nucleotide deletion,
		 	\=possible nucleotide insertion)
- 1	1	Į.	VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL
1	I		RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
1	į.		LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM
J	ļ	[LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII
1	1		EGCIRONKDERYSIKDLLNHAFFQEETGVRVELAERDDGEKIAI
1		1	KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG
5455	1359	377	YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
4	1	1	LTMVSPATRKSLPKVKAMDFITSTAILPLLFGCLGVFGLFRLLQ
]			WYRGKAYLRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNG
1	Į.	[GALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEIL
ł)	1	QCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMEINYFGPVALT
	i	1	KALLPSMIKRROGHIVAISSIQGKMSIPFRSAYAASKHATQAFF
1	}	1	DCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTT TAQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPG
-			LFFSLMASRARKERKSKNS
5456	2	2332	CGAGLVAAGAVLVLYPASRAGERTRVPGSPAPSSLPLHSPGACG
j	}		TEVDMDPQRSPLLEVKGNIELKRPLIKAPSQLPLSGSRLKRRPD
			QMEDGLEPEKKRTRGLGATTKITTSHPRVPSLTTVPQTQGQTTA
i	}		QKVSKKTGPRCSTALATGLKNQKPVPAVPVQKSGTSGVPPMAGG
1.			KKPSKRPAWDLKGQLCDLNAELKRCRERTQTLDQENQQLQDQLR
1			DAQQQVKALGTERTTLEGHLAKVQAQAEQGQQELKNLRACVLEL
			EERLSTQEGLVQELQKKQVELQEERRGLMSQLEEKERRLQTSEA
1			ALSSQAEVASLRQETVAQAALLTEREERLHGLEMERRRLHNQL
}		ı	QELKGNIRVFCRVRPVLPGEPTPPPGLLLFPSGPGGPSDPPTRL
			SLSRSDERRGTLSGAPAPPTRHDFSFDRVFPPGSGODEVFFFTA
i i			MLVQSALDGYPVCIFAYGQTGSGKTFTMEGGPGGDPOLEGLIDD
}			ALRHLFSVAQELSGQGWTYSFVASYVEIYNETVRDLLATGTRKG
i i			QGGECEIRRAGPGSEELTVTNARYVPVSCEKEVDALLHIAPOND
1 1			AVARTAQNERSSRSHSVFQLQISGEHSSRGLQCGAPISLVDLAG
1 1			SERLDPGLALGPGERERLRETQAINSSLSTLGLVIMALSNKESH
1 1			VPYRNSKLTYLLQNSLGGSAKMLMFVNISPLEENVSESLNSLRF
1 1			ASKVEPSVLFGTAQSNRKWKTDPDLCVCVCVCVCVCVCVCVCVP
5457	 2	1510	MSMYRVRGGRVAGGCFIGWRAPCPRAIK
2.3.	-	1540	DDFVERRRWIRTTCLVRSPPHVPVCGHACSWNGGSLDPLKGTPA
1			LLRSAERLMRKVKKLRLDKENTGSWRSFSLNSEGAERMATTGTP
1 1	I		TADRGDAAATDDPAARFQVQKHSWDGLRSIIHGSRKYSGLIVNK
1 1	ł		APHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPKKV
1 1	1		RKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVFGI
1 1	}		TSYDFHSESGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK
1 1			PLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANIETGEER
1 1	Ì		RLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASW
1			EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT
			GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI
L			ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA ASLCQSCPQECPAVCGVRGGHQRLDQCS
5458	6642	4022	FVPGLREPQWEPAQPSATMSAPSEEEEYARLVMEAQPEWLRAEV
1 1	!		KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA
			IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY
1	1		VRKVLELQTELKQLRNVLTNTQSENERLASVAQBLKEINQNVEI
, .	j		QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ
[[ļ	[VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET
1	1	j	LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA
			EPHNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS
] }	ì	1	DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG
	į	İ	SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG
1	İ	Í	DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ
}		j	HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS
1			DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML
1	ł		DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA
ŀ			DGGTGDSSPSPGSSLPSPLSDPRREPMNIYNLIAIIRDQIKHLQ
		1	AAVDRTTELSRORIASQELGPAVDKDKEALMEEILKLKSLLSTK
		L	"A" A STORY AND VINCATIME ETTING K STIPSTK

ID h	Predicted beginning nucleotide location corresponding	Predicted end nucleotide location corresponding	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide location	location	Glutamic Acid F=Phenvlalanine, G=Glycine,
	location		Giucamic Acid, 100 may
		COTTESTORALING	U_U_U_GE_iding T=Tsoleucine, K=LVSlne,
	corresponding		H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
		to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
}.	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
L	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		REQITTLETV_KANKQTAEVALANLKSKYENEKAMVTETMMKLR
			REQITTLRTV SKANKQ I AEVAHANDRSKI ENDEMORQLAAAEDE NELKALKEDAATFSSLRAMFATRCDEYITQLDEMQRQLAAAEDE
į.		1	NELKALKEDAATTSSLKAMFAIRCDEITIQDDIAQAQATTIADD
į		1	KKTLNSLLRMAIQQKLALTQRLELLELDHEQTRRGRAKAAPKTK
]		} -	PATPSVSHTCACASDRAEGTGLANQVFCSEKHSIYCD
5459	316	1262	RGGHRLSGMASNFNDIVKQGYVRIRSRRLGIYQRCWLVFKKASS
3435			KGPKRLEKFSDERAAYFRCYHKVTELNNVKNVARLPKSTKKHAI
.]			GIYFNDDTSKTFACESDLEADEWCKVLQMECVGTRINDISLGEP
		1	DILATGUERFOSERFNVYLMPSPNLGCYMGECALQITYEYICLW
		1	DVONDDUKT.TSWDI.SALRRYGRDTTWFTFEAGRMCETGEGLF1F
1		į	OTEN CEAT VOKUHSAALAIAEOHERLLQSVKNSMLQMKMSERAA
		Į.	SLSTMVPLPRSAYWQHITRQHSTGQLYRLQDVSSPLKLHRTETF
1 1		1	DAVECEU
11		L	RPGCRAGELSTGSRARERVRNRVSAPCGQDSRRCDPEVLRGRSP
5460	45	2097	GLGLAEMPSCGACTCGAAAVRLITSSLASAQRGISGGRIHMSVL
į I	•	1	GLGLAEMPSCGACTCGAAAVKEITSSEAAAVKEETGGGGGGGNKKS GRLGTFETQILQRAPLRSFTETPAYFASKDGISKDGSGDGNKKS
1 1		1	GRIGTFETQILQRAPLKSFIE TPATFASKUGISKUGSTRFVK ASEGSSKKSGSGNSGKGGNQLRCPKCGDLCTHVETFVSSTRFVK
i i		1	ASEGSSKKSGSGRSGRGGRQDKCFRCSD20111 CEKCHHFFVVLSEADSKKSIIKEPESAAEAVKLAFQQKPPPPPK
1 1		1	CEKCHHFFVVLSEADSKKSTIREFESHALA KIYNNIPANLRQQAE KIYNYLDKYVVGQSFAKKVLSVAVYNHYKRIYNNIPANLRQQAE
}		j	KIYNYLDKYVVGQSFAKKVLSVAVINITAKITAKITAKITAKI
{		1	VEKQTSLTPRELEIRRREDEYRFTKLLQIAGISPHGNALGASMQ
]		}	QQVNQQIPQEKRGGEVLDSSHDDIKLEKSNILLLGPTGSGKTLL
1	·	1	AQTLAKCLDVPFAICDCTTLTQAGYVGEDIESVIAKLLQDANYN
)	}	}	VEKAQQGIVFLDEVDKIGSVPGIHQLRDVGGEGVQQGLLKLLEG
1			TIVNVPEKNSRKLRGETVQVDTTNILFVASGAFNGLDRIISRRK
}	}	ì	NEKYLGFGTPSNLGKGRRAAAAADLANRSGESNTHQDIEEKDRL
Ι ,	4	į.	T DUTTE A DOLLER CM T PEFVGRLPVVVPLHSLDEKTLVQ1LTEPK
1	}	1	MAUT DOVOAL ESMOKCEL NVTEDALKALARLALERKTGARGLES
1		· ·	IMEKLLLEPMFEVPNSDIVCVEVDKEVVEGKKEPGYIRAPTKES
ì		1	CEREVISCOMEEGWPROADAANS
	<u> </u>	160	TNDDDDDVSDCGDADKWRRRRRPGAPEAAVMELPSGPGPERLFD
5461	1481	100	CURL DEDCET LLIVILLYAPVGFCLLVLRLFLGIHVFLVSCALPD
ł)	CIT PREVIOUS CAVICIVAROEDSGLEDHSVRVLISNHVTPYDH
i	į	1	NITED LITECTION INSPESSIVE SERVEN SER
1	}	1	ASTRUPPTPLLLFPEEEATNGREGLLRFSSWPFSIQDVVQPLTL
į .		1	QVQRPLVSVTVSDASWVSELLWSLFVPFTVYQVRWLRPVHRQLG
1]	}	EANEEFALRVQQLVAKELGQTGTRLTPADKAEHMKRQRHPRLRP
	,	1	QSAQSSFPPSPGPSPDVQLATLAQRVKEVLPHVPLGVIQRDLAK
}	1		QSAQSSPPSSPGPSPDVQHAT BAGKYRDSLPTASASKFPSSGPV TGCVDLTITNLLEGAVAFMPEDITKGTQSLPTASASKFPSSGPV
	l	1	TGCVDLTITNLLEGAVAFMPEDITRGTQSDF1ASASCTTSQEAD TPQPTALTFAKSSWARQESLQERKQALYEYARRRFTERRAQEAD
l	1	1	TPOPTALTFAKSSWARQESDQERAQADISTAKAAT TEMBERGER
5462	663	3353	KIKEROMSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSA
			RLSNGSFSAPSLTNSRGSVHTVSFLLQIGLTRESVTIEAQELSL
1		}	SAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSENILQLIT
1			SADEIHEGDLVEVVLSALATVEDFQIRPHTLYVHSYKAPTFCDY
1		j	CCEMINGLAROGI, KCEGCGLNYHKRCAFKIPNNCSGVRKRRLSN
1	1		VOLDEDGI GUDD DI OPEYVAL PSEESHVHQEPSKRIPSWSGRPI
1	1	1	LIMPUMING DURVIDUTE AVHSYTROTI COYCKRLLKGLFRQGMQC
-	Ţ		VDCVENCURPCASKVPRDCLGEVTFNGEPSSLGTDTD1PMD1DN
}	ł	1	NDING DESCRIPTION OF THE PROPERTY OF THE PROPE
1	1	1	CDETENNIT DI MRVVIOSIKHTKRKSSTMVKEGWMVHYTSRDNLRK
1	1	1	RHYWRLDSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNIS
1	ľ	1	QGSNPHCFEIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS
1	1	}	WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE
]		\	NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM
į.		1	NVDISTVYQIFADEVLGSGQFGIV IGGARACIGAD TITAL IPAN
ļ		l l	RFPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVVMEK
1		1	LHGDMLEMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHC
1			DLKPENVLLASAEPFPQVKLCDFGFARIIGEKSFRRSVVGTPAY
1	l		T.ADEVI.RSKGVNRSI.DMWSVGVIIYVSLSGTFPFNEDEDINDQ1
1			ON NEW VERNINGER SCEATELINNLLOVKMRKRYSVDKSLSHP
1	1		WLQDYQTWLDLREFETRIGERYITHESDDARWEIHAYTHNLVYF
1	1		WINTERSONDENDERDD
l l		1030	TI CUMMTTED CEUL DEVI. PDCTSSAAPVVKTVEDCGSLVNGQPC
5463	237	1012	YVMQVSAKDGQLLSTVVRTLATQSPFNDRPMCRICHEGSSQEDI

SEC	Predicted	Predicted end	
ID		nucleotide	Trimerio dollo Seguiene Confain. no cionol
NO:	nucleotide	location	Manageria and a
1	location	corresponding	Juliania Acia, Febbery alegina constrain
ł	corresponding	to first	n-nistidine, i=Isoleucine, K-liveine
}	to first	amino acid	Labercine, Mamethionine, NaAsparagine
ļ	amino acid	residue of	P=PIOLINE, O=Glutamine R-Argining
- 1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
L	sequence	4	COUCH, /=DOSSIDIE nucleotide deleti-
			\=possible nucleotide insertion)
1	ļ	j	LSPCECTGTLGT IHRSCLEHWLSSSNTSYCELCHFRFAVERKPR
ļ ·	ł		PLVEWLRNPGPQHEKRTLFGDMVCFLFITPLATISGWLCLRGAV
<u> </u>		1	DHLHFSSRLEAVGLIALTVALFTIYLFWTLVSFRYHCRLYNEWR
5464	195	677	RTNQRVILLIPKSVNVPSNQPSLLGLHSVKRNSKETVV
1	1		SPSMNPRKKVDLKLIIVGAIGVGKTSLLHQYVHKTFYEEYQTTL
1			GASILSKIIILGDTTLKLQIWDTGGQERVRSMVSTFYKGSDGCI
Ĺ			LAFDVTDLESFEALDIWRGDVLAKIVPMEQSYPMVLLGNKIDLA DRKYQSILENHLTESIKLSPDQSRSRCC
5465	5278	3348	KGDPREFIRVHREALECDYVSAHLHEWIDLIFGYKQQGPAAVEA
			VNVFHHLFYEGQVDIYNINDPLKETATIGFINNFGQIPKQLFKK
			PHPPKRVRSRLNGDNAGISVLPGSTSDKIFFHHLDNLRPSLTPV
- {	ļ		KELKEPVGQIVCTDKGILAVEQNKVLIPPTWNKTFAWGYADLSC
}		1	RLGTYESDKAMTVYECLSEWGQILCAICPNPKLVITGGTSTVVC
		1	VWEMGTSKEKAKTVTLKQALLGHTDTVTCATASLAYHIIVSGSR
1	1	1	DRTCIIWDLNKLSFLTQLRGHRAPVSALCINELTGDIVSCAGTY
ļ	j		IHVWSINGNPIVSVNTFTGRSQQIICCCMSEMNEWDTQNVIVTG
			DOG V V REWRMEPLOV PETPAPEDA EVI. PMO PDC DE A OTCO PAGE
1		! .	DEDSSUSEADEQSISODPKDTPSOPSSTSUPPDAACCDAMARIS
- i	1		I DSGSDDSRRWSDQLSLDEKDGFI FVNYSEGOTPAHLOGBT CUD
1			INTELLEGIAN ISKURPGYRWEROLVFRSKI.TMHTAFDDEDNIMIER
	i		I STALIGISKUHSKILVGDSRGRVFSWSVSDODGDGAADUURVDD
1		1	GGDSCSGCSVRFSLTERRHHCRNCGOLFCOKCSPEOSET VDT VT
5466	3	000	SSF VKVCQNCYYNLQHERGSEDGPRNC
		992	HACAHASAHASGRLVRWWRKRRSVMGIQTSPVLLASLGVGLVTL
	[Ì	I DIENGS I LVKKSKRPOVTI I DDNEKVI I DI I DVITTI OI DINGER
1	1		READPTANHTLGLPVGKHIYLSTRINGSIVIPPVTPVTEDEDOG
1			IVDDVIKVYLKGVHPKFPEGGKMSOVI.DSI.KVGDIAREBOOGGE
-			LTYTGKGHFNIQPNKKSPPEPRVAKKLGMIAGGTGITPMLQLIR
ľ			AILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLW
 			FTLDHPPKDWAYSKGFVTADMIREHLPAPGDDVLVLLCGPPPMV QLACHPNLDKLGYSQKMRFTY
5467	2103	4	GEALRYGTRGCRRDLPDPQARIFIQKKDLEEDESVTAAHLKSRG
	1		RSPRKIDQFCNSSNMVHGSVTFRDVAIDFSQEEWECLQPDQRTL
1	1 1		YRDVMLENYSHLISLAGSSISKPDVITLLEQBKEPWMVVRKETS
}	1 !		RRYPDLELKYGPEKVSPENDTSEVNLPKQVIKQISTTLGIEAFY
1			FRIDSE I ROFEGLOGYOEGNINOKMI SVEKI DTUTOUR CI TONT
	1 1	,	ARPIECKECGKYFSCGSNLIOHOSIHTGEKPYKCKECGKAEGETT
			TOLIKRORFHIGERIFECKECGKAFNI, DTOLNDUKNITUTTUTTUTTUT
1	1	Ī	ECKECGKSFNRSSNLTOHOSIHAGVKDVOCKECGKA ENDCOM T
1	1		VAUATHSNEKPFVCKECGMAFRYHYOLTEHCOTHTGEVDERGYD
1	1	ļ	CGAAF ILLIKUVRHQKIHTGEKPFECRECGKAFSI. MOI NDEEDE
ļ	1		THIO EXPERICACIONS PARSSITA VOHOSTHACT POPE COPE
	1 1		FIRGARII QHQKIHSNEKPFVCRECEMA FPVUCOL TEUER TYPE
J	1	1	DAFF & COLCGRAFINGSSLVOHOSIHTGERPVECKECCVA PRIVIL
i	1	i i	TOTAL THE CERPTECKECGKFFRRGON NOUDE TUROWERS I
L	1		ECKECGKAFRLHMHLIRHQKLHTGEKPFECKECGKAFRLHMQLI
5468	225	2976	RHOKLHTGEKPFECKECGKVFSLPTQLNRHKNIHTGEKAS
ĺ	1	t e	SFLTDLFQSLAQLENLCKQLYETTDTTTRLQAEKALVEFTNSPD
	İ		CLSKCQLLLERGSSSYSQLLAATCLTKLVSRTNPLPLEQRIDI
	. !	Į į	RNYVLNYLATRPKLATFVTQALIQLYARITKLGWFDCQKDDYVF
		1 ;	RNAITDVTRFLQDSVEYCIIGVTILSQLTNEINQVSATAFLIEA
l	1	1 1	DTTHPLTKHRKIASSFRDSSLFDIFTLSCNLLKQASGKNLNLND ESQHGLLMQLLKLTHNCLNFDFIGTSTDESSDDLCTVQIPTSWR
J			SAFLDSSTLQLSTIGRCEYEKTCALLVQLFDQSAQSYQELLQSA
j		1 5	SASPMDIAVQEGRLTWLVYIIGAVIGGRVSFASTDEQDAMDGEL
1	1	1	VCRVLQLMNLTDSRLAQAGNEKLELAMLSFFEQFRKIYIGDQVQ
f	1	I	KSSKLYRRLSEVLGLNDETMVLSVFIGKIITNLKYWGRCEPITS
ł	1	F	CTLQLLNDLSIGYSSVRKLVKLSAVQFMLNNHTSEHFSFLGINN
1	į	Į C	SNLTDMRCRTTFYTALGRLLMVDLGEDEDOVEORMI.DI.TAADE
1) A	VAQMESTNSFNEQEAKRTLVGLVRDLRGIAFAFNAKTCPMMIR
		E	WIYPSYMPILQRAIELWYHDPACTTPVLKLMAELVHNRSQRLQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	_		Codon, /=possible nucleotide deletion,
	amino acid	sequence	Codon, / apossible indicated deletas,
i	sequence	<u> </u>	\=possible nucleotide insertion)
			FDVSSPNGILLFRETSKMITMYGNRILTLGEVPKDQVYALKLKG
	[1	ISICFSMLKAALSGSYVNFGVFRLYGDDALDNALQTFIKLLLSI
		l	PHSDLLDYPKLSQSYYSLLEVLTQDHMNFIASLEPHVIMYILSS
		İ	ISEGLTALDTMVCTGCCSCLDHIVTYLFKQLSRSTKKRTTPLNQ
	[1	ESDRFLHIMQQHPEMIQQMLSTVLNIIIFEDCRNQWSMSRPLLG
	ł	1	LILLNEKYFSDLRNSIVNSQPPEKQQAMHLCFENLMEGIERNLL
	į	1	
			TKNRDRFTQNLSAFRREVNDSMKNSTYGVNSNDMMS
5469	134	2653	DQEFETSLVPWHLPMGWLCSGLLFPVSCLVLLQVASSGNMKVLQ
	1	1	EPTCVSDYMSISTCEWKMNGPTNCSTELRLLYQLVFLLSEAHTC
	j	Į.	VPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPS
	1		EHVKPRAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVN
İ	1		IWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAQ
i	j		CYNTTWSEWSPSTKWHNSYREPFEQHLLLGVSVSCIVILAVCLL
l			CYVSITKIKKEWWDQIPNPARSRLVAIIIQDAQGSQWEKRSRGQ
1	1		CIADITIKTERMENTI EMENDOS CHANTITION DE SANDE COCCAR
İ	1	1	EPAKCPHWKNCLTKLLPCFLEHNMKRDEDPHKAAKEMPFQGSGK
	1		SAWCPVEISKTVLWPESISVVRCVELPEAPVECEEEEEVEEEKG
	1	1	SFCASPESSRDDFQEGREGIVARLTESLFLDLLGEENGGFCQQD
	1	1	MGESCLLPPSGSTSAHMPNDEFPSAGPKEAPPWGKEQPLHLEPS
		1	PPASPTQSPDNLTCTETPLVIAGNPAYRSFSNSLSQSPCPRELG
Į	1	ł	PDPLLARHLEEVEPEMPCVPQLSEPTTVPQPEPETWEQILRRNV
ĺ	1	1	LQHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPGEAG
Ì	1	ı	YKAFSSLLASSAVSPEKCGFGASSGEEGYKPFQDLIPGCPGDPA
j	1	1	PVPVPLFTFGLDREPPRSPQSSHLPSSSPEHLGLEPGEKVEDMP
1	i	1	PADA DEL ESTA CONTROL DON CONTROL CONT
}	i	ł	KPPLPQEQATDPLVDSLGSGIVYSALTCHLCGHLKQCHGQEDGG
Į.	ł	•	QTPVMASPCCGCCCGDRASPPTTPLRAPDPSPGGVPLEASLCPA
1	1	1	SLAPSGISEKSKSSSSFHPAPGNAQSSSQTPKIVNFVSVGPTYM
į.	1	1	RVS
5470	17	1418	TACRIRTSLNRGIAAVKRDAVEMLASYGLAYSLMKFFTGPMSDF
31,0	1 -		KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI
1		l l	INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY
ļ	1		SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA
Ι.	(LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA
,	1		LILATORISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP
1	Į.	1	
1	i	1	YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA
Į.	1	}	LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF
i			PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL
1			GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT
1	1		EGEDSAMTDMPPTEEVTDIVEMREENE
	1868	658	RSSAPPGPQRAAAATAAAAAAGVEMAAAAAQGGGGGEPRRTEGV
5471	TROR	958	GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR
1			KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR
1			KIKVAIKKISPPENQIIQUILQRIDKEIQIDDKFKNEWVIGIKDIDK
1	1	}	ASTLEAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR
1			GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD
1		İ	HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
	}	}	NRPIPPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL
i	}	1	PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP
}		}	YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ
1		,	
L			PGVLEAP
5472	1469	753	LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR
1	1	1	DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTFHR
í	i		GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA
1		1	VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGYLGPAPEEA
1	I	1	IATQILACRGFSGHNLEYLLRVRDVMQLCGPQAQDEHLAAIVDA
1			VGTMLPCFCPTEQALALV
			FMNVKLLIQDLEDIEQRVPVMDAQYKIITKTAHLITKESPQEEG
5473	3	2119	EMMAKPPTONTENTE OKASAMBAGIKTI I VI MULI MERAMBU
1	1	1	KEMFATMSKLKEQLTKVKECYSPLLYESQQLLIPLBELEKQMTS
	l	1	FYDSLGKINEIITVLEREAQSSALFKQKHQELLACQENCKKTLT
}	1	1	LIEKGSOSVOKFVTLSNVLKHFDQTRLQRQIADIHVAFQSMVKK
]	1	1	TGDWKKHVETNSRLMKKFEESRAELEKVLRIAQEGLEEKGDPEE
	1	1	LLRRHTEFFSQLDQRVLNAFLKACDELTDILPEQEQQGLQEAVR
1	1	1	KLHKQWKDLQGEAPYHLLHLKIDVEKNRFLASAEECRTELDRET
1	L	ł	VOID ALLEN TANDERS OF THE PARTY

SEQ Predicted and nucleotide location (uncleotide location beginning) prepared to the positioning of the pos	SEO	1 5		
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Corresponding to first amino acid residue of amino acid amino acid residue of amino acid acid acid acid acid acid acid acid		beginning	nucleotide	(A=Alanine C-Cystoins D a
corresponding to first amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acid amino acid acid amino acid acid acid acid acid acid acid acid	NO:		location	Glutamic Acid B Despartic Acid, Es
Cotresponding to first amino acid services of services	- 1	location	corresponding	u-wighteding, F=Pnenylalanine, G=Glycine,
to first amino acid residue of amino acid amino acid amino acid amino acid acquence sequence P-Proline, O-Chutanine, N-Arginine, S-Cop acquence Sequence Sequence R-Trypbophan, Y-27cie, V-Valine, S-Trypbophan, Y-Valine, V-Valine, S-Trypbophan, Y-Valine, V-Valine, S-Trypbophan, Y-Valine, V-Valine, V-Valine, S-Trypbophan, Y-Valine, V-Valine, V-Valine, S-Trypbophan, Y-Valine, V-Valine, V-Valine, S-Trypbophan, Y-Valine, V-Valine,	1	corresponding	to first	
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residue of amino acid acquence surpripophan, "Typoshe, Kubuknown, "sscop Codon, /spossible nucleotide deletion, V-possible nuc				Partoline, OsGiutamine Parainine
amino acid sequence Sequence			4	Seserine, TeThreonine Vevaline
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ESSATS INEQUES KREADTAMHEGYERAYER EINSKRYTKRE ETSAHKERIKUTIEVSSENERANGOGDELAKISSERKAUTLIS EVERMISNINGDOVQYKETYNRSIEELISGSKRYOEGORKILDTE NIFERGOLLIHHIGGKTKEISKRROVGGOLGAGOGGGGILPDRG HBEIRKLESTILDGIERSKERGERIGYTLIKKMERFETNKETVVR TIPPTGSSEREFILESSIESSELEGTREFETEISIAVQAEN LWREASETPLOPONKOLLQQAAGSIKGVKKLEDTLEEFYVIDK LWREASETPLOPONKOLLQQAAGSIKGVKKLEDTLEEFYVIDK LORANGTIERSTUNGSAWTDETSKESSELEGTREFETEISIAVQAEN LORANGTORGANGTORGANGTVICHERSTYLDE LORANGTORGANGTORGANGTVICHERSTYLDE LORANGTORGANGTORGANGTVICHERSTYLDE LORANGTORGANGTORGANGTVICHERSTYLDE LORANGTORGANGTORGANGTVICHERSTYLDE LORANGTORGANGTORGANGTVICHERSTYLDE SA75 2 506 ARGUITERSTRONDELLAGIAGAATAMAAAAAABABEUGHTLA LORANGTORGANGTORGANGTVICHTREPTITHTTPTTITTYTYTY SAGMENICHTALGEMILLILEARRANGCORGANGTVICHTREPTITHTTPTTITTYTYTYT SAGMENICHTALGEMILLILEARRANGCORGANGTVICHTRESTELMS VORTHEART VORTHOUGHOUFFERDLREVORKOCTITHTEEHLVCVOK GEVENTVORTHOUGHOUFFERDLREVORKOCTITHTEEHLVCVOK GEVENTVORTHOUGHOUFFERDLREVORKOCTITHTEEHLVCVOK GEVENTVORTHOUGHOUFFERDLREVORKOCTITHTEEHLVCVOK GEVENTVORTHOUGHOUFFERDLREVORKOCTITHTEEHLVCVOK GEVENTVORTHOUGHOUFFERDLREVORKOCTITHTEEHLVCVOK GEVENTVORTHOUGHOUFFERDLREVORKOCTITHTEEHLVCVOK GEVENTVORTHOUGHOUFFERDLREVORTHUNGTHINTYTTYTTYTUT SAMMAVISPPAMBERLAGAAVILLERPRIPHITTYTTYTTYTUT SAMMAVISPPAMBERLAGAAVILLERPRIPHITTYTTYTYTUT GEVENTVORTHOUGHOUFFERDLREVORTHUNGGRINGHAAVINGGORIN AVIDEPOSTSVOHHILLISORIUVINGGRINGHAVINGGORIN AVIDEPOSTSVOHHILLISORIUVINGGRINGHAVINGGORIN AVIDEPOSTSVOHHILLISORIUVINGGRINGHAVINGGORIN AVIDEPOSTSVOHHILLISORIUVINGGRINGHAVINGGORIN AVIDEPOSTSVOHHILLISORIUVINGHAVINGSIT SAGMUSCI GESVUNSGATALAKAURUPTARANGTURARRANGA GUUSCI GESVUNSGATALAKAURUPTARANGTURARRANGA GUUSCI GESVUNSGATALAKAURUPTARANGTURARRANGA GUUSCI GESVUNSGATALAKAURUPTARANGTURARRANGA GUUSCI GESVUNSGATALAKAURUPTARANGTURARRANGA GUUSCI GESVUNSGATALAKAURUPTARANGTURARRANGA GUUSCI GESVUNSGATARANGTURARRANGTURARRANGA GUUSCI GESVUNSGATARANGTURARRANGTURARRANGTURARRANGTURARRANGTURARRANGTURARRANGTURARRANGTURARRANGTURARRANGTURARRANGTURARRANGTURARRANGTURARRANGTURARRANGTURARRANGTURARRANGTURARRANGTURARRANGTURARRANGT		l .	į.	RDP VRD1PG1CHV1LKELRAAIDSTYRKIMEDDDVWVDVTCDDG
EUROMISCHOUTESTENSELLISSERENGOORMEKILDTE EVERHISMISCHUTYKEISAKKROVOGOIAGAOGGEGIJPRO HEILRILBSTILDGIESERERGERIGVITEKSEPTINKETVUR TAPOTOSSIKERFLSPSIESILSSELEGTKEFEKTREIAVAGEN LVREASEILJEGGESERERGERIGVITEKSEFEKTESIAVAGEN LVREASEILJEGOPKOKLUGOGASI KROWKEILEGESVILDS S TPDVRQLOASERGIAVASWCSPRWFAGEEMAFVKSSMLLRGSTI LEKHKKNWEDLWSSDGHLIYTDOTTROH IEDKVHIMPMOG TINETG GECENTOPPOEKSKOLMGIVORDEKTISLGESTIDGLAUKPT LODSRINTAYVGSAWMTDETSWVSSPPPTATAAAAPADEVGRILD LODAVGGFYGOAYPPGTQUVYAANGGAVAPYQYPYAGLYGGO PANOVIIRERKRINNEDLALGHLAGAAATGALGSLEWYE SAMOMENSTLOALINSERSERSTENDERGTTIVHTPPNILTGYTRE VOGKMEDYLOALINISLAVSKLALLLEPPKEIEHOGANITVRTL STERNYTVOGFOVOVETEBULFAVORGATVANGGAVAPYQYPYAGLYGGO GEVPRAGWIRKHLEGEMYLLLATARDAVCSQVFRKVR SAMOMENSTLOALINISVRKALALLEPPKEIEHOGANITVRTL STERNYTVOGFOVOVETEBULFAVORGACTIVHTOPPTLAGSE BETRASEVLCSTRVOHVERLOVERGERGTOMLVOEPTLAGSE BETRASEVLCSTRVOHVERLOVERGREGTOMLVOEPTLAGSE BETRASEVLCSTRVOHVERLOVERGREGTOMLVOEPTLAGSE BETRASEVLCSTRVOHVERLOVERGREGTOMLVOEPTLAGSE BETRASEVLCSTRVOHVERLOVERGREGTOMLVOEPTLAGSE BETRASEVLCSTRVOHVERLOVERGREGTOMLVOEPTLAGSE BETRASEVLCSTRVOHVERLOVERGREGTOMLVOEPTLAGSE BETRASEVLCSTRVOHVERLOVERGREGTOMLVOEPTLAGSE BETRASEVLCSTRVOHVERLOVERGREGTOMLVOEPTLAGSE BETRASEVLCSTRVOHVERLOVERGREGTOMLVOEPTLAGSE BETRASEVLCSTRVOHVERLOVERGREGTOMLVOEPTLAGSE BETRASEVLCSTRVOHVERLOVERGREGTOMLVOHVERDIT SVOISTRACL ANGOVEROHRENDANTISSHERGENTISSIVANGERSITINISTRVOHVERGREGTOMLVOHVERDIT SVOISTRACL ANGOVEROHRENDANTISSHERGENTISSIVANGERSITINISTRVOHVERGREGTOMLVOHVERGREGOMLVOHV	i	1		EFOSWISINETQLKGIKGEAIDTANHGENKDAUDDTDNGUMODG
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SANDS IGESULVSSITHTVSRKIHTPSSKTFSPAFFSLVQLC LQQDPEKRPSASSLLSHVFFKQMKESQDSILSLLPPAYNKPSI SLPPVLPWTEPECDFPDEKDSYWEF 1044 RGMSRLRYSHEDELQLPREPELFETGRQLLDEVEVATEPAGSRI VQEKVFKGLDLLEKAAEMLSQLDLFSRNEDLEEIASTDLKYLLV PAFOGALTMKQVNPSKRLDHLQRAREHFINVLTQCHCYHVAEFE LPKTMNNSAENHTANSSMAYPSLVAMASQRQAKTQRYKQKKELE HRLSAMKSAVESGQADDERVEFYTLHHLQRHUIT SLEEIESIDQ EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKVFGA GYPSLPTMTVSDWYEQHRKYGALPDQGIARAAPEEFRKAAQQQE EQEEKEEDDEQTLHRAREWDDWKDTHPRGYGRINGNMG KTVRIWPPVVKGESTVFRAHTATVRSVHFCSDGGSFVTASDDKT VKVWATHRQKFLFSLSQHINWYCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSTTGEYFASGGSDQWVWKSNF DIGDHGEVYKVRPPPATLASSMGNLTVSILEQRLTLEEDKLKQC LENQQLIMQRATP 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT VKVWATHRQKFLFSLSGHINWYCAKFSPDGRLIVSASDDKTVK LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQWWWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLEDGWNWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLEDGWNWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLEDGWNWKSNF DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLEDGLKQC LENQQLIMQRATP 5480 444 1952 LSITSRMEAELUKGRLQATTDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREEWILDGISSGKEQEEMKKQNQQDQCHQIQVLEQSI LRLEKEIQDLEKAELQISTKERAILKKLKSIERTTEDIIRSVKV ERRERARESIEDIYANIPDLFKSYIPSFLREINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSYYANSNHSAAYNGTDGLAPVEVEELIKQASERNSKSPTEYH EPVYANPFYRPTTPOGETVTPGPNPORRIKKTWRGLGLEDDEN				ASGOVPFODMERTOMILIONILYGDDVCDI DICTEDOGRAPHICEL
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5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQODQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSYYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPORETVTPGPNFORRIKIKTWELGIGWNESI	1	1	ì	DVK1HKLLQHYQLHSAAVNGLSFHPSGNVI.TTAGGDGTT VTZ DT
5480 444 1952 LENQQLIMQRATP LENQQLIMQRATP LSITSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETVTPGPNFORFIKIKTNGLGIGWNEGI	1	1	Į.	MEGRILLYTLHGHOGPATTVAFSRTGEVEASCGSDEOLMANUSCHE
5480 444 1952 LSENGOLIMOKATP CHLKKKALREKWLLDGISSGKEQEEMKKQNQODQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPORETVTPGPNFORFIKIKTWELGIGWNESI	ŀ	}	1	DIGDHGEVTKVPRPPATIASSMENT TUGTI TOPE TO
1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPQRETYTPGPNFORRIKIKTWELGIGWNESI				TENOOPIWORALD
QHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPORETVTPGPNFORFIKIKTWELGIGWNESI	5480	444	1952	T.C.I.TCDMDEADY INCOME.
CHEKKKALREKWILDGISSGKEGEEMKKQNQQDQHQIQVLEQSI LRLEKEIQDLEKAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPORETVTPGPNFORFIKIKTWELGIGWNESI	į į	1	1	DIL SKILLALLVKGRLQAITDKRKIQEEISQKRLKIEEDKLKH
EREERAELQISTKEEAILKKLKSIERTTEDIIRSVKV EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPORETVTPGPNFORFIKIKTWELGIGWNESI	1	Į.		UHLKKKALKEKWLLDGISSGKEGEEMKKONOODOHOTOM BOOT
KALYAMEI KVEKDLKTGESTVIPSRLRKEINEEKEDDEQNR KALYAMEI KVEKDLKTGESTVLS I PLPSDDFKGTG I KVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPORETVTPGPNFORR I KI KTWELGLGWESCI	J	į	į.	DRIBERE IQUIE KAELOISTKEEATI.KKI.KGTPPTTPDTTDCTTGT
KADIAWETKVERDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPORETVTPGPNFOERIKIKTWELGIGWESI	1	1	i	EREERAKESIEDIYANIPDLPKSYIPSRIRKEINEEVEDDEOND
RSVIAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPTEYH EPVYANPFYRPTTPORETVTPGPNFOERIKIKTWELGIGWEGI	İ	J	į	KALYAMEIKVEKDLKTGESTVI.SSIDI DODDBYGDATANA
DEVIANDE INPITEDRETVIEGRET ATTENDED TO THE CONTROL OF C	i			KSVYAVSSNHSAAVNGTDGLADUEUDDT KGTGTKVYDDGQ
HNMGNGLSEERGNNFNHISPIPPVPHPRSVIQQAEEKLHTPOKR	- 1	1		EDVYANDRYPRITTED PRINTERS OF THE PROPERTY OF TH
RIMMGNGLSEEKGNNFNHISPIPPVPHPRSVIQOAEEKLHTPOKR				EFVIANCE INCITED RETUTE OF PROPERTY INTERFECT OF THE PROPERTY
			<u>l</u>	THE THE PROPERTY OF THE PROPER

		the state of and	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	location	to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	amino acid	p=Proline, Q=Glutamine, R=Arginine,
	to first	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	1	Codon, /=possible nucleotide deletion,
	amino acid	sedneuce	\=possible nucleotide insertion)
	sequence		LMTPWEESNVMQDKDAPSPKPRLSPRET1FGKSEHQNSSPTCQE
	_	1	DEEDVRYNIVHSLPPDINDTEPVTMIFMGYQQAEDSEEDKKFLT
	[GYDGIIHAELVVIDDEEEEDEGEAEKPSYHPIAPHSQVYQPAKP
	}		TPLPRKRSEASPHEKHKS
			NSPGSVCLCQCVCPSLLHCLPPLLLLLLLLLLLHESPQPPALRV
5481	3	1422	VATSSDRNFMNKHQKPVLTGQRFKTRKRDEKEKFEPTVFRDTLV
	1	}	OGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGSMLA
	1		PGGTRIDDGDKTKMTNHCVFSANEDHETIRNYAQVFNKLIRRYK
	}	(YLEKAFEDEMKKLLLFLKAFSETEQTKLAMLSGILLGNGTLPAT
		1	ILTSLFTDSLVKEGIAASFAVKLFKAWMAEKDANSVTSSLRKAN
			LDKRLLELFPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSLGTR
		1	LDKRLLEBFPVNRQSVDAFAKIFIDAGIKERGDFERVQQSIGIK
		1	KELQKELQERLSQECPIKEVVLYVKEEMKRNDLPETAVIGLLWT
1	[1	CIMNAVEWNKKEELVAEQALKHLKQYAPLLAVFSSQGQSELILL
1	1	1	QKVQEYCYDNIHPMKAFQKIVVLFYKADVLSEEAILKWYKEAHV
1		<u> </u>	AKGKSVFLDQMKKFVEWLQNAEEESESEGEEN
5482	1492	528	THVVMTGMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLSLRL
} -	}]	EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPS
ĺ		Į.	CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPA
ł	1	l	LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGP
ł	\	1	GAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDA
{	}	Į.	IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTP
	1	1	TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVP
	1	,	VMVPAQSQAGSLV
5483	1	788	FFFFKGCRAGRGNESDYRKLEEMHQRFLVSERSKDDLQLRLTRA
}		,	ENRIKOLETOSSEEISRYQEMIQKLQNVLBSERENCGLVSEQRL
1		1	KLQQENKQLRKETESLRKIALEAQKKAKVKISTMEHEFSIKERG
ł		(FEVOLREMEDSNRNSIVELRHLLATQQKAANRWKEETKKLTESA
1		1	RIRINNLKSELSROKLHTOELLSQLEMANEKVAENEKLILEHOE
1			KANRLORRLSQAEERAASASQQLSVITVQRRKAASLMNLENI
5484	3	1997	IMADMEDLFGSDADSEAERKDSDSGSDSDSDQENAASGSNASGS
1			ESDQDERGDSGQPSNKELFGDDSEDEGASHHSGSDNHSERSDNR
1	1		SEASERSDHEDNDPSDVDQHSGSEAPNDDEDEGHRSDGGSHHSE
}	1	i	AEGSEKAHSDDEKWGREDKSDQSDDEKIQNSDDEERAQGSDEDK
	Ī	ł.	LONSDDDEKMONTDDEERPQLSDDERQQLSEEEKANSDDERPVA
1	1	1	SDNDDEKQNSDDEEQPQLSDEEKMQNSDDERPQASDEEHRHSDD
}	1	!	EERODHKSESARGSDSEDEVLRMKRKNAIASDSEADSDTEVPKD
1		1	NSGTMDLFGGADDISSGSDGEDKPPTPGQPVDENGLPQDQQEEE
	l	i	PIPETRIEVEIPKVNTDLGNDLYFVKLPNFLSVEPRPFDPQYYE
1	}	}	DEFEDEEMLDEEGRTRLKLKVENTIRWRIRRDEEGNEIKESNAR
1	· ·	1	IVKWSDGSMSLHLGNEVFDVYKAPLQGDHNHLFIRQGTGLQGQA
į.	ł	1	VFKTKLTFRPHSTDSATHRKMTLSLADRCSKTOKIRILPMAGRD
1		ì	PECORTEMIKKEEERLRASIRRESQQRRMREKQHQRGLSASYLE
		i	PDRYDEEEEGEESISLAAIKNRYKGGIREERARIYSSDSDEGSE
1	į .	}	EDKAQRLLKAKKLTSDEVRPNLFNSRGLSCTQEPTALNEELTDQ
1			AGTN
5485	161	1074	KRKILSSMMDSEAHEKRPPILTSSKQDISPHITNVGEMKHYLCG
		1	CCAAFNNVAITFPIQKVLFRQQLYGIKTRDAILQLRRDGFRNLY
}			RGILPPLMQKTTTLALMFGLYEDLSCLLHKHVSAPEFATSGVAA
1			VLAGTTEAIFTPLERVQTLLQDHKHHDKFTNTYQAFKALKCHGI
		}	GEYYRGLVPILFRNGLSNVLFFGLRGPIKEHLPTATTHSAHLVN
		1	DFICGGLLGAMLGFLFFPINVVKTRIQSQIGGEFQSFPKVFQKI
}			WLERDRKLINLFRGAHLNYHRSLISWGIINATYEFLLKVI
5486	1404	142	IPGSTISWSPAAARGLSVCRCCRLHPASAMDLFGDLPEPERSPR
		1	PAAGKEAOKGPLLFDDLPPASSTDSGSGGPLLFDDLPPASSGDS
1		}	GSLATSISOMVKTEGKGAKRKTSEEEKNGSEELVEKKVCKASSV
1	1		TEGLEGYVAEREGEREEMODAHVILNDITEECRPPSSLITRVSY
1			FAVFDGHGGIRASKFAAONLHONLIRKFPKGDVISVEKTVKRCL
1		}	LDTFKHTDEEFLKOASSOKPAWKDGSTATCVLAVDNILYIANLG
1	1		DSRAILCRYNEBSOKHAALSLSKEHNPTQYEERMRIQKAGGNVR
1]		DGRVLGVLEVSRSIGDGQYKRCGVTSVPDIRRCQLTPNDRFILL
1			

SEO	Predicted	1 Day 25 3	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ĺ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
į	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	bequence	Codon, /=possible nucleotide deletion,
<u> </u>		 -	\=possible nucleotide insertion)
			ACDGLFKVFTPEEAVNFILSCLEDEKIQTREGKSAADARYEAAC NRLANKAVQRGSADNVTVMVVRIGH
5487	535	182	AVSLEQIRGLQTPAPVPLPLQPCPSNCDMERVTLALLLLAGLTA
J	}		LEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK
1	ł		CKCKSSQKQHSPVPEKAIPLITPGSATTC
5488	1072	259	AMAASGEPQRQWQEEVAAVVVVGSCMTDLVSLTSRLPKTGETIH
j].		GHKFFIGFGKGANQCVQAARLGAMTSMVCKVGKDSFGNDYIEN
			LKQNDISTEFTYQTKDAATGTASIIVNNEGQNIIVIVAGANLLL
i	ł	1	NTEDLRAAANVISRAKVMVCQLEITPATSLEALTMARRSGVKTL
}	1		FNPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAADAGE
ŀ		[AALVLLKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVKAVD
<u> </u>	ì	}	TTVSFKI
5489	81	893	GKGPVAAFIDQSNIFLTDPXIFLGQWREEPKMPLLLLGETEPLK
1		1	LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV
ľ	i .		LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD
ļ	1		IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDFDSF
ł	1		FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSEDVG
í			NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEEETAEGEEP
			GEDEDS
5490	81	893	GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGRTEPLK
1	-		LERDCRSPVEPWAAASPDLA_ACLCHCQDLSSGAFPNRGVLGGV
	}		LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD
1			IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDFDSF
ĺ			FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAOKEGSEDVG
į		•	NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEEETAEGEEP
5491			GEDEDS
5491	204	1194	GSAPRLSLGPTGAQARDPDWWARPPSRPYTQSKEDRPDTEGRSE
1 1			QGDMASSFLPAGAITGDSGGELSSGDDSGEVEFPHSPEIERTSC
			LAELFEKAAAHLQGLIQVASREQLLYLYARYKQVKVGNCNTPKP
1	1		SFFDFEGKQKWBAWKALGDSSPSQAMQEYIAVVKKLDPGWNPQI
1 1	!		PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCRENNIDH
1 1			ITKAIKSKNVDVNVKDEEGRALLHWACDRGHKELVTVLLQHRAD
1 1	[INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDGCLP
5492	3	1896	EEVTGCKTVSLVLQRHTTGKA
}	J	1036	ASKNPLSAVCTTGIMSSLAVRDPAMDRSLRSVFVGNIPYEATEE
1 1			QLKDIFSEVGSVVSFRLVYDRETGKPKGYGFCEYQDQETALSAM
[]		ĺ	RNLNGREFSGRALRVDNAASEKNKEELKSLGPAAPIIDSPYGDP
1 1			IDPEDAPESITRAVASLPPEQMFELMKQMKLCVQNSHQEARNML
1			LQNPQLAYALLQAQVVMRIMDPEIALKILHRKIHVTPLIPGKSQ SVSVSGPGPGPGPGLCPGPNVLLNQQNPPAPQPQHLARRPVKDI
[[1	PPLMQTPIQGGIPAPGPIPAAVPGAGPGSLTPGGAMQPQLGMPG
1 1	ļ		VGPVPLERGQVQMSDPRAPIPRGPVTPGGLPPRGLLGDAPNDPR
	}		GGTLLSVTGEVEPRGYLGPPHQGPPMHHASGHDTRGPSSHEMRG
1 1	1	1	GPLGDPRLLIGEPRGPMIDQRGLPMDGRGGRDSRAMETRAMETE
1	1	!	VLETRVMERRGMETCAMETRGMEARGMDARGLEMRGPVPSSRGP
; 1	1		MTGGIQGPGPINIGAGGPPQGPRQVPGISGVGNPGAGMQGTGIQ
j f	İ		GTGMQGAGIQGGGMQGAGIQGVSIQGGGIQGGGIQGASKQGGSQ
1 1			PSSFSPGQSQVTPQDQEKAALIMQVLQLTADQIAMLPPEQRQSI
			LILKEQIQKSTGAS
5493	1	1876	RAPMMTKAVPEEPRKPGRLTQALNSPLTWEHVWICVPGGTPDCL
i 1	i	-	TDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIELKKSLH
	1	}	VQKSDVDLMRTKLRRLEEENSRKDRQIEQLLDPSRGTDFVRTLA
[,		EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLE
)	J	EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKRQKKM
l		j	GSALLSLSRSVQELTEENQSLKEDLDRVLSTSPTISKTQGYVEW
1		İ	SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL
		j	HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEVKQLL
.]	}		QAKADLEKBLECAREGEEERREREEVLRERIQTLTSKLQELQEM
1	1	i	KKEEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSEEGLPRP
L		ľ	RSPCSDGRRDAAARVLQAQWKVYKHKKKKAVLDEAAVVLQAAFR
			THE TANK THE TANK TO THE TANK TO THE TANK TO THE TANK TO THE TANK

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	p=Proline, Q=Glutamine, R=Arginine,
İ	to first	amino acid	p=proline, Q=Glutamine, R=Alginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	 		GHLTRTKLLASKAHGSEPPSVPGLPDQSSPVPRVPSPIAQATGS
	1	l l	PVQEEAIVIIQSALRAHLARARHSATGKRTTTAASTRRRSASAT
	1	1	HGDASSPPFLAALPDPSPSGPQAVAPLPGDDVNSDDSDDIVIAP
	ţ	}	SLPTKNFPV
5494	71	536	RSKAKIGTPTREVPSTDMKVRRESSSSLTHRPAPSPATPRLLGT
5494	1 1	1 330	RRVLLGVSEGTGCADAMELVLVFLCSLLAPMVLASAAEKEKEMD
	1		PFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCKCSFNQKPRAP
		1	
	l	<u> </u>	GDEEAQVENLITANATEPQKAEN
5495	273	2168	DSLLLIQVDTMPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAG
	ì	İ	ELRPASLVVLPRSLAPAFERFCQVNTGPLPLLGQSEPEKWMLPP
			QGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFL
	1	1	GCSFSLEEALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCP
	1	1	LVVTMRPIPKDKLEGLVRACCSLGGEQGQPVHMGDPELLGIKEL
l	1	}	SKPAYGDAMVCPPGEVPVFWPSPLTSLGAVSSCETPLAFASIPG
	I		CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASQ
	1	1	KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSVLITT
	1		GFPTHFNHEPPEETDGPPGAVALVAFLQALEKEVAIIVDQRAWN
ł		1	LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAFLCKNGDPQT
}]	j	PRFDHLVAIERAGRAADGNYYNARKMNIKHLVDPIDDLFLAAKK
ĺ	1	1	IPGISSTGVGDGGNELGMGKVKEAVRRHIRHGDVIACDVEADFA
}	}		VIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAPGDQA
1			WTQALPSVIKBEKMLGILVQHKVRSGVSGIVGMEVDGLPFHNTH
i	1	(
ł		<u> </u>	AEMIQKLVDVTTAQV QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWIDYEG
5496	3	2408	QDTKMHETYKGNITPQLINKNITGKISAAIDVWAVIFSQLWIDISG
1	•	l l	MKSGKGRPISPVDSFPLSIWICQPTRYAESQKEPQTCNQVSLNT
1	}		SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSSDTFFR
}	1	1	FSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLILLSE
{	1	ł	NLRKDVEAVTGSPASOTSICIGILLRSAELALLLHPVDQANTLK
	1)	SPVSESVSPVVPDYLPTENGDFLSSKRKQISRDINRIRSVTVNH
		1	MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYLSDKH
1	Į.	1	LGKISEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVLNYRE
ł	1	1	DSNILSFDSDGNQNILSSTLTSKGNETIESIFKAEDLLPEAASL
1	i	1	SENLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCVSYKN
j	1	1	MKRSSSQMSLDTISLDSMILEEQLLESDGSDSHMFLEKGNKKNS
		1	TTNYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHDDLMS
i	ł		VVVFKITGVNGEIDIRGEDTEICLQVNQVTPDQLGNISLRHYLC
	İ	1	NRPVGSDQKAVIHSKSSPEISLRFESGPGAVIHSLLAEKNGFLQ
[1	CHIKNFSTEFLTSSLMNIQHFLEDETVATVMPMKIQVSNTKINL
1	1	1	CHIKNESTEE ETSPENTOUT PEDETANT AUGUSTONISTING
1	1		KDDSPRSSTVSLEPAPVTVHIDHLVVERSDDGSFHIRDSHMLNT
1	{	{	GNDLKENVKSDSVLLTSGKYDLKKQRSVTQATQTSPGVPWPSQS
1	}	1	ANFPEFSFDFTREQLMEENESLKQELAKAKMALAEAHLEKDALL
1			HHIKKMTVE
5497	1821	3308	SISKLLKRRSNIDAYLLSNSCAFFAPRLFSLASQIIREQQSPNV
1		}	CFIYKYSGFPSLECOCHFVSPHSSCYINFFSFPPPFFVCFQLSN
1			GFSHYSLSSESHVGPTGAGLFPHCLPASRLLPRVTSVHLPDYAH
	i	1	YYTIGPGMFPSSQIPSWKDWAKPGPYDQPLVNTLQRRKEKREPD
1	J	}	PNGGGPTTASGPPAAAEEAQRPRSMTVSAATRPGEEMEACEELA
			LALSRGLQLDTQRSSRDSLQCSSGYSTQTTTPCCSEDTIPSQVS
1	l l		DYDYFSVSGDQEADQQEFDKSSTIPRNSDISQSYRRMFQAKRPA
1	1	· ·	STAGLPTTLGPAMVTPGVATIRRTPSTKPSVRRGTIGAGPIPIK
1	1		TPVIPVKTPTVPDLPGVLPAPPDGPEERGEHSPESPSVGEGPQG
]	1		VTSMPSSMWSGQASVNPPLPGPKPSIPBEHRQAIPBSEAEDQER
1	1	1	VISMYSSIMSGUASVINFFDFGFAFSTFBBGRQATFBSBAEDQBR
1			EPPSATVSPGQIPESDPADLSPRDTPQGEDMLNAIRRGVKLKKT
			TTNDRSAPRFS
5498	2434	1492	ILTHQEIFTGEKPCECGKASIQMSHLSQQKIYSGENPFACKVCG
1	1		KVFSHKSNLTEHEHFHTREKPFECNECGKAFSQKQYVIKHQNTH
	1		TGEKLFECNECGKSFSOKENLLTHOKIHTGEKPFECKDCGKAFI
1	1		OKSNIJIRHORTHTGEKPFVCKECGKTFSGKSNLTEHEKIHIGEK
i			,
	}	j	PFKCSECGTAFGOKKYLIKHONIHTGEKPYECNECGKAFSQRTS
		-	PFKCSECGTAFGQKKYLIKHQNIHTGEKPYECNECGKAFSQRTS LIVHVRIHSGDKPYECNVCGKAFSQSSSLTVHVRSHTGEKPYGC
			PFKCSECGTAFGQKKYLIKHQNIHTGEKPYECNECGKAFSQRTS LIVHVRIHSGDKPYECNVCGKAFSQSSSLTVHVRSHTGEKPYGC NECGKAFSQFSTLALHLRIHTGKKPYQCSECGKAFSQKSHHIRH

PCT/US00/34263

SEO	Predicted	The diameter	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	I MEMIGRIE USCVSTAINA DENCARALIA NELLA N
l	location	corresponding	Glucamic Acid, F=Phenylalaning C_Clusical
j	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
J	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	(COUCH, /=POSSIBLE nucleatide deletion
	sequence		\=possible nucleotide insertion)
5499			QKIHTH
3,39	324	926	GFGQIGRGHKITTYPFSPRKSGRKGMAQSQGWVKRYIKAFCKGF
- 1	İ		FVAVPVAVTELDRVACVARVEGASMOPSLINDGGSOSSDUTT I NEL
1	1	į.	WKVKNFEVHRGDIVSLVSPKNPEOKIIKRVIALECDIVERTCHV
j	1		NRYVKVPRGHIWVEGDHHGHSFDSNSFGPVSLGLLHAHATHILW
5500	1978	1286	PPERWQKLESVLPPERLPVQREEE
		1	KPDWRLQNLPPRLYLWRSSRFGFGHLKKRLQMDFKIEHTWDGFP
1	j		VKHEPVFIRLNPGDRGVMMDISAPFFRDPPAPLGEPGKPFNELW DYEVVEAPFLNDITEQYLEVELCPHGQHLVLLLSGRRNVWKQEL
1	Į		PLSFRVSRGETKWEGKAYLPWSYFPPNVTKFNSFAIHGSKDKRS
	į.	1	YEALYPVPQHBLQQGQKPDFHCLEYFKSFNFNTLLGEEWKQPES
5501			DEMPTERCOI
3301	2927	2226	CRPPVSARVAPGHQGAVGGSGRRPARVEVVDAAARPSSRPFSLP
1	[AAIMLALISRLLDWFRSLFWKEEMELTI,VGI,OVSGKTTEIDDUX
}			SGQFSEDMIPTVGFNMRKVTKGNVTIKIWDICGODDFDSMWDDV
-			CRGVNAIVYMIDAADREKIEASRNELHNIJDKROLOGIDUR VEG
ì		1	NKRDLPNALDEKOLIEKMNLSAIQDREICCYSISCKEKDNIDIT
5502	3	824	
1			NSAFPVWVPERTALLTCPLGAAPGSSREAPGIAGPPNSTAMSKL GKFFKGGGSSKSRAAPSPQEALVRLRETEEMLGKKQEYLENRIQ
1	1		REIALAKKHGTQNKRAALQALKRKKRFEKQLTQIDGTLSTIEFQ
Í	1		REALENSHINTEVLRNMGFAAKAMKSVHENMDLNKIDDLMQEIT
1			EQQDIAQEISEAFSQRVGFGDDFDEDELMAELEELEGEELNKKM
ŀ	1		THIRLPNYPSSSLPAQPNRKPGMSSTARRSRAASSORAEREDDD
5503	216		INDLAAWAT
}	220.	654	KGVRRRGRVRSDSEDSHLGYFKMSFLLPKLTSKKEVDQAIKSTA
1	ļ		EKVLVLRFGRDEDPVCLQLDDILSKTSSDISKMAATVIJDUDOM [
L		İ	AVYTQYFDISYIPSTVFFFNGQHMKVDYGGEDPALRSIKAVRRT SPAGTLGEKPVNS
5504	58	3563	QLSFSFQAPVTFDDITVYLLQEEWVLLSQQQKELCGSNKLVAPL
}	1	j	GPTVANPELFRKFGRGPEPWLGSVQGQRSLLEHHPGKKQMGYMG
1	1		EMEVQGPTRESGQSLPPQKKAYLSHLSTGSGHIEGDWAGRNRKL
[į i	1	DAPKSIQKSWFVQFPWLIMNEEOTALFCSACDFVDCTDDVDCDr
1	}		TEGYTGPFKVETLKYHAKSKAHMFCVNALAAPDDTWAAPEDGTD
1	1		DPPGDVLASPEPLFTADCPIFYPPGPLGGEDGMAFI (DCGDAD)
	1	1	EDPGGDGAIPAMYLDCISDLROKETTDGTHSSSDTNTLVNDAVE
1	1		SCIQDPSAEGLSEEVPVVFEELPVVFEDVAVYFTREEWGMLDKR
1	1	j	QKELYRDVMRMNYELLASLGPAAAKPDLISKLERRAAFWIKDPN GPKWGKGRPPGNKKMVAVREADTQASAADSALLPGSPVEARASC
1			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQFPWLVIDPKETKL
1	1		FUSACLERPNLHDKSSRLVRGYTGDFKVFTT.VVDDVGVAVDT CT.
ł		j ,	NIVELKEDIPHTALVPEISSDLMANMEHFFNAAVCTAVIICDEL I
1	1		DFEKILQLLQSTGTVILGKYRNRTACTOFTKVISFTIKDETIRD
1	1	1	VKNSPCVSVLLDSSTDASEOACVGIYIRYFKOMENKESVITTAR
1	1 (LYSETADGYFETIVSALDELDIPFRKPGWVVGIGTDGSAMLSCD
	1] '	GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH
	1		IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR
	<u> </u>	1;	RRTLHALLVSWPALARHLORVAEAGGOIGHRAKGMLKLMRGFHF VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES
1	į	j:	LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV
j [*]			LIGIEYLQQRFDADRPPOLKNMEVFDTMAWPSGTET.ASECNDD
		1 1	LNLARY FECSLPTGYSEEALLEEWLGLKTIAOHI.PESMI.CKNAI
		1 2	AQHCRFPLLSKLMAVVVCVPISTSCCERGEKAMNDIDTDTDTDTTTV
		5	SNEV LNMLMMTAVNGVAVTEYDPOPAIOHWYLTSSGPPPCULTUR
l İ		10	-AQVPARSPASARLRKEEMGALYVEEPRTOKDDII.DCDEAADTT
5505	3312		COCIMEPPERLLYPHTSOEAPGMS [
·		1219 N	ICSPRSLSAAKMSNRNNNKLPSNLPQLQNLIKRDPPAYIEEFLQ
		1 5	INHIASHVELFKLOPNKPSKELAELUMEMAOT SUCVEDUL SAR
		=	POEVKOLLSCHTVLDPDLRMTFCKALILLRNKNLINPSSLLEL
			PELFRCHDKLLRKTLYTHIVTDIKNINAKHKNNKVNVVLQNFM

	_ _		Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	Glutamic Acid, Fernenylatanine, George Inc.
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
- {	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- {	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon. /=possible nucleotide deletion,
		Sequence	\-nossible nucleotide insertion)
	sequence	<u> </u>	VTMLRDSNATAAKMSLDVMIELYRRNIWNDAKTVNVITTACFSK
		1	VTKILVAALTFFLGKDEDEKQDSDSESEDDGPTARDLLVQYATG
	ì ·	1	KKSSKNKKKLEKAMKVLKKHRKKKKPEVFNFSAIHLIHDPQDFA
•].	EKLLKQLECCKERFEVKMMLMNLISRLVGIHELFLFNFYPFLQR
		Į.	FLQPHQREVTKILLFAAQASHHLVPPEIIQSLLMTVANNFVTDK
)	l	NSGEVMTVGINAIKEITARCPLAMTEELLQDLAQYKTHKDKNVM
		\	NSGEVMTVGINALKEITARCPHAMIEEHDQDHAQIRINGEVCPLDAV
		i	MSARTLIHLFRTLNPQMLQKKFRGKPTEASIEARVQEYGELDAK
	1		DYIPGAEVLEVEKEENAENDEDGWESTSLSEEEDADGEWIDVQH
	ł	i	SSDEEQQEISKKLNSMPMEERKAKAAAISTSRVLTQEDFQKIRM
	k	1	AQMRKELDAAPGKSQKRKYIEIDSDEEPRGELLSLRDIERLHKK
	1	į	PKSDKETRLATAMAGKTDRKEFVRKKTKTNPFSSSTNKEKKKQK
	1	1	NEMMMRYSONVRSKNKRSFREKOLALRDALLKKKKRMK
		1531	ERCOLOGORGGSAPGEGGSSAWPAPAHPLPEREREREALCPGRS
5506	1	1531	CSCGGGEETPGTTPVWSPLEGGGDEELRPNPYVRFPYRWWAVVV
		1	LAAFPSLGAGGETPEAPPESWTQLWFFRFVVNAAGYASFMVPGY
		1	LLVQYFRRKNYLETGRGLCFPLVKACVFGNEPKASDEVPLAPRT
	1	1	EAAETTPMWQALKLLFCATGLQVSYLTWGVLQERVMTRSYGATA
	1		TSPGERFIDSQFLVLMNRVLALIVAGLSCVLCKQPRHGAPMYRY
	1 .	ì	TSPGERFTDSQFEVLMNRVDADITARDSCAFERENCE SFASLSNVLSSWCQYEALKFVSFPTQVLAKASKVIPVMLMGKLV
	-{	1	SFASLSNVLSSWCQYEALKFVSFFTQVHARASKVII VILLIGUET
	1	1 '	SRRSYEHWEYLTATLISIGVSMFLLSSGPEPRSSPATTLSGLIL
	ì	1	LAGYIAFDSFTSNWQDALFAYKMSSVQMMFGVNFFSCLFTVGSL
	1	.	LEQGALLEGTRFMGRHSEFAAHALLLSICSACGQLFIFYTIGQF
	i .	1	GAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGGLGVAVVFAALL
		1	LRVYARGRLKQRGKKAVPVESPVQKV
5507	3704	1271	PRGTRRCRPAGRASRRARRRPPCPGPAAPGSLEIGGFGTAAGKK
3507	3,04	1	VAVADVOEGPMREHODOLOVLLVETKEDNQCNGECRACEKAGEK
l	· ·		CTUTKEAOAVLACFLDKHHDIIIIDHRNPRQLDAEALCRSIRSS
ì	}	Į	KISENTVIVGVVRRVDREELSVMPFISAGFTRRYVENPNIMACY
1	ł	l .	NELLOLEFGEVRSOLKLRACNSVFTALENSEDAIZITSEDRFIQ
1	ì		YANPAFETTMGYQSGELIGKELGEVPINEKKADLLDTINSCIRI
1	1	1	GKEWQGIYYAKKNGDNIQQNVKIIPVIGQGGKIRHYVSIIRVC
i	1	[NGNNKAEKISBCVQSDTHTDNQTGKHKDRRKGSLDVKAVASRAT
1	})	EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA
	1	ľ	LDRVLEILRTTELYSPOFGAKDDDPHANDLVGGLMSDGLRRLSG
]	1	1	NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEYWDFDI
ì	1	i	NEYVLSTKNTQMVSSNITTPISEDDVPFRIARATEMESTTOTE
1	1	1	FELEAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIE
			ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL
]	IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF
	· {		QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN
1			KPVNS INKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI
ł			KCADVSNPCRPLOYCIEWAARISEEYFSQTDEEKQQGLPVVMPV
		Ì	FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF
l			KYWKGI DEMKI RNI RPPPB
			LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN
5508	1151	691	VLKKVLVDQLVASPLLGVWYFLGLGCLEGQTVGESCQELREKFW
}	1	1	EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL
[1		
ł			KYRSPVPLTPPGCVALDTRAD
5509	1238	619	RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE
1	Į.	1	VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP
1	}		ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR
1	Ì	1	LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM
j	1	1	EDEUTWVDSSKIKRHVLEYNEERDDFDLEA
L		1195	PACAHUSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM
5510	96	1173	DEGEROPPEDSSEEAPPATONFI IPKKEIHTVPDMGKWKRSQAY
1		ļ	ADVIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID
	i		ETPPVDQPSRFGNKAYRTWYAKLDEEAENLVATVVPTHLAAAVP
ł		ı	ETPPVDQPSRFGNKAYRTWYAKLDBEAENDVAT VVFITTEATAV
		1	
			EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ
			TATUFKVFNRYLEVMRKLOKTYRMEPAGSQGVWGLDDFQFLPF1
			IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPF1 WGGSOLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT
			TATUFKVFNRYLEVMRKLOKTYRMEPAGSQGVWGLDDFQFLPF1

Deginning nucleotide location	SEQ	Predicted	T 22 - 2	
NO: nucleotide location corresponding to first amino acid amino acid residue of amino acid amino acid sequence		beginning	Predicted end	
location corresponding to first amino acid emino ac	70:	nucleotide		I IGTGLONENC, USLVSTBING DENGELSE E
Leleucine, Mambethionine, Napparagine, Peptoline, Gollutanine, Napparagine, peptoline, Gollutanine, Napparagine, peptoline, Gollutanine, Napparagine, peptoline, Gollutanine, Napparagine, peptoline, Gollutanine, Napparagine, peptoline, Seguence 5511 276 1980 Seguence Segue	ł	location		/ Caucanite Acto, rephenylalaning of di
to first amino acid residue of residue of sequence sequence sequence sequence sequence 5511 276 1980 1980 KISPVIAIR-PERILTYSTERVITESKEEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISELISEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISEVADFOLSVUSILLEKKND HSSPIDLOVAKILSEKLISEVADFOLSVUSIKASKRESPIDLOVAKILSE LGDVOALSEKURISEVADFOLSVUSIKASKRESPIDLOVAKILSE SOZVIKLISEKLISEVADFOLSVUSIKASKRESPIDLISEVANSKRESPIDLOVAKILSE HSSPIDLOVAKILSEKLISEVADFOLSVUSIKASKRESPIDLOVAKILSE HSSPIDLOVAKILSEKLISEVADFOLSVUSIKASKRESPIDLOVAKILSE HSSPIDLOVAKILSEKLISEVADFOLSVUSIKASKRESPIDLOVAKILSE HSSPIDLOVAKILSEKRISTIVATIVATIVALOVAKILSEVANSKRESPIDLOVAKILSE HSSPIDLOVAKILSEKRISTIVATIVALOVAKILSEKRISTIVATIVALOVAKILSE TRANTENDOPALOVATILSEKRISTIVATIVALOVAKILSEKRISTIVATIVALOVAKILSE 5514 1295 449 VARRSSINGANFERBALDFORSKINSTATIVALOVAKINSKERE FORDIVALIONAKILLERENTI TORKINITALOVAKINAKIL MENSALFYRES TYVAHTIGERORALOVATIVAKKYSEESE TORIVALIONAKILLERENTI TORKINITALOVAKINAKE SPITERCOPSKOROVANILLERENTTI TORKINITALOVAKINAKE SPITERCOPSKOROVANILLERENTTI TORKINITALOVAKINAKE VARSSINGANIPATIVATIVATIVATIVATIVATIVALOVAKINAKE VARSSINGANIPATIVATIVATIVATIVATIVALOVAKINAKE SPITERCOPSKOROVANILLERENTTI TORKINITALOVAKINAKE VARSSINGANIPATIVATIVATIVALOVAKINAKE VARSSINGANIPATIVATIVATIVATIVATIVALOVAKINAKE VARSSINGANIPATIVATIVATIVALOVAKINATIVALOVAKINA VARSSINGANIPATIVATIVATIVALITALOVAKINATIVALOVAKINATIVALOVAKINA VARSSINGANIPATIVATIVATIVALITALOVAKINATIVALOVAKINATIVALOVAKINATIVALOVAKINATIVALOVAKINATIVALOVAKINATIVALOVAKINATIVALOVAKINATIVALOVAKINATIVALOV	ì			
residue of amino acid sequence	1			P=Proline, O=Glutamine, N=Asparagine,
amino acid sequence Sequence	- 1			S=Serine, T=Threonine V-Valine
Sequence	i			W=Tryptophan, Y=Tyrosine Y-Unknown + a
SSII 276		1	sequence	COUCH, /=possible nucleotide dolar:
KLSRVIMIPPENLITSISAVPISOKEVADFOLSVDELLEKDNÜ HSRPIDIÇVQAKRLARKROTUVVESIORTVYPKINRELITK TVLQQVIEDGSKYCLKSELFSGLPOKKIVUFESSPNVAKKPHUR HSRPIDIGNPAMILKSELGHQVIRINDOMOMOFOLLGTOTOL FGYEEKLOSNPIORILFEVYVQVNKEADDKS VAKAAQEFFORLE LGGVOALSHOKKPRDISIEEVIRVYKLOVYPDISGESPYBEK SOBVLKLLESSGLLKTIKGTAVVDLSGKGPPSSICTVRKSDGT SVATATDLAAADIRMKNYNPDVMITVTOKGGKKHGQVSPOMLKT MGYDAAECQHVPFVVQGMKTRRGDVTFLEDVINDOTACLOFMON MASIKTTKELKNPQETASRVLALALIIQDFKGLLLSDYKFSMDR VPOSRGDTGVPLQYTHARLISLEEFTGVLINDOTACLOFMON MASIKTTKELKNPQETASRVLALALIIQDFKGLLLSDYKFSMDR VPOSRGDTGVPLQYTHARLISLEETGVLINDOTACLOFMON MASIKTTKELKNPQETASRVLALALIIQDFKGLLLSDYKFSMDR VPOSRGDTGVPLQYTHARLISLEETGVLINDOTACLOFMON MASIKTTKELKNPQETASRVLALALIIQDFKGLLLSDYKFSMDR VPOSRGDTGVPLQYTHARLISLEETGVLINDOTACLOFMON MASIKTTKELKNPQETASRVLALGFTBVCKM 1015 DPSLLETTTVGTVLUVLVLKSNNSRREPTITODPEAKYPSML LEKKELSSNTRRFRSGLSPSDHVLGLHGVGNYVOLLAKIDNELV RAYTPVSSDDDRGFVDLIIKIYFKNVHOOYBEGKHTQVLENM LOETIFFRGFGRGLFYGFDSPSDHULGHGVGNYVOLLAKIDNELV RAYTPVSSDDDRGFVDLIIKIYFKNUHOOYBEGKHTQVLENM LOETIFFRGFGRGLFYGFDSTRSLEFGNYLDGTSPKKTLADHILGMIA GGTGITPMLQLIRHTTUDFDGWSTPKKTLADHILGMIA GGTGITPMLQLIRHTTUDFDGWSTPKKTLADHILGMIA GGTGITPMLQLIRHTTUDFDGWSTPKKTLADHILGMIA GGTGITPMLQLIRHTTUDFDGWSTPKKTLADHILGMIA GGTGITPMLQLIRHTUDFDGWSTPFIKKTLADHILGMIA GGTGITPMLQLIRHTUDFDGWSTPFIKKTLADHILGMIA GGTGITPMLQLIRHTUDFDGWSTPFIKKTLADHILGMIA GGTGITPMLQLIRHTUDFTGWSTRSLEFGNATGT FAQETFEKQYKQTICLDFFFIKTLOFMIATURDGGSGTSSFTS TTPLAPERGOPGSRDTMSDSEESQDRGCKNVLFSSSPFPPSFPS PPTSRGOPGSRDTMSDSEESQDRGCKNVLFSSSPFPPSFPS PPTSRGOPGSRDTMSDSEESGDRGCKNVLFSSSPFPSSKTG GCMLDKXTGAQGVLUVDTTTGGSFSHEDMYTVVKKVSESSE TOPLVANACHOLGHHFTMTFFGHLAGTVVTANTUVMCPMSESSFT TOPLVANACHOLGHHFTMTFFGHLAGTVVTANTUVMCPMSESSFTTO FAQETFAGKYKGTGGMIKLGKHRTIKPEKHLKFCQENGFSSHFVSAKTG CYLLGSKTLFYR-ELLGGGTTGCWARADIUTTGTTSSLFTSTLFT TRAGTAGRGGSTGRCTTSVTANTUTDTTTSSLFTLYNT KRGGFAGETGRCTITSVTKAGAGNACVANTGGTSLADLATTUTDTTSSLFT KGFFAGETGRCTITSVTKAGAGNACVANTGGTSLADLATTUTDTSSLFOXT KRGGFAGETGRCTITSVTKAGAGNACVANTGGTSLADLATTUTDTSSLFWKGAGAGAGA FUNGGGGGGFFAFTASTLFFANTLAGDTINGVGRSVKE TYNOTGRG DDKCLANDFUNGGTSNLEGFTHRLLA	5511		<u> </u>	(\=possible nucleotide insertion)
TOLQQVIESGKYGLKSELTSGUPGVIVESESPONAKKPHVG HERSTIIGNPIANLKSALGHQVIVESESPONAKKPHVG HERSTIIGNPIANLKSALGHQVIVESESPONAKKPHVG HERSTIIGNPIANLKSALGHQVIVESESPONAKKPHVG HERSTIIGNPIANLKSALGHQVIVESESPONAKKPHVG FGVESELGOSPUGNETEVYQVONKENGDVSIGLTGFOLL LGDVQALSIMOKYRDLSIESTIRVYRRIGUVPDBYSGESFYREK SQEVLKLESKGLLAKTIKGTAVVUGKSGPDSSIGTVRRSGSG SUSTATRDLAAAIDEMKNNPDTMIYVPDKGQKKHFQQVFQMLKI MGYDABERCQNUPPGVVGMKTRGDUPTILDURELQEMLGN MASIKTTELKNPQETARRVGLAALIJOPKGLLLSDYKFSNDR VPQSRGDTGVYPLQYTHARLHSILESTFGGGYLNDBTACLOEFOS VSILQHLLRFDEVUKNSSOOPGPRHTVSYLLTISHLAAVAHKTL QIKOSPPEVAGARLHLFKAVRSVLANGKKLLGITPVCRM VPQSRGDTGVYLVLVLKSNNSRGEPTIQDPEAKYPLP. IRKEKISHMTRRFREGJSEDHVLGLPVGNYVQLLAKIDNBILVV RAYTPUSDDDRGFUHLIKIYYKNVLVLKSNNSRGEPTIQDPEAKYPLP. IRKEKISHMTRRFREGJSEDHVLGLPVGNYVQLLAKIDNBILV GGTGITFMGLIREITUNDSDRTRBSLIFANGVSPTGDHIVFSINK IGETIFFRGPRGRIFYHGPGANGJIRVYSGFVTADMIKEHLPPPAK TILLVGCAPPLUCTAAHNLEKLGYTQDHIFTY RAYTPUSDDDRGFUHLIKIYTKNVLYDSFRTEDDILVRRELE BIARTHPDQPDLWYTLDRPDIGKYSSGFVTADMIKEHLPPPAK TSTLLLVGCAPPLUCTAAHNLEKLGYTQDHIFTY ARSTFRKGYKGYTGLIFFLRRITLPGCANFSSHEVPSSFPP PPTSRCOPGSSBTMSDSESESGDRGLKTUVLGGASGKTSITTT ARSTFRKGYKGYTGLIFFLRRITLPGCANFSSHEVPSAKTG GKMLDKYIYGAGGVLLVYDITTYQSFRNLEBDHTVVKKVSESSS TOPLVALVORKIDLEHMRTTKPRKHLRFTLGENSSSHEVPSAKTG DSVPLCPGVVAABILGIKLNKARIEGSGRVVKADIVNYNGEPMS TVMPPRSSMCAVQ VNRFSWIMONFEGHALPGTFFFIIGLWRCTKSILKYICKKGKRT CYLGSKKTLFYR-EILGITIVCMALTGROPTYPTSAKTG VKGGHNOLLIGHHFTNYFFPGLLGVADLICTTISSLPVSLITEL MERALLPVARAFTLYBERHLDIFFHGLUVLVVLVTGUVAFLGLVAL EFLURNNULBELLRSSLILLGGSSFFFENDEGOFTHAPVERSLIFTL MERALLPVARAFTLYBERHENDIFFHGRENDEGOFTHYPSGGFANDIM DHEN ILPLTIIGFCHTAAVTIVUVGMWYAFITNLVKSLKRLGSS FVEGVLUKARRERGSEEFM PTKGGFAGETGRCTISVIKRAGMPKPVVQYNINNEELYSIL KEPIHLLVFRILLUNPRDREVUTIESVLCPSHFPETLIRVLPKX KEPIHLLVFRILLUNPRDREVUTIESVLCPSHFPETLIRVLPKX KEPIHLLVFRILLUNPRDREVUTIESVLCPSHFPETLIRVLPKX KREGTGRFTITSVLGKRAMPKVRVOYGNESLUPPINGE VLNCGGALFFGRGGGGGGGGSTAVUTDLGGRVATE VVDCTGRIPDWCGANLHKEHFTYSSFFFWGAGGAGGG KRYGGGGGGCANACHGGISAPPSASSFFFFFRSFFFFFRANGDURINGFSTEK VXNCGGGGFFFFFTASSFFFFFRANGDULLGUNGGGGGGG KRYGGGGGGCANGTSTEDDVUTGGFSTASSF		276	1980	KLSRVLNLPPENLITSISAVPISOKEFVADEOLGUDGILDVEN
HERST I IONFTANLEREISGLPOKET VURGEGGFOLLEGGEOL FOYEEKLOSNELOHLEVYVOUNKEAADDES VARAAGEFFORLE LOGVOALSHOKKERDISTEST INVYVOYDE VSEESES YEEK SOEVLKLLESKGLLKTIKGTAVVOLSCHIOPESSICTVARSDOT SLYATINGLAAAIDRIKKINFOTHI VYLOYBUSGLESSY TEK SOEVLKLLESKGLLKTIKGTAVVOLSCHIOPESSICTVARSDOT SLYATINGLAAAIDRIKKINFOTHI VYLOYBUSGKKHEPQOVPOKIKI MASIKITIKELKINPOTARROVLALDID VKILLIADIYKISMOR VYOSKODTGVELQYTHARLISLEETTECGYLINDFINTALOEPOS VSLICHLIRFPELLVIKSSODFOPRHI VSYLLITISHLAAVAHKTL OIKUSPPEVAGARIHLEKAVRSULADIYKISMORREEFITLODEAKYPLPI IEKEKISHITTRIRFRIGERIDI JIVANKILLIGITPVCRM DFSILLITITVTGVIVULVIKISMISRREEFITLODEAKYPLPI IEKEKISHITTRIRFRIGERIDI JIVANHOVYEEGGKHTQVYLENM VOORTITPMLQLIREITKOPSDETRIRSLIFANOTEEDILLVIRELE EIAATHEPOPDLWYLDEPSIGKKISTOPEPKKTLADHILOMIA GGTGITPMLQLIREITKOPSDETRIRSLIFANOTEEDILLVIRELE EIAATHEPOPDLWYLDEPPIGKTAAHINLEKLGYTODHI FIT ARWILESSOSPEPPAGAETFGKISCERVILESSSPPPEBEGFPE PPTSRGOFGSRDIMSDESEESODROLKIVULGDGASGKTSLITTC FAQSTFGKKYKOTIGLDPFIRRITLPGKTVLTOG VIDOGGTTG CKMLDKYIVAGGOLLVYDITTYOG PENLEDHYTVIKVESESE DSVELCPGKVAAELIGIKLNKRAEIGOSGCWVKADIVANVOEPHS STUHPPSSMCAVO VARSEMIHMENTERFERGSCRUVERSSPPPEBEGFSHPESSERT DSVELCPGKVAAELIGIKLNKRAEIGOSGCWVKADIVANVOEPHS STUMPPSSMCAVO VARSEMIHMENTERFERGSCRUVERSTULTTISSESTENISSITEL MLSRALFVERFIFYNHTHGREBULDIFVHOLLULVVELTIGLVAEL EFIVENNVLUELLESSILLLGGSSFFFFYINTPSSITEL MLSRALFVERFIFYNHTHGREBULDIFVHOLLULVVELTIGLVAEL EFIVENNVLUELLESSILLLGGSSFFFFYINTPSSITEL MLSRALFVERFIFYNHTHGREBULDIFVHOLLULVVELTIGLVAEL EFIVENNVLUELLESSILLLGGSGFFFAVIDLGETISSILVSLIKK KREITLIVFRILLVINFRODRIVUT IESULCPSHPERTLTRVLYSL KREITLIVFRILLVINFRODRIVUT IESULCPSHPERTLTRVLYSL KREITLIVFRILLVINFRODRIVUT IESULCPSHPERTLTRVLYSL KREITLIVFRILLVINFRODRIVUT IESULCPSHPERTLTRVLYSL KREITLIVFRILLVINFRODRIVUT IESULCPSHPERTLTRVLYSL KREITLIVFRILLVINFRODRIVUT IESULCPSHPERTLTRVLYSL KREITLIVFRILLVINFRODRIVUT IESULCPSHPERTLTRVLYSL KREITLIVFRILLVINFRODRIVUT IESULCPSHPERTLTRVLYSL KREITLIVFRILLVINFRODRIVUT IESULCPSHPERTLTRVLYSL KREITLIVFRILLVINFRODRIVUT IESULCPSHPERTLTRVLYSL KREITLIVFRILLVINFRODRIVUT IESULCPSHPERTLTRVLYSL KRALGTKTFRI HTPPAKANCVANG				MSRPDIQVQAKKLAEKLRCDTVVSEISTGODTUNIEKINDELI TIL
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5516 3 735 NSREPPQAGFGPSPKKSPTASSFLFPWRPLASSFWMGAQGAQES IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGPTWAG KMYGPGGGKYFSTTEDYDHEITGLRVSVQVKLGDSW DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDR YFYFGKLDGQISSAYPSOEGOVLVGIYGOYOLLGIYE	1 1			KKALGTKTED THTDDAYANGIANI GOT THE TOTAL THE THE THTDDAYANGIANI GOT THE TOTAL THE
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I TOTAL TOTA				TDGTSDLBLKI BALCHEBANGASSARAGRRNALPDIQSSAA
TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK DAWADAWVRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMEA	5518	3	1375	DAWADAWVRAWDI NIMDERCI NI CI I TOTALIN
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THIMPSNIN PDGFEAVKKPDCYYS I GRENYNOYD I NEW PDDA PDV			<u> </u>	THIMPSNNPDGFEAVKKPDCYYSIGRENYNOYDI,NPNPPDAPPY
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I IGALISKS LTPDDDVFOYLAHTYAS RNPNMKKGDECKNYMYEDN			, ,	IGALISKSLIPDDDVFOYLAHTYASRNPNMKKCDECKNYMNEDN
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SFWNNNKASLIEYIKQVHLGVKGQVFDQNGNPLPNVIVEVQDRK			·	ST WINDHIM TASEL EY I KQV-HLGVKGQVFDQNGNPLPNVIVEVQDRK

SEQ Predicted		
	redicted end	Amino acid segment containing signal peptide
10 (DEATMITTIES	ucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO: nucleotide 1	ocation	Glutamic Acid, F=Phenylalanine, G=Glycine,
location	orresponding	H=Histidine, I=Isoleucine, K=Lysine,
	o first	L=Leucine, M=Methionine, N=Asparagine,
to first	mino acid	P=Proline, Q=Glutamine, R=Arginine,
amino acid	esidue of	S≈Serine, T=Threonine, V=Valine,
residue of	mino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	Codon, /=possible nucleotide deletion,
Q	,0400	\=nossible nucleotide insertion)
sequence		UTCPVPTNKYCEVYLLLLPGSYIINVTVPGHDPHITKVIIPEKS
		QNFSALKKDILLPFQGQLDSIPVSNPSCPMIPLYRNLPDHSAAT
1		KPSLFLFLVSLLHIFFK
<u> </u>		IKSKLNQQVEVQESEWRLTEAKGPTMGKESGWDSGRAAVAAVVG
5519 87	477	IKSKLNQQVEVQESEWRETEARGFINGREDGHEDGHETVET
		GVVAVGTVLVALSAMGFTSVGIAASSIAAKMMSTAAIANGGGVA
1		AGSLVAILQSVGAAGLSVTSKVIGGFAGTALGAWLGSPPSS
5520 117	943	PTEGROKVLKTFTVPRSALAMTKTSTCIYHFLVLSWYTFLNYYI
5520 111		SOEGKDEVKPXTLANGARWKYMTLLNLLLQTIFYGVTCLDDVLK
1		PTKCCKDIKFLTAFRDLLFTTLAFPVSTFVFLAFWILFLYNRDL
 		IYPKVLDTVIPVWLNHAMHTFIFPITLAEVVLRPHSYPSKKTGL
. 1		TLLAAASIAYISRILWLYFETGTWVYPVFAKLSLLGLAAFFSLS
. 1		YVFIASIYLLGEKLNHWKWVSVQILQRWRLESVGICFQWPDWKS
Į Į		PAKHQLVKNIR
5521 546	911	KILNMQKSCEENEGKPQNMPKAEEDRPLEDVPQEAEGNPQPSEE
		GVSQEAEGNPRGGPNQPGQGFKEDTPVRHLDPEEMIRGVDELER
1		LREEIRRVRNKFVMMHWKQRHSRSRPYPVCFRP
5522 1224	637	GSRPLGQRSREKMWVFGYGSLIWKVDFPYQDKLVGYITNYSRRF
5522 1224		WOGSTDURGVPGKPGRVVTLVEDPAGCVWGVAYRLPVGKEEEVK
1 1		AVIDEREKGCYRTTTVIFYPKDPTTKPFSVLLYIGTCDNPDYLG
1 (PAPLEDIAEQIFNAAGPSGRNTEYLFELANSIRNLVPEKADEHL
)		FALEKLVKERLEGKONLNCI
1 1		SKGKKRMGSSMSAATARRPVFDDKEDVNFDHFQILRAIGKGSFG
5523 3	1280	SKGKKRMGSSMSAATAKKPVFDDLEDVATSHT QT
1 1 . 1		KACIAÖKEDIEKWAWKANNKÖÖCTEKDEAKKATUDDDIEKEDIA
1 1		HVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVQFSEDTV
1 1 1		RLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI
1 . 1		ATIIKDGERATALSGTKPYMAPEIFHSFVNGGTGYSFEVDWWSV
1 1		GVMAYELLRGWRPYDIHSSNAVESLVQLFSTVSVQYVPTWSKEM
		VALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVEPG
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į į į		SSQSENDYLQDCLDAIQQDFVIFNREKLKRSQDLPREPLPAPES
		DDAAFDUFDEAERSALPMCGPICPSAGSG
	2318	DEPENDER DESSOGOSGAGGCF PSPTMELRCGGLLFSSRFDSG
5524 85	2310	NLAHVEKVESLSSDGEGVGGGASALTSGIASSPDYEFNVWTRPD
\ j		CARTEFENGNRSWFYFSVRGGMPGKLIKINIMNMNKQSKLYSQG
1 1		MAPFVRTLPTRPRWERIRDRPTFEMTETQFVLSFVHRFVEGRGA
		TTFFAFCYPFSYSDCQELLNQLDQRFPENHPTHSSPLDTIYYHR
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		RFAGKRIFFLSSRVHPGETPSSFVFNGFLDFILRPDDPRAQTLR
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		INTOWER OCCUSADD HINDEAUKOTE PAEOKLINS VWIMPQQSAGLE
		NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQQSAGLE BCARDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE
		NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQQSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE NMLYDKLISINSAHFDFOGCNFSEKNMYARDRRDGQSKEGSGRV
		NIQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQQSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE MMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV NIVYAGCTINSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA
		NIQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQQSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE MMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV NIVYAGCTINSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA
	·	NIQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQOSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA EPSPYTYELFROVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL
	·	NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQOSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL BALMILKUVDNSRGLSSTLNYGVNKKRGLRTPPKSHNGLPVSCSE
		NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQOSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE NTLSBARSFSTGTSAGGSSSSQQNSPQMKNSPSPPFHGSRPAGL
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5525	834	NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQOSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL RAWMKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFFFHGSRPAGL PGLGSSTQKVTHRVLGPVRGKPYWEPLQHVFGCLGHCWGK
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5525 105	834	NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQQSAGJE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE NMLYRLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFFFHGSRPAGL PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV
5525 105	834	NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQQSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA FPSRYTVELFBQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFPFHGSRPAGL PGLGSSTQKVTHRVLGPVRGKPYWEPLQHVFGCLGHCWGK SNTLDFERHLFIMGQOISDQTQLVINKLPEKVAKHVTLVRESGS LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ
5525 105	834	NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQQSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA FPSRYTVELFBQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFPFHGSRPAGL PGLGSSTQKVTHRVLGPVRGKPYWEPLQHVFGCLGHCWGK SNTLDFERHLFIMGQOISDQTQLVINKLPEKVAKHVTLVRESGS LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ
5525 105	834	NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQQSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE NMLYRLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFFFHGSRPAGL PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ SSTSEEPDENSSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP
5525 105	834	NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWIMPQOSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMXGNSFSDESTQVE NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL RAWMLKHVRNSRGLSSTLNYGVNKKRGLRTPPKSHNGLPVSCSE NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFPFHGSRPAGL PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ SSTSEEDENSSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP
5525 105 5526 3	834	NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWIMPQOSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSPPFHGSRPAGL PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV VVRVVCTXINKSSGIVEASRINNLYQFIQLYKDITSQAAGVLAQ SSTSEEPDENSSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP TEDDMANYILNMADEAGQPHRP
		NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQQSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV AIYKASGIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA FPSRTTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFPFHGSRPAGL PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ SSTSEEPDENSSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP TEDDMANYILNMADEAGQPHRP RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT
		NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQQSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDMGRASPPPPPA FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFFFHGSRPAGL PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV VVRVVCTXINKSSGIVEASRINNLYQFIQLYKDITSQAAGVLAQ SSTSEEPDENSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP TEDDMANYILNMADEAGQPHRP RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR
		NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWIMPQQSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV A1YKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFPFHGSRPAGL PGLGSSTQKVTHRVLGPVRGKPVWEFLQHVFGCLGHCWGK SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ SSTSEEPDENSSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP TEDDMANYILNMADEAGQPHRP RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLITTRAVT QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR LDDDPPPSTLLKDYQNVPGIEKVDDVVKRLLSLEMANKKEMLKI
		NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQQSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDNGRASPPPPPA FPSRYTVELFBQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFPFHGSRPAGL PGLGSSTQKVTHRVLGPVRGKPYWEPLQHVFGCLGHCWGK SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ SSTSEEPDENSSSVTSCQASLMMGRVKQLTDEEECCICMDGRAD LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP TEDDMANYILNMADEAGQPHRP RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVKRAQSR LDDDPPPSTLLKDYQNVPGIEKVDDVVKRLLSLEMANKKEMLKI KQEQFMKKIVANPEDTRSLEARIIALSVKIRSYEBHLEKHRKDK
		NLQNEAQCGHSADRHNAEAWKQTEPAEQKLNSVWINPQQSAGLE ESAPDTIPPKESGVAYYVDLHGHASKRGCFMYGNSFSDESTQVE NMLYPKLISLNSAHFDFQGCNFSEKNMYARDRRDGQSKEGSGRV AIYKASGIIHSYTLECNYNTGRSVNSIPAACHDMGRASPPPPPA FPSRYTVELFEQVGRAMAIAALDMAECNPWPRIVLSEHSSLTNL RAWMLKHVRNSRGLSSTLNVGVNKKRGLRTPPKSHNGLPVSCSE NTLSRARSFSTGTSAGGSSSSQQNSPQMKNSPSFFFHGSRPAGL PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK SNTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS LTYEEFLGRVAELNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV VVRVVCTXINKSSGIVEASRINNLYQFIQLYKDITSQAAGVLAQ SSTSEEPDENSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP TEDDMANYILNMADEAGQPHRP RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR

SEO	Predicted	I Dwodd at 3	
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	M=Aldnine, C=Cvsteine, D=Asnay+ic Acid R
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
f	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
į.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ſ	residue of	amino acid	W=Tryptophan, Y=Tvrosine, Y=Unknown +-Cha-
- 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
5527			RRNPDSPAKAIPKTLKDSO
332/	3225	565	LLRKYLLHQNPLLLRHQPNRTCISFSATMKLKDTKSRPKQSSCG
1			KPUTKGIKVVGKWKEVKIDPNMFADGCMDDLVCFFFI.TDVOLVS
į.			PAKNPSSLFSKEAPKRKAQAVSEEEEEEGKSSSPKKKTKLKKE
			KNVATEGTSTQKEFEVKDPELEAOGDDMVCDDPEAGEMTSENLY
l l			QTAPKKKKNKGKKGLEPSQSTAAKVPKKAKTWI PEVHDQKADVS
- 1		1	AWKDLFVPRPVLRALSFLGFSAPTPIQALTLAPAIRDKLDILGA
1	İ		AETGSGKTLAFAIPMIHAVLOWOKRNAAPPPSNTEAPPGETRTE
1	İ	1	AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEARAKTGGT
i		-	VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEENLDKEQTGN LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQHIDAVAR
1		1	FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWELIKEKH
j		}	YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNDSQYNPK
ŀ			RQTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLLMQKIGM
ĺ	ł	 ·	RGKPKVIDLTRNEATVETLTETKIHCETDEKDFVI.VVFI.MOVDC
- 1			RSLVFANSISCIKRLSGLLKVLDIMPLTI.HACMHOKOPI.DNI PO
İ			FARLEDCVLLATDVAARGLDIPKVOHVIHYOVPRTSETVUDGG
1	1		RTAKATNEGLSLMLIGPEDVINFKKIYKTIKKNEDI DI EDWOTE
1	· I		YMDVVKERIRLARQIEKSEYRNFQACLHNSWIEQAAAALEIELE
1			EDMYKGGKADQQEERRRQKQMKVLKKELRHLLSQPLFTESQKTK
			YPTQSGKPPLLVSAPSKSESALSCLSKQKKKKTKKPKEPQPEQP OPSTSAN
5528	3	895	GPFLSACRMWGACKVKVHDSLATISITLRRYLRLGATMAKSKFE
1			YVRDFEADDTCLAHCWVVVRLDGRNFHRFAEKHNFAKPNDSRAL
1			QLMTKCAQTVMEELEDIVIAYGQSDEYSFVFKRKTNWFKRRASK
]	<u> </u>		FMTHVASQFASSYVFYWRDYFEDOPLLYPPGFDGPXAAVPCMCT
1		•	LKDYLSWRQADCHINNLYNTVFWALIOOSGI.TPVOAOGRI.OGTI
İ			AADKNEILFSEFNINYNNEPPMYRKGTVLIWOKVDENMYKETET
5529	48	640	PTEMEGKKMAVTRTRTKPCKPSHLPRAPCLRWI.
ļ		040	TFRLVSAHLKTRKLINPEAAERRWRDWDSRQGWLSVKMQRVSGL
			LSWTLSRVLWLSGLSEPGAAROPRIMEEKALEVYDLIRTIRDPE
	1		KPNTLEELEVVSESCVEVQEINEEEYLVIIRFTPTVPHCSLATL IGLCLRVKLQRCLPFKHKLEIYISEGTHSTEEDINKQINDKERV
	<u> </u>		AAAMENPNLREIVEQCVLEPD
5530	4541	2606	AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK
1	1		FOPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDTWSLCVTLEMI
1	1		VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDI.TTPMI.OP
	1		DPKKRASLEEIENHPWLOGVDPSPATKYNTPLUSVKNI SEPRIM
j]		SIIQRMVLGDIADRDAIVEALETNRYNHITATYFILAERILDEV
] [QEKEIQTRSASPSNIKAOFROSWPTKIDVPODI.EDDI.TATDI CII
ſ		Į.	ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP
1	1		PASLKPTASGRKCLFRVEEDEEDEEDKKPMSLSTQVVLRRKPS VTNRLTSPKSADU NO LEFECTED HERMAN
1]		VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMNI ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF
	1	ľ	TYSWHRRDSSEGPPGSEGDGGGQSKPSNASGGVDKASPSENNAG
	1	ł	GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK
1	1]	LMSLCLGSQLHGSTKYIIDPONGLSFSSVKVOEKSTWKMCT Ser
j]		GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLOLDEG
5531	24		EKTISVNIQRNPKEGLLCASSPASCCHVI
	"	515	GSQPRAPRPRDSMERPEPELIROSWRAVSRSPLEHCTUL PARIE
i :	}	}	ALEPOLLFLFQYNCRQFSSPEDCLSSPEFLUHTRKVMIATDAM I
]			INVEDESSIEEYLASLGRKHRAVGVKLSSFSTVGESLLVMLEVC
5532	3395	1402	LGPAFTPATRAAWSQLYGAVVOAMSRGWDGE
		· .	SDWMVVGKRKMI I EDETEFCGEELLHSVLQCKSVFDVLDGEEMR
	I		RARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG
		1	KPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGMTLK
1	1	i	GPNDFKLEDFYSASSELFEPYYGEGGIDGDGDITRPENISAFRN FYLDNTDRKGULFI MADGGESUEGOENI OFFI GVOL
	1	ļ	FVLDNTDRKGVHFLMADGGFSVEGQENLQEILSKQLLLCQFIMA LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFERVCLFKPITS
			RPANSERYVVCKGLKVGIDDVRDYLFAVNIKLNQLRNTDSDVNL
			TWATER STRANGE WAS TREMANDED AND

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, O=Glutamine, R=Arginine,
	amino acid	residue of	S-Serine T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of		Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		VVPLEVIKGDHEFTDYMIRSNESHCSLQIKALAKIHAFVQDTTL
		1	VVPLEVIKGDHEFTDYMIKSNESHCSDSIKAMAKIMI VQDIID
ĺ	1	1	SEPRQAEIRKECLRLWGIPDQARVAPSSSDPKSKFFELIQGTEI
į	Į.	ì	DIFSYKPTLLTSKTLEKIRPVFDYRCMVSGSEQKFLIGLGKSQI
1		l	YTWDGROSDRWIKLDLKTELPRDTLLSVEIVHELKGEGKAQRKI
1		ł	SAIHILDVI.VI.NGTDVREOHFNORIQLAEKFVKAVSKPSRPDMN
1	1	1	PIRVKEVYRLEEMEKIFVRLEMKIIKGSSGTPKLSYTGRDDRHF
1	4		VPMGLYIVRTVNEPWTMGFSKSFKKKFFYNKKTKDSTFDLPADS
ì	(1	IAPFHICYYGRLFWEWGDGIRVHDSQKPQDQDKLSKEDVLSFIQ
ł	{ ·	(1
ì	\	1	MHRA
5533	94	789	MKERRAPQPVVARCKLVLVGDVQCGKTAMLQVLAKDCYPETYVP
3333	1	1	TVFENYTACLETEEORVELSLWDTSGSPYYDNVRPLCYSDSDAV
1	i	1	LLCFDISRPETVDSALKKWRTEILDYCPSTRVLLIGCKTDLRTD
]		}	LSTLMELSHQKQAPISYEQGCAIAKQLGPEIYLEGSAFTSEKSI
1	1		HSIFRTASMLCLNKPSPLPQKSPVRSLSKRLLHLPSRSELISPT
}]	1	
1			FKKEKAKXCSIM
5534	3	605	LVRGRARAANPGRVGAMDGLRQRVEHFLEQRNLVTEVLGALEAK
		I '	TGVEKRYLAAGAVTLLSLYLLFGYGASLLCNLIGFVYPAYASIK
		i	AIESPSKDDDTVWLTYWVVYALFGLAEFFSDLLLSWFPFYYVGK
1	,	1	CAFLLFCMAPRPWNGALMLYQRVVRPLFLRHHGAVDRIMNDLSG
1	ł	· t	RALDAAAGITRNVKPSQTPQPKDK
L			KSFMDSEARLCSLVELSDTQDETQKSDSENEDLKIDCLQESQEL
5535	1029	332	NLQKLKNSERILTEAKQKMRELTVNIKMKEDLIKELIKTGNDAK
1		1	NLOKIKASEKI LITEAROMAKEDI VITICIKEDELIKEDI SENKOL SOVAM
1	{	[SVSKQYTLKVTKLEHDAEQAKVELTETQKQLQELENKDLSDVAM
4	\	1	KVKLQKEFRKKVDAAKLRVQVLQKKQQDSKKLASLSIQNEKRAN
1	1	i	ELEQSVDHMKYQKIQLQRKLQEENEKRKQLDAVIKRDQQKIKVI
1			LSYIPAKYNMKC
5535	942	282 .	AAATAASLSPRGCRLRTPSSDVSPSRAJPPSAAPLPTGRAQMSP
5536	342	}	SGRLCLLTIVGLILPTRGQTLKDTTSSSSADATIMDIQVPTRAP
1	1	i i	DAVYTELQPTSPTPTWFADETPQPQTQTQQLEGTDGPLVTDPET
}	1	1	HKSTKAAHPTDDTTTLSERPSPSTDVQTDPQTLKPSGFHEDDPF
l l	1	1	FYDEHTLRKRGLLVAAVLFITGIIILTSGKCRQLSRLCRNHCR
1	•	· · · · · · · · · · · · · · · · · · ·	FYDERTERREGEDVAAVEFITGIIIIIISGRERGESKEET
5537	3	2391	RARVSSPQLRVFRSGRPRRLRVLRINRTSVALRLAGTGRFVAKT
1	*	1	PGHPGSWEMGLLTFRDVAVEFSLEEWEHLEPAQKNLYQDVMLEN
1		1	YRNLVSLGLVVSKPDLITFLEQRKEPWNVKSEETVAIQPDVFSH
1		1	YNKDLLTEHCTBASFQKVISRRHGSCDLENLHLRKRWKREECEG
Ì		1	UNGCYDEKTFKYDOFDESSVESLFHQQILSSCAKSYNFDQYRKV
1	i	1 .	PTHSSLLNOOEEIDIWGKHHIYDKTSVLFRQVSTLNSYRNVFIG
}		1	EKNYHCNNSEKTLNQSSSPKNHQENYFLEKQYKCKEF3EVFLQS
1 .	· 1	1	MHGQEKQEQSYKCNKCVEVCTQSLKHIQHQTIHIRENSYSYNKY
1	1	1	DKDLSQSSNLRKQIIHNEEKPYKCEKCGDSLNHSLHLTQHQIIP
1	I	1	DADDSOSSNERROTTRINEBAFTACEACGDOMMINICATIVE CVACCEC
1	ł	1	TEEKPYKWKECGKVFNLNCSLYLTKQQQIDTGENLYKCKACSKS
1	1	}	FTRSSNLIVHQRIHTGEKPYKCKECGKAFRCSSYLTKHKRIHTG
1	ł	1	EKPYKCKECGKAFNRSSCLTQHQTTHTGEKLYKCKVCSKSYARS
1	·		SNLTMHORVHTGEKPYKCKECGKVFSRSSCLTQHRKIHTGENLY
1	ł.	l	KCKVCAKPFTCFSNLIVHERIHTGEKPYKCKECGKAFPYSSHLI
1	1		RHHRIHTGEKPYKCKACSKSFSDSSGLTVHRRTHTGEKPYTCKE
1	1		CGKAFSYSSDVIQHRRIHTGQRPYKCEECGKAFNYRSYLTTHQR
1	t	1	SHTGERPYKCEECGKAFNSRSYLTTHRRRHTGERPYKCDECGKA
ı	į		SHTGERPY KUBEUGKAPNSKS I DI IMRKRITGERF I KUDEUGKA
i		1	FSYRSYLTTHRRSHSGERPYKCEECGKAFNSRSYLIAHQRSHTR
1	1	,	EKL
5538	926	161	HSMMMKIPWGSIPVLMLLLLLGLIDISQAQLSCTGPPAIPGIPG
1 3338	1 22		IPGTPGPDGOPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNP
1	1	1	GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI
1	1	1	NVPLRRDQTIRFDHVITNMNNYEPRSGKFTCKVPGLYYFTYHA
Į.	ļ		SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ
1	1		SSKGNLCVNLPRGREKAQRVVII CDIMIRIT QVII COMMEN
1	1	1	GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA
5539	38	1258	HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG
			TVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK
1	l l	1	DETYGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCS
ĺ	[SDSFNEDIAAFAKQVRSERPLFSSNPELDNLVIQAIQVLRFHLL
1	1	1	

SEO	Predicted	Trimodiana and	
ID	beginning	Predicted end	The second containing class and the second
NO:	nucleotide	location	I W-Midilie, C=CVS[eine, N-Achartic X-13 e
- (location	corresponding	Glucamic Acid, F=Phenvlalaning G_Classing
-	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
-	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=Possible nucleotide insertion\
1	1		ELEKVHOLCONFCHRYITCLKGKMPIDLVIRDPDCCCPEDEEDV
] !			FASCESTEPDQNNMWIRDHEDSGSVHT.GTPGPSSCGTASOSCONIO
- -	1		SDQGDGLDTSVASPSSGGEDEDLDOERRRNKRRGTEDVIATNIM
			RAWDFQHLSHPYPSEEOKKOLAODTGI.TTI.OMMMETNADDDTY
			QPMIDQSNRTGQGAAFSPEGQPIGGYTETOPHVAVRPPGSVGMS
5540	148	3440	FUTEGEMHAT
		1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
- [1	PSGAAAPGCALPRGQALEGPRSCRRPOPMARRYDELBUYDGTUD
		l	GPAALASFPETVPAVPGPYGPHRPPOPLPPGI.DSDGI.VPPVDET
1 1		1	YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
1 1		}	FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
1 1			KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
1 1		}	SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
1 1			LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
FE			QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5541	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
			PSGAAAPGCALPRGQALEGPRSCRRPOPMARRYDELDUVDGTUD
1 1			GPAALASFPETVPAVPGPYGPHRPPOPI.PPGI.DCD.GT.VPPVDET
			IGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVGCCDC
1 1			I FREDRIAFAKOVRSERPLESSNPELDNIMI OA TOST PEUT I EL E
1 1			NGKMPIDLVIEDRDGGCREDFEDYPASCPSI,PDONNITWIPDUED
1 1	ľ		SGSVHLGTPGPSSGGLASOSGDNSSDOGVGLDTSVACRECGED
1 1	ļ		EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
		•	LAQDTGLTILQVNNWFINARRIVOPMIDQSNRTGQGAAFSPEG QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5542	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
			PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
1 1			GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDBI
1	J		IGHPUFPLLALVFEKCELATCSPRDGAGAGLGTPPGGPVGCCPG
1 1			FNEDNTAFAKQVRSERPLFSSNPELDNIMTOATOW PEUT PER
1 1	1		AGAMPIDEVIEDRDGGCREDFEDYPASCPSI.PDONNITHIDDURD (
ł ļ	Į.		SGSV-LIGTPGPSSGGLASOSGDNSSDOGVGI.DTGVACACCORD
1 1	I		EDEDQEPKRNKKRGIFPKVATNIMRAWI.FOHI.SHDVDCPPOVVO
j j		•	LAQUIGLILLQVNNWFINARRRIVOPMIDOSNPICOGA A PEDEC
5543	2405	665	QPIGGITETEPHVAFRAPASVGDEFGTRKEEWHVT.
1 1		885	RWVREQPWPLRTSEAVKTPALRPFPGPRGVSPFPKPDWGKSPAP
			KRPFSDSGAFWSPERRPGVLEAPRRRPVPASFRAVPPKPTRVHG
1 1	1	ļ	SSASRDRVLARTMIVADSECRAELKDYLRFAPGGVGDSGPGEEQ KBSRARRGPRGPSAFIPVEEVLREGAESLEQHLGLEALMSSGRV
1	1		DNLAVVMGLHPDYFTSFWRLHYLLLHTDGPLASSWRHYIAIMAA
1	1	i	ARHQCSYLVGSHMAEFLQTGGDPEWLLGLHRAPEKLRKLSEINK
)			LLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTHCHSLS
j	Į	1	SFVFGCGILPEGDADGSPAPQAPTPPSEQSSPPSRDPLNNSGGF
1	1	j	ESARDVEALMERMOOLOESLLRDEGTSOEEMESPEELEVERGET
		į.	VIPSADILEPSPHPDMLCFVEDPTFGYEDFTRRGAOADDTFDAO
	1	1	DYTWEDHGYSLIQRLYPEGGOLLDEKFOAAYSI.TVNTTAMUGGU
		I	DISVLRRAIWNYIHCVFGIRYDDYDYGEVNOLLEDNIKUVIV
I		1	ACYPEKTTRRMYNLFWRHFRHSEKVIIVNLLLLEARMOAALLYAL
5544	1895		RAITRYMT
	1070	514	LGGLLGRQRLLLRMGAGRLGAPMERHGRASATSVSSAGEQAAGD
J			PEGRRQEPLRRRASSASVPAVGASAEGTRRDRLGSVSGDTGVCD
l	1	1	QRVESLRKKRPLFPWFGLDIGGTLVKLVYFEPKDITAEEPPPPU
1	1	}	ESLKS IRKYLTSNVAYGSTGIRDVHLELKDI.TI.CGPKGNLUBID
1]	[.	FPIHDMPAFIQMGRDKNFSSLHTVFCATGGGAVKFRODELTICD
l	1	4 .	LQLCKLDELDCLIKGILYIDSVGFNGRSOCYYFENPADSWYCOY
		[-	LPFDLKNPYPLLLVNIGSGVSILAVVSKDNYKRVTGTSI GGGTR
			Mild Charlet TEFFALEMACOCOCCUCTOR TO Second
ſ	i	1 :	FGLCCLLTGCTTFEEALEMASRGDSTKVDKLVRDIYGGDYBRFG
		1 2	LPGWAVASSFGNMMSKEKREAVSKEDLARATT.TTTTMNTGGTAD
			LPGWAYASSFGNMMSKEKREAVSKEDLARATLITITNNIGSIAR MCALNENINQVVFVGNFLRINTIAMRLLAYALDYWSKGQLKALF BEHEGYFGAVGALLELLKIP

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID (beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H-Histidine, I-Isoleucine, K-Lysine,
ĺ	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 -	\=possible nucleotide insertion)
5545	802	131	GAMWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVL
5545	1 332	1	KLLNTHHRVRLHSHDIKYGSGSGQQSVTGVEASDDANSYWRIRG
	1	I	GSEGGCPRGSPVRCGOAVRLTHVLTGKNLHTHHFPSPLSNNQEV
	1	Į.	caegeogegodi.dl.wtvrcsgohwereaavrfQhvgtsvflsvt
1	1	1	GEQYGSPIRGQHEVHGMPSANTHNTWKAMEGIFIKPSVEPSAGH
	1	1	I DET.
	L	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
5546	1592	146	RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
	i	1	LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
	l	1	SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
1	{	1	NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK
}	,		NVHKVNLNTIKRCBLIDINPDSQEDDFRITSIKVV
	1		KPTORKE SAME SCOTT TO THE TOP OF
	}	1	AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
1	1		FVSKTEEELQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH
ŀ)	1.	RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI
1	1	1	EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL
1	1	1	CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRGRFGKRVA
5547	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
) 334.	1	1	RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
\	l .	Ĭ	taururi.Ti.SkTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
1	1		SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
1	[ļ	MULICUNI NTIKECILIDYNPDSOELDFRHYSIKVVPVGASRGMK
1	1		VILOEKEPNMSRLODISELLATGAGLSESEAEPDGDHNITELPQ
	1	}	AVAGRGNMRAOOSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
ł			FYSKTEERIOATLEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH
1	i .	1	PKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDD1
1			PYFCOAUGFAPSEDLFPEAKOKRLAKSPGRKRKRWEMDRGRGRL
İ		1	CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRGRPGKRVA
		2153	DOTGPPETIAFTFPRSTMEPLCPLLLVGFSLPLARALRGNETTA
5548	1	2153	DSNETTTTSGPPDPGASQPLLAWLLLPLLLLLLLVLLLAAYFFRF
			RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI
}	ì	ł	PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN
1	l l	1	REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK
1	}	1	FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY
		İ	WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR
	1	ì	LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC
1	ŧ		SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ
ł	1	1	TDMQYTF1YQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK
1	1	\	TDMQYTF1YQALLEIILIGDIEHDVSSHSKRIQIIAQVIKQIIPYDFNR IGLBEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR
1		į.	IGLEEFRKETNVKIMKENMKIGNDFAMMKGAKVIQUIAHTVKDFW
1	l	}	VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW
[1	RMIWEWKSHTIVMLTEVQBREQDKCYQYWPTEGSVTHGEITIEI
1			KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG
Ì	(IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL
	1		SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ
			DFIDIFSDYANFK
5549	915	256	FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ
7525	1	1	CLAECSACTKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME
ļ	}		VEETERI.FORFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAP
	1		PKI.DKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD
ł	1	. [NEDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL
		1210	PVPVVFI.KMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV
5550	2364	1210	CI. TAFTTMALLTIMEFSVYODTWMKYEYEVDKDFSSKLRINIDI
1	1		TUDANCOVUGADVI.DI.AETMVASADGLVYEPTVFDI.SPQQKENQ
1		[RMLQLIQSRLQBEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN
	1		ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN
{		1	FSHRIDHLSFGELVPAIINPLDGTEKIAIDHNQMFQYFITVVPT
		j	FSHRIDHLSFGELV9AIINPLOGIEKIAIDHAQGIFMKYDLSSL KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL
1		1	KLHTYKISADINQFSVTEKEKIINNAGSNGVOGITAKIDAGO
-		}	MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC
1	1	1	CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH
5551	211	1700	MORDHTMDYKESCPSVSIPSSDEHREKKKRFTVYKVLVSVGRSE

SEC	Predicted		
ID		Predicted end	
NO:	nucleotide	nucleotide	I M-Midille, C=CVSteine, D=Acceptio Acid a
1	location	location	Totucamic Acid. F=Phenvlalanine C-cl
- 1	corresponding	corresponding to first	A=HISTIGINE, I=ISOleucine, K=Isysine
	to first	amino acid	L=Leucine, M=Methionine, N=Acnaracine
- !	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ĺ	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
- (amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence		Codon, /=possible nucleotide deletion,
		 	\=possible nucleotide insertion)
1		j	WFVFRRYAEFDKLYNTLKKQFPAMALKIPAKRIFGDNFDPDFIK
ſ			ORRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSDPSEDE DERSSQKLHSTSQNINLGPSGNPHAKPTDFDFLKVIGKGSFGKV
1	į		LLAKRKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKH
			PFLVGLHYSFQTTEKLYFVLDFVNGGELFFHLQRERSFPEHRAR
1	}		FYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTDFGLC
:			REGIALSDITTTFCGTPEYLAPEVIRKOPYDNTVDWWCI CAVI V
ı	j .	}	EMUYGLPPFYCRDVAEMYDNILHKDISI.PPGVSI.TAWS II PRI I
	1		EKDRQNRLGAKEDFLEIONHPFFESI.SWADIJJOVVIDDDENDANI
1	1	ł	AGPDDIRN PDTAFTEETVPYSVCVSSDYSIVNASVI, RADDAFVG
5552	2748	930	FSTAPPSEDLFL
ſ	- 1	1 330	LGPAAGAAMGKKHKKHKAEWRSSYEDYADKPLEKPLKLVLKVGG
- 1	İ		SEVTELSGSGHDSSYYDDRSDHERERHKEKKKKKKKKKKKKKKEKHL
ſ	1		DDEERRKRKEEKKRKREREHCDTEGEADDFDPGKKVEVBPPPDR PVRACRTOPAENESTPIQQLLEHFLRQLQRKOPHGFFAFPVTDA
ļ	ļ		IAPGYSMIIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNA
			MTYNRPDTVYYKLAKKI LHAGFKMMSKQAALLGNEDTAVEEPVP
ı	1	į.	LVVPVQVETAKKSKKPSREVISCMFEPEGNACSI.TDGDAPEGU
J		1	ADVERAADEARDRINRFLPGGKMGYLKRNGDGS1.1.VSIADER ED
i	ĺ		DADESETHPYDLSSLSSKLLPGFTTLGFKDEPRNKUTPLEGATER
1	}		ALSMUNNSVFGDLKSDEMELLYSAYGDETGVOCALSLOFEUVDA
- (1		GS18KKVVDDLLDQITGGDHSRTLFOLKORRMIDMUDDDER VIG
]		DTLGDSSSSVLEFMSMKSYPDVSVDISMLSSLGKVKKELDPDDS
			HLNLDETTKLLQDLHEAQAERGGSRPSSNLSSLSNASERDQHHL GSPSRLSVGEQPDVTHDPYEFLQSPEPAASAKT
5553	74	1095	LGREAVYLVSRMDGPVAEHAKQEPFHVVTPLLESWALSQVAGMP
1	1		VFLKCENVQPSGSFKIRGIGHFCQEMAKKGCRHLVCSSGGNAGI
1	1		MAAIAARKLGIPATIVLPESTSLOVVORLOGEGAEVOLTGETTED
1	1		EANURAGELAKROGWENVPPFDHPLIWKGHASIJOEL KAVII DTD
1	1.		FGALVLAVGGGGLLAGVVAGLLEVGWOHVPTTAMETUCAUCENA
1	1		ATTAGELVTLPDITSVAKSLGAKTVAARALECMOUCKTUGETARE
			DTEAVSAVQQLLDDERMLVEPACGAALAAIYSGLLRRLQAEGCL PPSLTSVVVIVCGGNNINSRELQALKTHLGQV
5554	166	2318	CSGRTGGRGSLRPAENVCLTCKLSGAETRGLLCPALRTWIMKVL
1	1 (GRSFFWVLFPVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQ
1	1 1		WVRDSCKKLSGLLROKNAVLNKI,KTATGAVRKDVGI CDEBVI BO
	1		VALUE TO THE TRUE SENS OF TO A VALUE OF THE TRUE OF TRUE O
1	1 . 1		QRUBALKERALKEETEYMELLAARKHOVENI,VNMOUONOGT OUT
1	1		DEILEDVRKAADRLEERIEEHAFDDNKSVKCVNFFAVT DVRWDD
	()	1	TWO KUNI TRREVEDULGESMEIDSONNOYI, TROPPORTED A DIE
}	1 1	ļ	HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLN
İ	1		SIKSİVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPC
l	1)	YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS
Ī	1 1		ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK
i	1 1	}	DIMES KONKEILILGISAFIFLMI, TVTEI, I, DVSMFI, COET 2021
ŀ	1	İ	VSSQGPVVIEEIATSIEPIRDFLATVFFASTGI-HVFDTFSIAVEL
	1 1	l	TVUVELIUSVVVMKFLLAALVLSLILPRSSOVTKWTVCACI ACV
			SEEF VLGSKARRAGVISREVYLLILSVTTLSLLLADIM.WDD A T
5555	212	1425	TRCVPRPERRSSL
	}	1	LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNPTRDR
		,	GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK KAYKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY
i]]	DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPR
		[GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAFGKRKCNCRQE
		í	PIKT IQLGPGRFQMTQEVGCDECPNVKLVNEERTTEVETERGURD
i		1	GMEIPFIGEGEPHVDGEPGDLRFRIKVVKHDIFERDGDDI.VPNR
	(f	11SUVESTVGFEMDITHLDGHKVHISRDKITRPGAKLWKKCEGI
		1	PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQK
5556	5835		A LINGTYGI
			RTRGMSKNCVPMEFEEYLLRMFQGTFYLLQKITKDNNAHTVKSR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
,	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	Sagerine
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
			Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence	<u> </u>	LEELDESYIEKFTDFLRLFVSVHLRRIESYSQFPVVEFLTLLFK
		1	YTFHQPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNRYE
	1	1	YTTHQPTHEGITSCEDINIER EDITIONAL PRI DDDOOTEWOPVI.P
	1	1	DALVLLLTEVLNRIQFRYNQAQLEELDDETLDDDQQTEWQRYLR
	1		QSLEVVAKVMELLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSGS
	1	1	GHRLNITAENDCRRLHCSLRDLSSLLQAVGRLAEYFIGDVFAAR
	i	1	FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHAQ
]	1	SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIST
	Ì	l	KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDASA
	1	4	I.PL.VDKAOVLVCRALSNILLLPWPNLPENEQQWPVRSINHASLI
	l .	\	CALSRDYRNI, KPSAVAPORKMPLDDTKLIIHQTLSVLEDIVENI
	1	1	SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFFL
	ł	1	TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGCR
	1		VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERPS
	1	1	PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENEP
	1	1	PDVKAELFELLFKTLINNWKIFFASIVLINS VQASIALEQUINEL
	1		QFSAIMQAFGQSFLQPDIHLFKQNLFYLETLNTKQKLYHKKIFR
	1	į.	TAMLFQFVNVLLQVLVHKSHDLLQEEIGIAIYNMASVDFDGFFA
		l	AFLPEFLTSCDGVDANQKSVLGRNFKMDRVRRERGRAKRRAEWA
	l l		RKPGTCAARRGHIEASGRGLCPPCSLAAAHEMPADLVL
5557	1712	491	VILGAGLRDKDMWIPVVGLPRRLRLSALAGAGRFCILGSEAATR
5557		ł	KHLPARNHCGLSDSSPQLWPEPDFRNPPRKASKASLDFKRYVTD
	1	1	PRI ARTI ACTVI GKPSRPPHLLLECNPGPGILTQALLEAGAKVV
	1	1	ALESDETE DULESI GKNLDGKLRVIHCDFFKLDPRSGGVIKPP
	1	1	AMSSEGI.FKNI.GIEAVPWTADIPLKVVGMFPSRGEKRALWKLAY
	i	1	DIVECTSTVKFGRTEVNMFIGEKEFOKLMADPGNPDLYHVLSVI
	1	l	WOLACETKVI.HMEPWSSFDIYTRKGPLENPKRRELLDQLQQKLY
	l l		I.TOMIPPONIFTKNLTPMNYNIFFHLLKHCFGRRSATVIDHLRS
	1	1	LTPLDARDILMQIGKQEDEKVVNMHPQDFKTLFETIERSKDCAY
Į	}	1	KWLYDETLEDR
l			RAGCTHPQVPADLGAPAEPRRPQKTCVCLLQPQPGGQRGPTTMI
5558	1509	96	TGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRS
	,	j	LLKLKMVQVVFRHGARSPLKPLPLEEQVEWNPQLLEVPPQTQFD
{	1	i	YTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFA
1	}	ì	LGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLA
ł	ì	j	GLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTA
	1	•	GPLOCOKECLI I HADEMDSEADIAN I OSCUPRIO ELICANIMO DE CARANTO DE CAR
j	}	1	SLOPGISEDLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLPS
Ì	1 .	i	CPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES
ì	1	į	NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPP
1	1	}	FAVDLTMELYQHLESKEWFVQLYYHGKEQVPRGCPDGLCPLDMF
i	1		LNAMSVYTLSPEKYHALCSQTQVMEVGNEE
5559	150	1983	PLAATAHFAKMSRVAKYRRQVSEDPDIDSLLETLSPEEMEELEK
3359	1	1	FLDVVDPDGSVPVGLRORNOTEKQSTGVYNREAMLNFCEKETKK
1	[1	1.MODEMSMDESKOVETKTDAKNGEERGRDASKKALGPRRDSDLG
1	1	l	WEDWDGGT.KKSFSRDRDEAGGKSGEKPKEEKIIRGIDKGRVRAA
1		1	UDKKEAGKDGRGEERAVATKKEEEKKGSDRNTGLSRDKDKKREE
Į .	1	1	MYDYAKKEDDEKVKGERRNTDTRKEGEKMKRAGGNTDMKKEDEK
1			VKRGTGNTDTKKDDEKVKKNEPLHEKEAKDDSKTKTPEKQTPSG
1			PTKPSEGPAKVEEEAAPSIFDEPLERVKNNDPEMTEVNVNNSDC
1	į		ITNEILVRFTEALEFNTVVKLFALANTRADDHVAFAIAIMLKAN
j	1	1	ITNEILVRFTEALEFNIVVALIFALINII IODDINTLELRFHNQRHICG
1	1	[
1			KILISHNDOMITIOKO IZI CVUDDI ACDDMTVITNI I QDNMIKI
			CKTEME LAKILKENTTILKLGYHFELAGPRMTVTNLLSRNMDKC
			GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDKC
			GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDKC ROKRLOEOROAQEAKGEKKDLLEVPKAGAVAKGSPKPSPQPSPF PSPKNSPKKGGAPAAPPPPPPPLAPPLIMENLKNSLSPATQRKN
			GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDKC ROKRLOEORQAQEAKGEKKDLLEVPKAGAVAKGSPKPSPQPSPH PSPKNSPKKGGAPAAPPPPPPPLAPPLIMENLKNSLSPATQRKN GDKYLPAOEKNSRDOLLAAIRSSNLKQLKKVEVPKLLQ
5560	9	921	GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNILLSRNMDKC ROKRLQEORQAQEAKGEKKOLLEVPKAGAVAKGSPKPSPOPSPH PSPKNSPKKGGAPAAPPPPPPLAPPLIMENLKNSLSPATQRKN GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ GSWFFSALSVSMACLSPSOLOKFQODGFLVLEGFLSAEECVAN
5560	9	921	GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNILLSRNMDKC RQKRLQEQRQAQEAKGEKKDLLEVPKAGAVAKGSPKPSPQPSPH PSPKNSPKKGGAPAAPPPPPPPLAPPLIMENLKNSLSPATQRKN GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ SSVVEFSALSVSMACLSPSQLQKFQQDGFLVLEGPLSAEECVAN OORIGEIVAEMDVPLHCRTEFSTOEEEQLRAQGSTDYFLSSGDI
5560	9	921	GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNILSRNMDKC RQKRLQEQRQAQEAKGEKKDLLEVPKAGAVAKGSPKPSPQPSPH PSPKNSPKKGGAPAAPPPPPPLAPPLIMENLKNSLSPATQRKM GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ SSVVEFSALSVSMACLSPSQLQKFQQDGFLVLEGFLSAEECVAM QQRIGEIVAEMDVPLHCRTEFSTQEEEQLRAQGSTDYFLSSGDI TBERFFKGVFDFKGNFLVPPEKSINKIGHALHAHDPVFKSITHS
5560	9	921	GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNILSRNMDKC RQKRLQEQRQAQEAKGEKKDLLEVPKAGAVAKGSPKPSPQPSPH PSPKNSPKKGGAPAAPPPPPPLAPPLIMENLKNSLSPATQRKM GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ SSVVEFSALSVSMACLSPSQLQKFQQDGFLVLEGFLSAEECVAM QQRIGEIVAEMDVPLHCRTEFSTQEEEQLRAQGSTDYFLSSGDI IRFFFEKGVFDEKGNFLVPPEKSINKIGHALHAHDPVFKSITHS EVOOTLAPSLGLOMPDVVOSMYIFKOPHFGGEVSPHQDASFLYT
5560	9	921	GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDKC RQKRLQEQRQAQEAKGEKKDLLEVPKAGAVAKGSPKPSPQPSPH PSPKNSPKKGGAPAAPPPPPPLAPPLIMENLKNSLSPATQRKM GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ SSVVEFSALSVSMACLSPSQLQKFQQDGFLVLEGFLSAEECVAN QQRIGEIVAEMDVPLHCRTEFSTQEEEQLRAQGSTDYFLSSGDM IRFFFEKGVPDEKGNFLVPPEKSINKIGHALHAHDPVFKSITKS FKVQTLARSLGLQMPVVVQSMYIFKQPHFGGEVSPHQDASFLYM EDUCRYLGVWIAVEDATLENGCLWFIPGSHTSGVSRRMVRAPVC
5560	9	921	GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDKC RQKRLQEQRQAQEAKGEKKDLLEVPKAGAVAKGSPKPSPQPSPH PSPKNSPKKGGAPAAPPPPPPLAPPLIMENLKNSLSPATQRKM GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ SSVVEFSALSVSMACLSPSQLQKFQQDGFLVLEGFLSAEECVAN QQRIGEIVAEMDVPLHCRTEFSTQEEEQLRAQGSTDYFLSSGDM IRFFFEKGVPDEKGNFLVPPEKSINKIGHALHAHDPVFKSITKS FKVQTLARSLGLQMPVVVQSMYIFKQPHFGGEVSPHQDASFLYM EDUCRYLGVWIAVEDATLENGCLWFIPGSHTSGVSRRMVRAPVC
5560	9	921	GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDKG ROKRLQEOROAQEAKGEKKOLLEVPKAGAVAKGSPKPSPOPSPH PSPKNSPKKGGAPAAPPPPPPLAPPLIMENLKNSLSPATQRKM GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ SSVVEFSALSVSMACLSPSOLOKFQODGFLVLEGFLSAEECVAN QQRIGEIVAEMDVPLHCRTEFSTQEEEQLRAQGSTDYFLSSGDM IRFFFEKGVYPDEKGNFLVPPEKSINKIGHALHAHDPVFKSITKS FKVQTLARSLGLQMPVVVQSMYIFKQPHFGGEVSPHQDASFLYM EPLGRVLGVWIAVEDATLENGCLWFIPGSHTSGVSRRMVRAPVG SAPGTSFLGSEPARDNSLFVPTPVQRGALVLIHGEVVHKSKQNM CDREDOAYTEHLMEASGTTWSPENWLOPTAELPFPQLYT
5560		921	GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNILLSRNMDKC RQKRLQEQRQAQEAKGEKKDLLEVPKAGAVAKGSPKPSPQPSPR PSPKNSPKKGGAPAAPPPPPPPLAPPLIMENLKNSLSPATQRKN GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ SSVVEFSALSVSMACLSPSQLQKFQQDGFLVLEGFLSAEECVAN OORIGEIVAEMDVPLHCRTEFSTOEEEQLRAQGSTDYFLSSGDE

SEQ	Predicted		
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide	(A=Aldnine, C=Cvsteine, D=Aspartic Acid p
1	location	location	Glucamic Acid, F=Phenylalanine C_Cl
- 1		corresponding	H=H1Stldine, I=Tsoleugine V-Tagina
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
1	to first	amino acid	Parrollne, QaGlutamine Razginine
j	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- {	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
1			QLLAPTYFSAPGVMNFGNPSYPYAPGALPPPPPPHLYPNTQAPS
	1	İ	OVYGGUTYYNDDOOGUODYDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
	ł	1	QVYGGVTYYNPAQQQVQPKPSPPRRTPQPVTIKPPPPEVVSRGS
5562	342	1385	_,, -
ı		2303	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH
	1		LOSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP
j		1	LASFLDFITYSYMIDNVILLITGTLHQRSIAELVPKCHPLGSFE
1	1	1	QMEAVNIAQTPAELYNAILVDTPLAAFFODCISEODI.DEMNIET
1	ļ	J	TRATLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRDARITT
	1	İ	INSEGTELSKEDRAKLEPHCGRLYPEGLAGIARADDYFOUKNUM
1	ì	i	DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLABLNOFUE
5563			GVFIAFVKLKEQECRNIVWIAECIAORHRAKIDNVIDIR
1 2203	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSOADVI.NI.VOCETLEDI ELU
1		j	LQSTDYGNFLANEASPLTVSVIDDRIKEKMUVEEPUMDNUN VED
1			LASFLDFITYSYMIDNVILLITGTLHORSTARLADKCHDLGCDD
ł	1		QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI
1	i		IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
1			INSFGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA
i	1		DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNOFHF
			GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIP
5564	3	914	RVRRDKRAVWTARGRRRCGDSMSGGWMAQVGAWRTGALGLALLL
1	1		LLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRTSGLC
1	1 1		VPLTWRCDRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCT
}	!		GVSDCSGGTDKKLPMCSBI ACI ACRI PORT CONTROL OF THE CO
ł	i i		GVSDCSGGTDKKLRNCSRLACLAGELRCTLSDDCIPLTWRCDGH
1]		PDCPDSSDELGCGTNEILPEGDATTMGPPVTLESVTSLRNATTM
	1		GPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLV
5565	993	138	TATLLLLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP
1]		RWNSPNPARAGSISRPORAPGSVSAVAMTAAVFFGCAFIAFGPA
Į į	1 !		LALYVFTIATEPLRIIFLIAGAPFWLVSLLISSLVWFMARVIID
1			NKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSIN
1			PGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGPGTVGIH
1 1	1		GDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVL
j l			LINULVSAUTFISSYYGINLASAFIILVIMGTWAFLANGGCODG
5566	2043	1232	LANCILCODKNFLLYNORSR
1 1		1232	SHIQHHGRGAQAPVKMVSWMISRAVVLVFGMLYPAYYSYKAVKT
1		:	KNVKEYVRWMYWIVFALYTVIETVADQTVAWFPLYYELKIAFV
1 1			IWLLSPYTKGASLIYRKFLHPLLSSKERETDDVTVOAVERGVER
j j	j		INVERTIGATION INTERPRETATION INTERPR
1 1	1		DEPVGQRPYQPLPEAKKKSKPAPSESAGYGTDLKDGDEVTDEER
!!	1		EGPISONEMLTHKGPRRSQSMKSVKTTKGRKEVRYGSI.KVKVKV
5567	1554		RPUVIF
	1004	233	EFLGSGVSPDLANEDGLTALHQCCIDDFREMVQQLLEAGANINA
1		İ	CDSECWIPHRAATCGHLHLVELLIASGANIJAUNTDGMMDVDI
[Ĭ	l	CDDEQTLDCLETAMADRGITODS I FAARAVDELPMI DDIRECT O
, ,	J		AGADLHAPLDHGATLLHVAAANGFSEAAAI.I.T.FHDASI.CAVDOD
]			GWEPLHAAAYWGQVPLVELLVAHGADI.NAKSI.MDETPI.DVCCDE
}	į	1	EVANALLEUKHKHDALLRAOSRORSI.LRRPTSSAGSPGWARDDY
			SUIQRIDLYRKQHAQEAIVWOOPPPTSPEPPFDNDDPOTCARI D
	Ţ	i	PPPPEEDNPEVVRPHNGRVGGSPVRHLYSKRLDRSVSYQLSPLD
}	1	1	STIPHTLVHDKAHHTLADLKRORAAAKI.ORPPPEGPEGPEGPERPP
5568			GLPGDIVTPQPDCGFRAGGDPPI,I,KI,TAPAVPADVPDPDCGCC
2268	1731	587	AEDROPASRRGAGTTAAMAASGFGCRSWCLCPEVPSATFFTALL
- 1			SLLVSGPRLFLLQQPLAPSGLTLKSEALRNWQVYRLVTYIFVYE
1		Į	NPISLLCGAIIIWRFAGNFERTVGTVRHCFFTVIFAIFSAIIFL
ı			SFEAVSSLSKLGEVEDARGFTPVAFAMLGVTTVRSRMRRALVFG
Ī		1	MVVPSVLVPWLLLCASHLTDOROFS CONTROL CONT
į.	i		MVVPSVLVPWLLLGASWLIPQTSFLSNVCGLSIGLAYGLTYCYS TDLSGPVALKLDOTEREGIAND
1		j	IDLSERVALKLDQTFPFSLMRRISVFKYVSGSSAERRAAQSRKL
1		1	NPVPGSYPTQSCHPHLSPSHPVSQTQHASGQKLASWPSCTPGHM
_		i	PILPPIQPASGLCYVONHFGPNPTSSSVVPASAGTGICTOPPER
5569	2		VNSPGIVISGALGTPGAAGSKESSRVPMP
 -	<u>-</u> L	635	QTPCPLAWERGSRSEDISVPGQKPPTCSSFSGMDVGPSSLPHLG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
-	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Truntonhan Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon. /=possible nucleotide deletion,
	amino acid	sequence	_nossible nucleotide insertion)
	sequence		LKLLLLLLLPLRGQANTGCYGIPGMPGLPGAPGKDGYDGLPGP
	1	ì	KGEPGIPAIPGIRGPKGQKGEPGLPGKPGKNGPMGPPGMPGVPG
	ł	ſ	PMGIPGEPGBEGRYKQKFQSVFTVTRQTHQPPAPNSLIRFNAVL
	1	1	PWGIPGEPGREGKIKOKIOSALIAIKOINOPERINSBERINS
i		1	TNPQGDYDTSTGKFTCKVPGLYYFVYHASHTANLCVLLYRSGVK
]	1	VVTFCGHTSKTNQVNSGGVLLRLQVGEEVWLAVNDYYDMVGIQG
	1.	1	SDSVFSGFLLFPD
	264	946	RDRRDRGGVATSTEEPARPRAPQSRGPGPVSQTGRGRERGGGDT
5570	204	1	MSS DS DGKRRMDTDVVKLIESKHEVTILGGLNEFVVKFYGPQGT
	1	ì	PYEGGVWKVRVDLPDKYPFKSPSIGFMNKIFHPNIDEASGTVCL
		1	DVINGTNTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH
	i	1	RPEBYKQKIKBYIQKYATEEALKEQEEGTGDSSSESSMSDFSED
ļ	· [ł	
}		1	EAQDMEL
5571	264	946	RDRRDRGGVATSTEEPARPRAPQSRGPGPVSQTGRGRERGGGDT
	1	1	MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEFVVKFYGPQGT
	\	}	PVEGCVWKVEVDLPDKYPFKSPSIGFMNKIFHPNIDEASGTVCL
1	1	1	DUINOTWIALVOLINIFESFLPOLLAYPNPIDPLNGDAAAMYLH
1	1	1	RPEEYKQKIKEYIQKYATEEALKEQEEGTGDSSSESSMSDFSED
İ	l)	EAODMEL
_			RTDYRTGIPGRRFRVMAAGDGDVKLGTLGSGSESSNDGGSESPG
5572	2802	2085	DAGAAAEGGGWAAAALALLTGGGEMLLNVALVALVLLGAYRLWV
1	ł	1	DAGAAAEGGGWAAAALALLIGGGEMIIIN VADVAD VADVAS PND
1	1		RWGRRGLGAGAGAGEESPATSLPRMKKRDFSLEQLRQYDGSRNP
1	1		RILLAVNGKVFDVTKGSKFYGPAGPYGIFAGRDASRGLATFCLD
ł	Į.		KDALRDEYDDLSDLNAVQMESVREWEMQFKEKYDYVGRLLKPGE
1	1	· ·	PRORYTHEEDTKDHNKOD
	2562	219	VENETENA EDOGPEARATATPCOSGRERAGEAAEDGVKMAAF
5573	2562	219 .	SEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAET
1	1	1	GSGKTGAFSIPVIQIVYETLKDQQEGKKGKTTIKTGASVLNKWQ
1	1	}	MNPYDRGSAFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYE
ļ			VSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTGKKSHNKQFD
	ì	İ	NYGEEFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKN
1	1	· I	QALFPACVLKNAELKFNFGEEEFKFPPKDGFVALSKAPDGYIVK
1 .	· 	f	QALFPACVLKNAELKENFGEEEF & FFFALOF VALSIGAT DOILL
1	j	}	SQHSGNAQVTQTKFLPNAPKALIVEPSRELAEQTLNNIKQFKKY
(1	i	IDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTPGRLDDLVST
}		1	GKLNLSQVRFLVLDEADGLLSQGYSDFINRMHNQIPQVTSDGKR
}	1		LOVIVCSATLHSFDVKKLSEKIMHFPTWVDLKGEDSVPDTVHHV
1	ì	į	VVDVNDKTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMWSEA
1	Ì		TRILKGEVAURAIKEHKMDOAIIFCRTKIDCDNLEQYFIQQGGG
1		1	PDKKGHQFSCVCLHGDRKPHERKQNLERFKKGDVRFLICTDVAA
ì	1	1	RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA
1	1		TEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEE
1	}	}	HLNCTISQVEPDIKVPVDEFDGKVTYGQKRAAGGGSYKGHVDIL
1	1		HLNCTISQVEPDIKVPVDEFDGKVIIGQKKAAGGGIKGAVDID
	{		APTVQELAALEKEAQTSFLHLGYLPNQLFRTF
5574	1731	952	NEGLEVFKEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG
33,4	1	1	LICITOTI VAMI I PSWKTSSYVGASIVTAVGFSKGLWMECATHS
Ī		}	TCTTOCDTYSTLLGLPADIOAAQAMMVTSSAISSLACIISVVGM
i	į	l	PCTUFCOESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD
1	}	1	FYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSCQRN
1		1	RSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
	_1		LLWALPCPPPTAAAVLLSSTGLMELLEKMLALTLAKADSPRTAL
5575	456	766	LLWALPCPPPTAGAVERSS TGEREDUS MIRES TELESCOPET KTAS
l	1	(LCSAWLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR
1	{	j	SPDIGRNSPHYLMFP
5576	249	2146	RSWGAPWFWRMRLLRRRHMPLRLAMVGCAFVLFLFLLHRDVSSR
1 33.0	1	1	FEATER DWI.KSI.VSRKDHVI.DLMLEAMNNLRDSMPKLQIRAPEA
1	1	,	COTLESTNOSCLPGFYTPAELKPFWERPPQDPNAPGADGKAFQK
j			SKWTPLETQEKBEGYKKHCFNAFASDRISLQRSLGPDTRPPECV
1			DOKFRRCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK
1		ł	DOKEKCOPLATIBULIVE INTERNATIONAL OF THE TENENT OF THE TENENT POLICY OF THE TENENT OF T
	1	1	EIILVDDASTEEHLKEKLEQYVKQLQVVRVVRQEERKGLITARL
1			LGASVAQAEVLTFLDAHCECFHGWLEPLLARIABDKTVVVSPDI
		1	VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFGWETLPPHEKQRR
1			KDETYPIKSPTFAGGLFSISKSYFEHIGTYDNQMEIWGGENVEM

SEO	Predicted	T Bu- 42 - 4 - 3	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	Managanine, Cacysteine, Danspartic hold Ra
:	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i i	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		(\=possible nucleotide insertion)
- 1	Ì		SFRVWQCGGQLEIIPCSVVGHVFRTKSPHTFPKCTSVTAPNOVD
]			LAEVWMDSYKKIFYRRNLQAAKMAOEKSFGDISERLOLDEOLDC
1			HNESWYLHNVYPEMFVPDLTPTFYGAIKNLGTNOCLDVGENNPG
1		j	GKPLIMYSCHGLGGNQYFEYTTQRDLRHNIAKQLCLHVSKGALG
		ļ	LGSCHFTGKNSQVPKDEEWELAQDQLIRNSGSGTCLTSQDKKPA
5577	3	1275	MAPCNPSDPHQLWLFV
}		"2"	RNSDCSCGEISVHCLPWVLFILDLKVESSMFCPLKLILLPVLLD
1			YSLGINDINVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTL SPGEHAKDEYVLYYYSNISVPIGRFQNRVHLMGDILCNDGSILL
1			QDVQEADQGTYICEIRLKGESQVFKKAVVLHVLPEEPKELMVHV
	ŀ		GGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKLRM
ł			SVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCS
1	1		I HLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNOLVTTV
]	}		GIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNTKKTNDETV
[[•	EXPCHEERCEGEKHIYSPIIVREVIEEEEPSEKSEATVMTMUDI
5578	3	783	WPSLRSDRNNSLEKKSGGGMPKTOOAF
		163	AVESMAS PGACRAPPELPERNCGYREVEYWDQRYQGAADSAPYD
Ì	i		WFGDPSSFRALLEPELRPEDRILVLGCGNSALSYELFLGGFPNV
1			TSVDYSSVVVAAMQARYAHVPQLRWETMDVRKLDFPSASFDVVL EKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSRVLVPGGRFI
			SMTSAAPHFRTRHYAQAYYGWSLRHATYGSGFHFHLYLMHKGGK
			LSVAQLALGAQILSPPRPPTSPCFLQDSDHEDFLSAIQL
5579	3	1540	RNSGLARGASALARHGGGLAGGVGWDCGACASRCQGVMEGLLTR
			CRALPALATCSRQLSGYVPCRFHHCAPRRGRRIJI.SPVFOPONT [
1 :			REDRVLSLQDKSDDLTCKSORLMLOVGLIYPASPGCVHILDVTV
}			RAMEKLVRVIDQEMQAIGGOKVNMPSLSPARI,WOATHRWDI.MCV
1 1			BLLRLRDRHGKEYCLGPTHEEAITALIASOKKISYKOLDELLYO
1 1			VTRKFRDEPRPRFGLLRGREFYMKDMYTFDSSPEAAQQTYSLVC
			DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA
1 1	ĺ		ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEVGHTFYLGT KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRILAAAIEVLSTED
1 1	İ		CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYDHITEAVPQ
}			LHGEVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHF
5580			EVWCQNTGEVAFLTKDGVMDLLTPVOTV
3300	1681	450	ADAGTRCIPGFVVPSGAGYSAPAORGRRSSGRMRAAAADGITTAD
[Į		WRLLQCCELEAGELGMAVPAAAMGPSALGOSGPGSMAPWCSVSS
1 1	1		GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGPRLASG
1 1	1		SFDKTASVFLLEKDRLVKENNYRGHGDSVDOLCWHPSNPDT.FUT
1 1			ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK
1 1	ļ	1	DDVVTFIDAKTHRSKABEQFKFEVNEISWNNDNNMFFLINGNGC INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS
1 1		I	LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA
	1	ĺ	EVETGDXLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR
-EEn-			EAGTVKLFGLPNDS
5581	54	947	GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS
	1	j	CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYDAADA
1 [l		YNPSLYPTNSPSYAPEFQFLHSAYATLLMKOAWPONSSSCOTTC
j i			TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTOSNTADDDV
] [1	1	SPSPNPYQTAMYPIRSAYPQONLYAOGAYYTOPVYAAOPHUTUU
1 1	ļ	ļ	TIVVQPNSIPSAIYPAPVAAPRTNGVANGMVAGTTMAMSAGTT I
5582	5775	2739	TTPOHTAIGAHPVSMPTVPAQGTPAYSYVPPHW
[=		IITMMMVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI
			EKGLQFIQSTLPLKQEEYEAFLLKLVQNLFAEGNDLFREKDYKQ
		1	ALVQYMEGLNVADYAASDQVALPREILCKLHVNRAACYFTMGLY EKALEDSEKALGLDSESIRALFRKARALNEIGRHKEAYECSSRC
	-	Į.	SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG
	1		TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF
	[PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDS1.51.
	į	ł '	VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSpt.pp
			ASFGLVMDPSKKLAASVLDALDPPGPTLDPLDLLPYSETRLDAL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
į	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
,	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
ţ	to first	amino acid	P=Proline, Q=Glucamine, Ranginine,
1	amino acid	residue of	S=Serine, T-Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 -	\=possible nucleotide insertion)
	sequence	 	DSFGSTRGSLDKPDSFMEETNSQDHRPPSGAQKPAPSPEPCMPN
	1	1	TALLIKNPLAATHEFKQACQLCYPKTGPRAGDYTYREGLEHKCK
	}	ì	POLICELESSEDOTWKRIRPRPTKTSFVGSYYLCKDMINKQDC
	\$	1	VVCDNCTFAVHOFETDVWTEERKGTLNRDLLFDPLGGVKRGSLT
	-	1	INVIJERHOGIFTFLCEICFDSKPRIISKGTKDSPSVCSNLAAK
		1	LEBYMNKCLVHTVRSTSLKYSKIROFQEHFQFDVCRHEVRYGCL
]	}	PEDSCHEAUSFIELKVWLLOOYSGMTHEDIVQESKKYWQQMEAH
	1	l	AGKASSSMGAPRTHGPSTFDLQMKFVCGQCWRNGQVVEPDKDLK
	ļ		YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYD
	1	ļ	ICSAKARACWIREKKVIIIVIIIVIIIVIIVIIVIIVIIVIIVIIVIIVIIVI
	}	ŀ	DMWLKKHNPGKPGEGTPISSREGEKQIQMPTDYADIMMGYHCWL
	1	1	DMWLKKHNPGK2GEGIPISSREGBRQIQIDII ISCUARREPMGEFR
	1	}	CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFR
	1	l .	LCDRLQKGKAC?DGDKCRCAHGQEELNEWLDRREVLKQKLAKAR
	1	}	KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE
5583	1 3	1265	SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE
5363	1	1	IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD
		l l	QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
	1		HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL
	1	ł	CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC
	į.	į.	CONVUTDERKTIEVHVEKGMKDGOKILFHGEGDQ&PELEPGDVI
	1	1	TUT DOVINGUEOPPCHOLIMKMKIOLSEALCGFKKIIKTLDNKI
	{		LATTICK ACEVIKHGOL RCVRDEGMPIYKAPLEKGILLIQFLVIF
	1	1	PEKHWLSLEKLPQLEALLP?RQKVRITDDMDQVELKEFCPNEQN
	1	\	MECUPEAVEEDEDGPOAGVOCOTA
	<u> </u>	1000	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
5584	3	1265	IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD
	l l	l l	QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
	1	1	QGGEQATREGGSGSTSTSOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOT
	}	}	CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC
	1	1	SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI
ļ	1	ì	SGAKVIREKKIIEVHVEKSMEDGATIL IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
}	,	l l	IVLDQKDHSVFQRRGHDLIMATKIQLSKAPLEKGILIIQFLVIF LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF
ł	1	ł	PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN
ì	1	\	PEKHWLSLEKLPQLEADLPPRQKVRIIIDDWIDGVIDIOLIU
Į	1	1	WRQHREAYEEDEDGPQAGVQCQTA
5585	2619	915	LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM
3302		1	YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS
1	ł		SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD
İ	(Į.	ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG
l	ì	Į.	THE CUCA PAIL PLANT PER TIRLLE FVGFSGNKDYGLLQLEEGAS
Į.	1	1	CHERROLL COMPLICATION OF THE CHERRY LINK
Į.	1	}	VDVGA TELELAGRIEVIKGNIDAAIRREECCEAQQHWKQFHHM
{	i	[CYWEL-MWCETYKGOWKMSYFYADLLSKENCWSKATYIYMKAAIL
1	į)	DECKEDURDEGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
(ı	\	DDVECENDICI DVDALEMMYTWNGYAVIGKQPKLTDGILEIITA
\		}	AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS
1		į	ISANEKKIKYCHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ
ļ		1	NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL
1			NYKNYSMESKTHFKTQAATLQAKSSIENGSKEN LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM
5586	2619	915	LPAGTPESSLHEADDQCMTADDFDTMQFSEADSTDCFRTADDM
1		1	YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS
)	}		SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD
1	1		ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG
1			VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS
	1		GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR
]		1	VDVCATELELAGRIEVIKGNIDAAIRREECCEAQQHWKQFHH
1	1	1	CVWELMWCETYKGOWKMSYFYADLLSKENCWSKATYLYMKAALI
1	1	l	CMCCVEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTERFALKK
1	1	Į.	DRYESCNETSI.DVDAI.EMMYTWNGYAVIGKQPKLTUGILEIIII
		· ·	THE PARTY OF THE PROPERTY OF T
		Į.	AREMT.EKGPENEYSVDDECLVKLLKGLCLKILGKVQEAELMING
			AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS
			ISANEKKIKYDHYLIPNALLELALLIMEQDRNEEAIKLLESAK
	7 1768	148	AEEMLEKGPENEYSVDDECLVKLLKGLCLKILGRVQEAEEMI ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAK NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL SSAVPDGAVGRPVAVAVGGPPHSCRCRPCCLMAAIGVHLGCTS

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G≈Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
	to first amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
1	residue of	residue of	S=Serine, T=Threonine, V=Valine
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
	 	 	\=possible nucleotide insertion)
- [· ·		CVAVYKDGRAGVVANDAGDRVTPAVVAYSENEEIVGLAAKQSRI
Í		1	RNISNTVMKVKQILGRSSSDPQAQKYIAESKCLVIEKNGKLRYE IDTGEETKFVNPEDVARLIFSKMKETAHSVLGSDANDVVITVPF
1			DFGEKQKNALGEAARAAGFNVLRLIHEPSAALLAYGIGQDSPTG
			KSNILVFKLGGTSLSLSVMEVNSGIYRVLSTNTDDNIGGAHFTE
1		<u> </u>	TLAQYLASEFQRSFKHDVRGNARAMMKLTNSAEVAKHSLSTLGS
1	1	ł	ANCFLDSLYEGODFDCNVSRARFELLCSPLFNKCIEAIRGLLDO
1	J .		NGFTADDINKVVLCGGSSRIPKLOOLIKDLFPAVELLNSIPPDE
į.		ĺ	VIPIGAAIEAGILIGKENLLVEDSLMIECSARDILVKGVDESGA
1		}	SRFTVLFPSGTPLPARRQHTLQAPGSISSVCLELYESDGKNSAK
- 1			EETKFAQVVLQDLDKKENGLRDILAVLTMKRDGSLHVTCTDQET GKCEAISIEIAS
5588	3	589	TPPPPEQAMVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGK
			LVSLEKYRGSVSLVVNVASECGFTDQHYRALQQLQRDLGPHHFN
			VLAFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKTAVTGTC
			AHPAFKYLAQTSGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEEV
5589	1884		RPQITALVRKLILLKREDL
	1004	553	LRQAWHEGGIGQTDKERGAAALPGEEGDPTRGRSLGRASWESGS
į	}		PRRPRSPFSSFLPRPICLSLEARPCSIEDRRNWSLIGRPGAPAS
1			GLNRSSGLWLGPDRCRPRSRCSCRVMENPSPAAALGKALCALLL ATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPLF
1	1		RPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALM
1	ļ		KEIEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRHSLVSF
	ĺ		VVRIVPSPDWFVGVDSLDLCDGDRWREONALDLVPVDAGTDGG=
1			TFSSPNFATIPODTVTEITSSSPSHPANSFYYPRLKALPDIADV
			TLLRLRQSPRAFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLW
			SSWGLCGGHCGRLGTKSRTRYVRVQPANNGSPCPELEEEAECVP DNCV
5590	72	896	LCSSGALRLLPAMVAWRSAFLVCLAFSLATLVQRGSGDFDDFNL
1	J		EDAVKETSSVKQPWDHTTTTTTNRPGTTRAPAKPPGSGLDLADA
1	ì		LDDQDDGRRKPGIGGRERWNHVTTTTKRPVTTRAPANTLGNDFD
			LADALDDRNDRDDGRRKPIAGGGGFSDKDLEDIVGGGEVKDDKG
1 1			KGDGRYGSNDDFGSGMVAEPGTIAGVASALAMALIGAVSSYISY
}			QQKKFCFSIQQGLNADYVKGENLEAVVCEEPOVKYSTLHTOSAE
5591	68	1494	PPPPPBPARI
1	· ·	2272	AGSSRAAAERLLVSAGCRSLAGRASGVLLLPAELLPGEEEAMA
]]	}		LRVTRNSKINAENKAKINMAGAKRVPTAPAATSKPGLRPRTALG DIGNKVSEQLQAKMPMKKEAKPSATGKVIDKKLPKPLEKVPMLV
	1		PVPVSEPVPEPEPEPEPEPVKEEKLSPEPILVDTASPSPMETSG
1 1		i	CAPAEEDLCQAFSDVILAVNDVDAEDGADPNLCSEYVKDTVAVT.
1 1		!	RQLEEEQAVRPKYLLGREVTGNMRAILIDWLVOVOMKERLLORT
		{	MIMIVSIIDRFMQNNCVPKKMLOLVGVTAMFIASKYFFMYDDRI
1 1	Ĭ		GDFAFVTDNTYTKHQIRQMEMKILRALNFGLGRPLPLHFTRRAS
1 1			KIGEVDVEQHTLAKYLMELTMLDYDMVHFPPSQIAAGAFCLALK
Ll			ILDNGEWTPTLQHYLSYTEESLLPVMQHLAKNAAMVNQGLTKHM TVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV
5592	242	924	YGESKDWNQKDLLSALVLTTVNCLPTPIMAKSAEVKLAIFGRAG
1 1	ļ	ļ	VGKSALVVRFLTKRFIWEYDPTLESTYRHQATIDDEVVSMEILD
]		Ì	TAGQEDTIQREGHMRWGEGFVLVYDITDRGSFEEVLPLKNILDE
	1	1	IKKPKNVTLILVGNKADLDHSROVSTEEGEKLATELACAFVECS
ji	į	į	ACTGEGNITEIFYELCREVRRRRMVQGKTRRRSSTTHVKOAINK
5593	3	7777	MLTKISS
		1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
i i	1	į	SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE
[ļ	DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR
		{	BLDLYDNQIKKIENLEALTELBILDISFNLLRNIEGVDKITRLK KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLB
	ļ	1	SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR
]	ì	ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELO
	<u>-</u>		EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV

			the state of the s
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	p=proline, O=Glutamine, R=Arginine,
	amino acid	residue of	S-Scripe T-Threonine, V-Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	1	Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		/=possible nucleotide inscience,
			MLALPSVRQIDATFVRF
5594	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
555		1	SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE
		1	DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR
	1	ì	ELDLYDNQIKKIENLEALTELEILDISFNLLRNIEGVDKLTRLK
	1	1	KLELVNNKISKIENLSNLHOLOMLELGSNRIRAIENIDTLTNLE
	1	l	SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR
	}	· l	ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQ
	l	l	EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV
	1	[
			MLALPSVRQIDATFVRP
5595	3	1476	ARWNGRWVQVPAWPGPGCGTNASGERQRQLPRAWRPVGRTLGSE
	-		PIALAWSPPLYLFPIPLPSWAVSQPTPTLGTMFADLDYDIEEDK
	}	}	LGIPTVPGKVTLQKDAQNLIGISIGGGAQYCPCLYIVQVFDNTP
			AALDGTVAAGDEITGVNGRSIKGKTKVEVAKMIQEVKGEVTIHY
	1	į.	NKLOADPKOGMSLDIVLKKVKHRLVENMSSGTADALGLSRAILC
	1	1	NDGLVKRLEELERTAELYKGMTEHTKNLLRAFYELSQTHRAFGD
		1	VESVIGUREPOPAASEAFVKFADAHRSIEKFGIRLLKTIKPMLT
	}	· I	DLNTYLNKAIPDTRLTIKKYLDVKFEYLSYCLKVKEMDDEEYSC
	1 .	· ·	IALGEPLYRVSTGNYEYRLILRCRQEARARFSQMRKDVLEKMEL
	1 .	Í	LDQKHVQDIVFQLQRLVSTMSKYYNDCYAVLRDADVFPIEVDLA
	1	}	HTTLAYGLNQEEFTDGEEEEEEDTAAGEPSRDTRGAAGPLDKG
	1	1	
	ì	1	GSWCDS
5596	698	219	GAVLAPSSLPAAELAAQGESQSLEDLSNTSRPTSEVYKISFIFP
	l l	[NGDKYDGDCTRTSSGIYERNGIGIHTTPNGIVYTGSWKDDKMNG
	· (į.	FGRLEHFSGAVYEGQFKDNMFHGLGTYTFPNGAKYTGNFNENRV
	1	1	KGEGEYTHIQGTRMDVVTFHFTSCSQT
5597	+3	731	ISCHMANGOSSLPASWRSVTLTHVEYPAGDLSGHLLAYLSLSP
5597	1 3	1 .32	VEVIVGEVILIIEKRELHTISELGGLALNEGVNWLIKNVIQEPR
ļ	ļ	1	PCGGPHTAVGTKYGMPSSHSQFMWFFSVYSFLFLYLRMHQTNNA
[ł.	1	RFLDLLWRHVLSLGLLAVAFLVSYSRVYLLYHTWSQVLYGGIAG
ì	1	1	GLMAIAWFIFTQEVLTPLFPRIAAWPVSEFFLIRDTSLIPNVLW
!			FEYTVTRAEARNRQRKLGTKLQ
			GIGPIAASFIPCKVASLYIFLSPPPPPSVSGVPYSPANSSWSCAL
5598	326	2440	VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLLAVALGFFEG
1	1	ì	DAKFGERNEGSGARRRCLNGNPPKRLKRRDRRMMSQLELLSGG
f	l .		DAKFGERNEGSGARRRRCLINGNPPRRBRRRDRRIMDECCVI.LEE
1	· I	1	EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
ì	{	1	IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR
1	{	1	GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
}		1	OMERYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
}			I.FILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL
t		ſ	STAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
1		}	NPHOVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM
1	1		ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
1	1	1	TNOPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS
1			SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
	ļ		SARILQII KGKDI ESEPSDBEL KPESKOTBYDI CI CTCCCCDCVPCC
i		į.	YGSYVFGDRNGNFLTLQQSPVTKQWQBKPLCLGTSGSCRGYFSG
1	1		HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE
1			CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
5599	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
1	1		VDLICSGVPPHPPAPSPCCSGOTMLKMLSFKLLLLAVALGFFEG
1	1		DAKEGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG
	j	}	EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
[IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR
	l	(GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
1		i	QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
		j	
		l	QMEEYDKVEETSKKHKMNCFCTQEVVSGBRQFVCABROODSGE
			LEILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL
			LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLI SLAFHDNYKKNGKLYVSYTTNOERWAIGPHDHILRVVEYTVSRK
			LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK NPHOWDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM
			LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLI SLAFHDNYKKNGKLYVSYTTNOERWAIGPHDHILRVVEYTVSRK

SEQ	Predicted	Predicted end	2000
σı	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion}
			SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
			YGSYVFGDRNGNFLTLQQSPVTKOWOEKPLCLGTSGSCRGVESG
1			HILGFGEDBLGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE
5600	1977	1244	CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
	1377	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE
		1	EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF
			SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA
	}	1	FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
[İ	AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC TFYHPTINVPPRHALKWIRPQTSE
5601	1977	1244	STEM SCHI WOLDDA ADDA SERVE
			SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF
			SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA
	! '		FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
			AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC
			TFYHPTINVPPRHALKWIRPQTSB
5602	246	766	YHTSCTVWRTAKEALENTEVPVGCLMVYNNEVVGKGRNEVNQTK
ı			NATRHAEMVAIDQVLDWCRQSGKSPSEVFEHIVI,YVTVFPCIMC
ſ			AAALRIMKIPLVVYGCQNERFGGCGSVINIASADIPNTGRPEGC
			IPGYRAEEAVEMLKTFYKQENPNAPKSKVRKKECOOILNMF
5603	1	565	FRGRTPISGERGCAOYPIPATPARSCENRTMPGAGDCGVARAR
			WLGTGLLGLFLLPVTLSLEVSVGKATDIYAVNGTEILLPCTFSS
1			CFGFEDLHFRWTYNSSDAFKILIEGTVKNEKSDPKVTI,KDDDP1
1	1		TLVGSTKEKRNNISIVLRDLEFSDTGKYTCHVKNPKENNLQHHA
5604	1	1506	TIFLQVVDRRMQ
	*	1206	EDIFPAQLLKLQRHERVWQQEPPVRDHRSWGGSGAGGVAGREWT
1			DOGOVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG
			GGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ
1	İ		RLDGILSETIPIHGRGNFPTLELQPSLIVKVVRRRLAEKRIGVR
1			DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI
1			SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE
			NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG
1 1		i	LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL
1			ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL
i i	1		ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV
			QPVFTCQQQTYSTWLPCN
5605	35	1821	SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALCI.
1 1	1		MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFO
1	1		KALRSLRRYPLPLRSGKEAKILOHFGDGLCRMI,DERT,OPHPTSC
1	i	İ	GDHAPDSPSGENSPAPQGRLAEVODSSMPVPAOPKAGGSGSVWP
1 1	l		AKHSGARVILLVLYREHLNPNGHHFLTKEELLORCAOKSPRVAP
	ľ		GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAOKLAESE
1			GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP
]		ļ	GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF
			VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ
	1		KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG
1			FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE
1			SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG
j í	ì	Ì	VSGEKAAALVDRYSTPASLLAAVDACATPKEQETLLSTIKCGRL
5606	3	1099	QRNLGPALSRTLSQLYCSYGPLT GRSRCPGPGAPGCTMGDBGGLBGAPALVENING
[]	ļ		GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK
	1	1	LSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA
]]	į	į	IEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG
	1	ĺ	VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVEC
		ĺ	KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRRVG
	1	1	SSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGR
	ì	i	TCNKTSKAIDGCELLCCGRGFHTAQVELAERCSCKFHWCCFVKC
			RQCQRLVELHTCR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
5607	521	141	PRICHPAEAMPS PGTVCSLLLLGMI.WLDLAMAGSSFLSPEHQRV
3607	521	1	QQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAP
	!		FDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK
		983	WFQSPLRQADPGPPRHTLFMDFVAGAIGGVCGDAVGYPLDTVKV
5608	2	763	RIQTEPKYTGIWHCVRDTYHRERVWGFYRGLLLPVCTVSLVSSE
	İ	1	VFGTYRHCLAHICRLRFGNPDAKPTKADITLSGCASGLVRVFLT
		1	SPTEVAKVRLQTQTQAQKQQRRLSASGPLAVPPMCPVPPACPEP
		1	KYRGPLHCLATVAREEGLCGLYKGSSALVLRDGHSFATYFLSYA
		Í	VLCEWLSPAGHSRPDVPGVLVAGGCAGVLAWAVATPMDVIKSRL
	Į.	i	VLCEWESPAGASKPDVPGVEVAGGCAGVEAMATTTTTDV11CCPAEDIM
		i	QADGQGQRRYRGLLHCMVTIVREEG?RVLFKGLVLNCCRAFPVN
			MVVFVAYEAVLRLARGLLT
5609	1628	304	AKGVWVLPSPPPRPGRGALVSGSGLRRGRSGTSWRPRRMNHKSK
	1		KRIREAKRSARPELKDSLDWTRHNYYESFSLSPAAVADNVERAD
			ALQLSVEEFVERYERPYKPVVLLNAQEGWSAQEKWTLERLKRKY
			RNQKFKCGEDNDGYSVKMKMKYYIEYMESTRDDSPLYIFDSSYG
	Į.		EHPKRRKLLEDYKVPKFFTDDLFQYAGEKRRPPYRWFVMGPPRS
	1		GTGIHIDPLGTSAWNALVQGHKRWCLFPTSTPRELIKVTRDEGG
	1	1	NQQDEAITWFNVIYPRTQLPTWPPEFKPLEILQKPGETVFVPGG
	1	1	WWHYVLNLDTTIAITQNFASSTNFPVVWHKTVRGRPKLSRKWYR
	i	1	ILKQEHPELAVLADSVDLQESTGIASDSSSDSSSSSSSSSSDSD
	i	i	SECESGSEGDGTVHRRKKRRTCSMVGNGDTTSQDDCVSKERSSS
	1		R
L	54	1196	LERTPASADMAWTKYOLFLAGLMLVTGSINTLSAKWADNFMAEG
5610	34	1 1150	CGGSKEHSFQHPFLQAVGMFLGEFSCLAAFYLLRCRAAGQSDSS
ļ	ļ	1	VDPQQPFNPLLFLPPALCDMTGTSLMYVALNMTSASSFQMLRGA
1	j	1	VIIFTGLFSVAFLGRRLVLSQWLGILATIAGLVVVGLADLLSKH
{		1	DSQHKLSEVITGDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLRA
ļ	i	1	VGTEGLFGFVILSLLLVPMYYIPAGSFSGNPRGTLEDALDAFCQ
!	ľ	ì	VGQQPLIAVALLGNISSIAFFNFAGISVTKELSATTRMVLDSLR
İ	1		TVVIWALSLALGWEAFHALQILGFLILLIGTALYNGLHRPLLGR
			LSRGRPLAEESEQERLLGGTRTPINDAS
			FVLPNRLGIPGSTFRGPGACASSSSLAASAKPGAGGSPALAMSG
5611	2	577	ELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPE
ł	\	ļ	ELSNRFQGGRAFGILLNARQERRIABINGS ICOQRESSES ELSNRFQGGRAFGILLNARQERRIABING ICOQRESSES ELSNRFQGGRAFGILLNARQERRIABING ICOQRESSES ELSNRFQGGRAFGILLNARQERRIABING ICOQRESSES ELSNRFQGGRAFGILLNARQERRIABING ICOQRESSES ELSNRFQGGRAFGILLNARQERRIABING ICOQRESSES ELSNRFQGGRAFGILLNARQERRIABING ICOQRESSES ELSNRFQGGRAFGILLNARQERRIABING ICOQRESSES ELSNRFQGGRAFGILLNARQERRIABING ICOQRESSES ELSNRFQGGRAFGILLNARQERRIABING ICOQRESSES ELSNRFQGGRAFGILLNARQERRIABING ICOQRESSES ELSNRFQGGRAFGILLNARQERRIABING ICOQRESSES ELSNRFQGGRAFT ELSNRFQGGRAFT ELSNRFQGGRAFT ELSNRFQGGRAFT ELSNRFQGGRAFT ELSNRFQGGRAFT
ł	\	Į.	KLTAFKEKYMEFDENNEGETDENSUKANTEKTOVFKINDERKOV
1			ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP
1		<u> </u>	KPVGPPPERDIASLP
5612	1	721	ASRDGYMDATIAPHRIPPEMPQYGEBNHIFELMQAMWLCKHLNS
]	į		SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA
1	1 .		EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL
1		ı	IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET
1			AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS
1			NHRTNAPFTPRVLLLGPVGS
5613	115	1279	RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD
1 2013	1	_=	KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST
		}	AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF
			FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH
1		ļ	GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH
	1	1	AHGHGHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI
[1	ASAIMMONFGLMIADPICSILIAILIVVSVIPLLRESVGILMOR
1		\	TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKL
		.	IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM
			LLSRNEHACPLQAGLGLTQRKPKAIRGREGRATNQGQGETQNER
5614	3	1268	LLSRNEHACPLQAGLGLIQRAPAAIRGRESAAIRQCQCDIQRAR APWGARQRLGVMAELQQLQEFEIPTGREALRGNHSALLRVADYC
1		1	APWGARQREGVMAELQQLQDFELYIGKEADKGMIGALDKVADIC
1			EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRMLD
1			LQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVQRLPPG
1			QKVIAPENLPPLTPYCRRPLNFGCLDDIGHGIKDLSTQLSRTGT
I	1	1	LSRKSIKAPATPASATLGRPPRIPEPVHLPVVPDGRLSAASSAS
1	i		SLASAGSAEGVGGAPTPKGQAAPPAPPLPSSLDPPPPPAAVEVF
1			ORPOTLEELSPPPPDEELPLPLDLPPPPPPLDGDELGLPPPPPGF
l		1	GPDEPSWVPASYLEKVVTLYPYTSQKDNELSFSEGTVICVTRRY
1	i .	1	U. Mar Dir variante de la constante de la cons

SEO	Predicted	I punding a second	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide location	Note that the control of the contr
	location		
į.	corresponding	corresponding to first	1 "-" TOUTOUTUE, ISISOIPHOIDE V-Territor
i	to first	amino acid	D=Deucine, M=Methionine N-According
ı	amino acid	residue of	(Fariotine, Oagintamine Dalvainia.
l	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
- 1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	1 Codon, /=possible nucleotide deletion
			\=possible nucleotide insertion)
5615	9	1558	SDGWCEGVSSEGTGFFPGNYVEPSC
j		1 .550	ALGRRRPGDPREMEAAATPAAAGAARREELDMDVMRPLINEQNF
i	1		DGI SDEEREQEDEPVOKHYOI, DDAFCI CENAMI MITT I MANTER COM
1			LIGUPLA LANAGIVLGPISLVFIGITSVUCMUTI VDCGVDV OV D
- 1			TAKSING ISDIVSEAMEVSPWSCTAKOA AMCDCIATORET TITMOS
	1 .		GFCSVIIVFLAENVKOVHEGFLESKVRISMOSMOSMOSMOSMOSMOSMOSMOSMOSMOSMOSMOSMOS
1	İ		DRIEDCE LPETILLVFIRELKNI, FVT, SET, AMICMAYOT VITTAGE
1	· ·		1 V KNIL POPHNUPI VAGWKKYPLFFGTAVFA FFGTGVALDI FNO
- 1	ſ		MALSIAR PUALNIGMGIVITLYVTIATICVMCRUDETVCCTMIN
1			LPQDVWLYQSVKILYSFGIPVTYSIQFYVPAEIIIPGITSKFHT
			KWKQICEFGIRSFLVSITCAGAILIPRLDIVISFVGAVSSSTLA
<u> </u>	1		LILPPLVEILTFSKEHYNIWMVLKNISIAFTGVVGFLLGTYITV
5616	1	719	BELLIFIPAVVAGTPOSPFLNI,NSTCI,TSGI,Y
1	[,15	DDFVRCGPQSAAMGASARLLRAVIMGAPGSGKGTVSSRITTHFE
· ·	1		LKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIPDDVMTRLAL
1	1 1		HELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV
1			IKQRLTARWIHPASGRYYNIEFNPPKTVGIDDLTGEPLIQREDD
L			KPETVIKRLKAYEDQTKPVLEYYQKKGVLETFSGTETNKIWPYV YAFLQTKVPQRSQKASVTP
5617	176	765	PWRCRCSPPRCACAMARROUPERS
İ	1 1		PWRGRGSRPRGAGAMAEEQVNRSAGLAPDCEASATAETTVSSVG
1	i		TCEAAGKSPEPKDYDSTCVFCRIAGRODPGTELLHCENEDLICF KDIKPAATHHYLVVPKKHIGNCRTLRKDQVELVENMVTVGKTIL
l	1		ERNNFTDFTNVRMGFHMPPFCSISHLHLHVLAPVDQLGFLSKLV
			YRVNSYWFITADHLIBKLRT
5618	3	1692	YLNYINLKSENKLSGKEDLWEKLQYLWKSTLNLPEDLLRVPDES
	1		LFLNSGGDSLKSIRLLSEIEKLVGTSVPGLLEIILSSSILEIYN
ı	1 1		HILQTVVPDEDVTFRKSCATKRKLSNINQERASGTSLHQKAIMT
	1		FICHNEINALVVLSRGSOILSINSTREITRIGUCGGROOPS
1.	1		VINIVALIAGENS PVLIGKS KDPS CVAKVS RRGK DAT CTOVARDITY
1	1	•	VKWASDIGACVDASPLVVIPTFDKSSTTVVIGSUSUDMVAUDDI
	1		SGRVKWEQILGDRIESSACVSKCGNFIWGCVNGIWWII VONGO
İ	1		EXIMMFTTEDAVKSSATMDPTTGLIYIGSHDOHAVAIDIVDVVG
ł	1		VWASKUGGIVESSPCLNLIPHHI.VPATI.CCT.T.AMPRATORY
1	Ī		KHSCGK-LESSPOCCSOYICIGCUDGNT.I.CETTLECEOUTGORGES
1	1		GPIFSSPCISPSEOKIFFGSHDCFTVCCNMVGHI OWVERNMOD:
	1		I TATEFAFHININGSNEMLLAAASTDGKVWII.ESOSGOI.OSTOPER
5619	2160	1477	GEALSSEAATESWITTGCKDNAAACIDITGCNOR
Í	1	14//	DSPVLPTSGNVISTAQPAQPWSAVEAALRSLGSPPGAGRGCPCP
	j j		AUSTREAD TO A COLOR OF THE PROPERTY OF THE PRO
1	1		RSCPUPEPLEELLRAGSSTRPOPT.TSSCCGMCGMVcpr gracer
1]		LWGTKGRGSGSPSSPGCCLHPPAQHSQDLPLVHVDVGWQPPLGP
	1 1		TVGLRPGLLGERQRGALRAGDPQCQCPLPATVREDLGVPSPWAA ECSPPATP
5620	930	182	
1		1	PLPPPTLAMPLTRSEYDRGVNTFSPEGRLFQVEYAIEAIKLGST
1			AIGIOTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGCAMSG
1 1		ł	LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNLALQFG
			EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQCDAR
		į	AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEEKLNA TNIELATVQPGQNFHMFTKEELEEVIKDI
5621	3	819	VVEFVEVEATOANUANEGA GOVOGA
]]	!	[VVEFVEYTATDANVKNESLSSVQQLGIKMTVRYGKFLSLLKDGA
i I		ľ	ENDLTWVLKHCERFLKQQQTSIKSSLLCLQGNYAGHDWFVSSLP MIMIGDKEKTFQFLHQFSRLLTSAFLWLPRLHISSYLPNDTVES
1 1	1	1	GIHPVYFCSTHYIEMLLKABLPLVFSAFHMSGFAPSQICLQWIT
[]		Ť	QCFWNYLDWIRICHYIATCVFLGPDYQVYICIAVPKHLQQDILQ
	1	į	HTQTQDLQVFLKEEALHGFRVSDYFEYMEILEQNYRTVLLRDMR
<u> </u>		1	NIRLOST
5622	1122		AASTKDAVSRKRSHSASEKSGTGTSISKRLNMNPQIRNPMKAMY
1]	PGTFYFQFKNLWEANDRNETWLCFTVEGIKRRSVVSWKTGVFRN
	1	1	QVDSETHCHAERCFLSWFCDDILSPNTKYQVTWYTSWSPCPDCA
			GEVAEFLARHSNVNLTIFTARLYYFQYPCYQEGLRSLSQEGVAV
			- TYPE-TARGET STREET ST

Predicted Predicted Predicted Predicted Predicted Programming Design				Amino acid segment containing signal peptide
NO: location corresponding to first amino acid residue of samino acid sequence seque	SEQ		Predicted end	Amino acid segment containing signal popular
location corresponding to first amino acid residue of amino acid residue of amino acid sequence				Clutamic Acid F=Phenylalanine, G=Glycine,
LeLeucine, M-Methionine, Na-Naparaghe, amino acid residue of amino acid sequence screen, T-Threonine, Na-Valine, amino acid sequence screen, T-Threonine, Na-Valine, amino acid sequence screen, T-Threonine, Na-Valine, amino acid sequence screen, T-Threonine, V-Valine, was separated and sequence screen, Y-Threonine, V-Valine, was separated and sequence screen, Y-Threonine, V-Valine, was supported and sequence screen, Y-Threonine, V-Valine, was supported and sequence screen, Y-Threy Colon, Y-Possible nucleotide deletion, Y-Possible nucleotide sequence screen, Y-Threy Stry of the sequence seque	NO:		location	w_wightedine T-Teoleucine, K=Lvsine,
to first anino acid anino acid residue of anino acid sequence sequence sequence Servine				T-Tougine M-Methionine N=Asparagine,
amino acid residue of amino acid sequence sequence Secrime, Trivreonime, V-Valine, Sequence				n preline O-Glutamine R-Arginine.
### ### ##############################				Paproline, Quedicamine, Navaganary,
amino acid sequence Codon, /-possible nuclectide insertion				SESETINE, TEINTEDITINE, V-VALUE,
Sequence Sequence				W=Tryptopnan, islyrosine, n-ommoni,
5623 3 954 FLOFFTRADTISHNGOWLFFTFFFFANKALKRRILESEL 0 0 0 RKILITPOTTOTHE LIQUITLE LLIPSICSSESTOLLEANNSLYV TTTKS TITPNTESLOKINVTPTTOTTPKOTITMELLKINSLING AFFLENSKOBLARTITOVRKNOSI ISINVTTSVITLANASTLOS SKEKTETOSSIKTTET POSVLOPDASPEKTOTITSTELLKINSLING SKEKTETOSSIKTTET POSVLOPDASPEKTOTITSTEVTI PORV SOSVUTGTEGGINASTISTSSESSI ILIPVITALIVITLSVEVI VGLYMNCKRADPGTPENGRIDOPOSKESVELLIVKITLSTEVTI VGLYMNCKRADPGTPENGRIDOPOSKESVELLIVKITLSTEVTI SAGGKTKIN 159 898 FGWAAAAGALPOYNGPARALVSCREELSLESAGSLOLERKRRIDS SCSRKIMPTHRALVCLEDBIGFATQOREI IVSALVKILEANNM IVYKDMVIRMQOETTFOQVMSQIANVKKOMILLEKSEFSALRAN NEKKILEHLGIKOVOMBEVI IVOTITKIK EDENGEKSKYRELIVSIA LENIKYLLGISTICVALGETYRIK LENIKYLLGISTICVALGETYRIK LENIKYLLGISTICVALGETYRIK LENIKYLLGISTICVALGETYRIK LENIKYLLGISTICVALGETYRIK LENIKYLLGISTICVALGETYRIK LENIKYLLGISTICVALGETYRIK LENIKYLLGISTICVALGETYRIK LENIKYLLGISTICVALGETYRIK LENIKYLLGISTICVALGETYRIK LENIKYLLGISTICVALGETYRIK LENIKYLLGISTICVALGETYRIK LENIKYLLGISTICVALGETYRIK LENIKYLLGISTICVALGETYRIK LENIKYLLGISTICVALGETYRIK LENIKYLLGISTICVALGETYRIK CREPADERKIKULUSELDISCOLUTAFFTENTH GOMRISLVSSRIRIT EPEPAAVLERQRARGETOPALTETELEPE LISSRASYSGKADUWSLOVALFTMLAGGRIVAPETOPALTET CREPADERKIKULUSELDISCOLUTAFFTENTH GOMRISLVSSRIRIT EPEPAAVLERGEBORRAVALHOPTISTITT CREPADERKAVLUSELDISCOLUTAFFTENTH CORMISLAVSSRIRIT EPEPAAVLERGEBORRAVALHOPTISTITT CREPADERKAVLUSELDISCOLUTAFFTENTH CORMISLAVSSRIRIT EPEPAAVLERGEBORRAVALHOPTISTITT CREPADERSAVLUSELDISCOLUTAFFTENTH CORMISLAVSSRIRIT EPEPAAVLERGEBORRAVIA CREPADERKAVLUSELDISCOLUTAFFTENTH CORMISLAVSSRIRIT EPEPAAVLERGEBORRAVIA CREPADERKAVLUSELDISCOLUTAFFTENTH CORMISLAVSSRIRIT EPEPAAVLERGEBORRAVIA CREPADERKAVLUSELDISCOLUTAFFTENTH LIVKKYSMINENTENTICHTARDET CORMIA WERDENDERGE LIVKKYSMINENTENTICHTARDET CORMIA WERDENDERGE LIVKKYSMINENTENTICHTARDET CORMIA WERDENDERGE LIVKKYSMINENTENTICHTARDET CORMIA WERDENDERGE LIVKKYSMINENTENTICHTARDET CORMINANTENTICHT SEVLEPSI COLUMNICATION CORMINENTENTICHTARDET LIVKKYSMINENTENTICHTARDET CORMINANTENTICHT SEVLEPSI COLUMNICATION CORMINATION CORMINANTENTICHT LIVKKYSMINENTENTICHTARDET COLUMNICATI		amino acid	sequence	Codon, /=possible indefedence deleter,
Second color		sequence		\=possible nucleotide insertion
Section				1
RKKILIPSTOTMELLQVTILELLPSICSSSTGVLERANNSLY TITKPSITTPMTESICKGNVTPTTOTTPKGTITTMELKNSLMST ATPLISKOBGLKATTTDVRKNOSIISNVTTYSVILPRAVSTIGS SKPKETROSSIKMETE 1GSVLOPASPEKTGILISTUTIPEN SOSOVIGTEGGKNASTSATSSSYSSILLPVVIALIVITLSVPVIL VGLYRMCKKADDPERNERDOPOSKESVALLTVATISEGGER SAGGKTKN FORMADAGGALPVRIGPAPALVSCREELSLSAGSLOLERKRRDFT SSCSRKINPOTRALVGLEDBIGPATQOASTIVSALVAKILEANDI 1VYKDMVTRKOGGTFFOOMSGLANVKKUMILISESFSALMAS NEKIKLELHGUKQOVMBEVIEVRTDTRKLETERSGERSALKAS NEKIKLELHGUKQOVMBEVIEVRTDTRKLETERSGERSALKASIL EKKLELESTITLATVALGFYRLMI 1.80 TIPSSAAGKRREDDNILDTEREVGKRARSGOPRIPPCLUBLSPH AGSLSSKKRELDDNILDTERVOKRARSGOPRIPPCLUBLSPH TAPDRATAVATASRIGPVILLBERGGRAVALHGESHK LUNIKYLLGSITFLLTVALGFYRLMI GUMMSILVSSRIRTSRIPSVILLBERGGRAVALHGELDLISPSY TAPDRATAVATASRIGPVILLBERGGRAVALHGELDLISPSY TAPDRATAVATASRIGPVILLBERGGRAVALHGELLBLISSK CREFVFADDRERKKLVLERLBGSGLVLTGPDDSIMOKHACPAVVOP LISSRASYSGRADWSLGVALFTMLAGNTYLGVELLSDVANFAT GUMMSILVSSRIRT EPPERAVLFRAMATALAKTORILHBUKD DEMULATESILMERAQVOPDGLALDLERBERGRAVILDELLBE LISSRASYSGRADMSLGVALFREDFILLFVERFANTOTILLHBUKD DEMULATESILMERAQVOPDGLALDLERBERGEVILVEN TYVOKKYSOMBELIKGBKRELFILARDFFORILDESDAFMELRAK EEBELINKLRILSSGSFETUTINERKYLFFYKLTGFON TYVOKKYSOMBELIKGBKRELFILARDFFORILDESDAFMELRAK EEBELINKLRILSSGSFETUTINERKYLFFYHLIVALTHJUTHJGJVIRF RIHLYKGRRRYGGKKKIH REPKLAGHGAGKONVYEFHLEFILDLYKEPFYYKLTGROV TENVIHFKAQGHGAKSONVYEFHLEFILDLYKEPSVYKLTGROV TENVIHFKAQGHGAKSONVYEFHLEFILDLYKEPSVYKLTGROV TENVIHFKAQGHGAKSONVYEFHLEFILDLYKEPSVYKLTGROV TENVIHFKAQGHGAKSONVYEFHLEFILDLYKREPSVYKLTGROV SEPLESSIGNENGHTIGHT FITGTMEROMKAVVEFYTLMSALE TENVIHFKAQGHGAKSONVYEFHLEFILDLYKREPSVYKLTGROV TENVIHRKAQGHGAKSONVYEFHLEFILDLYKREPSVYKLTGROV TENVIHRKAQGHGAKSONVYEFHLEFILDLYKREPSVYKLTGROV TENVIHRKAQGHGAKSONVYEFHLEFILDLYKREPSVYKLTGROV TENVIHRKAQGHGAKSONVYEFHLEFILDLYKREPSVYKLTGROV TENVIHRKAQGHGAKSONVYEFHLEFILDLYKREVENDALDHAN LIVRYGCILGKSSTYDTHTVANDRYCOMLAVVETINAATOVT SPULDSLOLLGKHETERVENDELGGLGGGSTROSANVSSORG TENVILLBERGGOVENDENGHGAGGSTROSANATSSYSGG GOMPGEGILTGNEKTHGVENDENGLGGLGGNALDLANDLYTHALDLYTHA TENVIHRANDLANDRATATATTATATATATATATATATATATA		1		Q STREET TO THE TOTAL PROPERTY OF THE PROPERTY
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ATPLITS(DBGLKATITOVRKNDS IISNIVIVISVILLINIVISTUS) SKYKTET(DSSILKTET) GSULOPDASPSKITGLITSIPVITIENT SOSOVIGTEGGINASTSATSRSYSSIILDVVIALIVITISJEVIL VGLYNNCKARDAPOTPENGINOPOSDKESVILLIVKITSIESGEB SAGKKIN FORMAARGALDOVHGPAPALVSCREELSLSAGSLOLERKRRDFT SCHARARGALDOVHGPAPALVSCREELSLSAGSLOLERKRRDFT SCHARARGALDOVHGPAPALVSCREELSLSAGSLOLERKRRDFT IVYDDVIVINOPOSITPOOWNSOILNVEKMILLIKSEFSAURAB MEKILLELHOLKOOVNDEVITKVRTDTELDENLEKSRVAKHLESHK NEKILLELHOLKOOVNDEVITKVRTDTELDENLEKSRVAKHLESHK LINIKILASSIPPCLIVOLLEPVELMI TIPSSARAGRAPPRAGALEALSTOCARAHAERGEMRATPLAAP AGSISAKKRIELDDBLOTERPVOKRARSGPOREDPELLEPEDP TADDRATAVATASRIGPVILLEPBERGRAVQAHCPPGTEFTCR VYPVORALAVELPVALPPRIKVARPTYEVLAGTQLLYAPFTETH GOMMSLVASRIRITPEPRAVULREGGARAVALHCHOGGIVLRULKL CREVFADRERKKULERLIBSCULTREDABELTAGTILLEPBERG DEMPLAPTESILMEAAQVUPOGLGLDAREERGDBEVVLKO RRGAYALPAGLARAPACIVACHLOREPAGRAVALHGKIARPYVELP LISSRASYSGRAADWSLGVALFTHLAGHTPGOSEPVLKOK RRGAYALPAGLARPAGNOVELTREAVARAFRETELIVREDDWORPATST TENVLHEKAQCHGAKGONVYEPHLEFILDLVKEPOYHALTGOVN TENVLHEKAQCHGAKGONVYEPHLEFILDLVKEPOYHALTGOVN TENVLHEKAQCHGAKGONVYEPHLEFILDLVKEPOYHALTGOVN TENVLHEKAQCHGAKGONVYEPHLEFILDLVKEPOYHALTGOVN SPULPSILIQLIGRNFILIFITEGTMEEMONKAVVEPTURASIE TERVSFYHLICIDDMKVLTHALTYTHI DIJVJGGLABAVSVIQ SIPIFNETGREFFILPVVKKKVENFSFFLQIYLINIFIGLYINF RHLYKORRRYGOKKKHI FRAGGRAVALPAGGAKGANOVYEPHLARYTIM THAUPGICLABAVSVIQ SIPIFNETGREFFILPVVKKKVENFSFFLQIYLINIFIGLYINF RHLYKORRRYGOKKKHI TURVENGOKKHI TURVENGOKKHI TURVENGOKKHI TURVENGOKKHI TURVENGOKKHI TURVENGOKKHI TURVENGOKKHI TURVENGOKKHI TURVENGOKHI TURVENGOKHI TURVENGOKKHI TURVENGOKHI TURVENGOKHI TURVENGOKHI TURVENGOKHI TURVENGOKHI TURVENGOKHI TURVENGOKHI TURVENGOKHI TURVENGOKHI TURVENGOH TURVENGOKHI TURVENGOKHI TURVENGOKHI TURVENGOH TURVENG	5525			RKKILTPSTGTMELLQVTILFLLPSICSSNSTGVLEAANNSDVV
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SQSQVIGTEGGINASTASTASTSYSSILLEVVIALIVITISTISEGGER SQGKYKN SGYRALOPOTPERSINDOPOSDKESVKLITVKTISIESGER SQGKYKN SGYRALOPOTHALVCLLENNGPATQAGEITVSALVKLIEANIM IVVKDMVTRNOGITTGQWASQLANVKKUMILEKSEFSALRAF EKIKLELHOLKQOVNDEVIKVRTDTELDFRILESSRAGEIVSIAN EKKIKLELHOLKQOVNDEVIKVRTDTELDFRILESSRAKEIVSIAN EKKIKLELHOLKQOVNDEVIKVRTDTELDFRILESSRAKEIVSIAN EKKIKLELATEIVALHARQODRAITOTDEKETERVELYSIAN EKKIKLELATEIVALHARQODRAITOTDEKETERVELYSIAN EKKIKLELATEIVALHARQODRAITOTDEKETERVELYSIAN EKKIKLELATEIVALHARQODRAITOTDEKETERVELYSIAN EKKIKLELATEIVALHARQODRAITOTDEKETERVELYSIAN EKKIKLELATEIVALHAROPEVALATOTDEKETERVAGEKIKLESISIA EKKIKLELATEIVALHAROPEVALATOTDEKETERVAGEKIKLESISIA EKKIKLELATEIVALATOTOTEKETERVAGEKIKLESISIA EKKIKLELATEIVALATOTOTEKETERVAGEKIKALESISIA EKKIKLELATEIVALATOTOTEKETERVAGEKIKALESISIA EKKIKLELATEIVALATOTOTEKETERVAGEKIKALESISIA EKKIKLELATEIVALATOTOTEKETERVAGEKIKALESISIA EKKIKLELESTATAILATOTILLASIA EKKIKLELESTATAILATOTILLASIA EKKIKLELESTATAILATOTILLASIA EKKIKLELESTATAILATOTILLAPIA PERDEGRANJAAN OLEHAPITAILATOTILLAPIA PERDEGRANJAAN OLEHAPITAILATOTILLAPIA PERDEGRANJAAN OLEHAPITAILATOTILLAPIA PERDEGRANJAAN OLEHAPITAINA EKKIKLESISIA PERDANJAKAN OLEHAPITAINA EKKIKLESISIA PALIVAN ANAN OLEHAPITAINA EKKIKLESISIA PALIVAN ANAN OLEHAPITAINA OLEHAPITAINA EKK				ATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPNAVSTLQS
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SSGSRLYPDTHALVCLLENNEGPTQUESTYORATIVANIALIEANS IVYRDWYTWRQSITTQQWSQTANVKRWILLEANSH REXILLELRIPUMARQQUSTAVVKRWILLESHKALESHK REXILLELRIPUMARQQUSALTQTOTRKLEFEVAGKTMLESHK LDNIKYLAGSIFTCLTVALGFYRLWI 11280 AGSLSRKRELBIDNIDTERPVQKRARSGPQRDJPCLLDLSPJP TAPDRATAVATASRLGFYVLLSPEBGGRAYQALPCPTGTEYTCR VYPVQGALAVLEFYARLPFHKIVARPTEVLAGTQLLYAFFTRTH GDMHSLVRSRRIFIPEDEAVLFRQMATALAHCHGGETYTCR VYPVQGALAVLEFYARLPFHKIVARPTEVLAGTQLLYAFFTRTH GDMHSLVRSRRRIFIPEDEAVLFRQMATALAHCHGGETYTCR VYPVQGALAVLEFYARLPFHKIVARPTEVLAGTQLLYAFFTRTH GDMHSLVRSRRRIFIPEDEAVLFRQMATALAHCHGGETURDLKI CRFVFADREKKLVLENDEDSCVLTGFGDSLKDKHACFAYVGPE LISSRAYSGKAADVUSLGVALFTHLAGHYPFQDSEPVLLFGKI REGAYALPAGLSAPARCLURCLLREPEABRAITATGILLHFMLRQ DPMLAFTSHLWRAAQVVDPOLLDDAREBEGDREVVLVG PPFALGSVAMENQVLTHVAVQCHRERLVESDVQNPAIST TENVLHKAQGRGAKGDNVYEFHLEFLDLVKPEPVVLTGQVN ITVQKKVGQWBELTKQBER PLFLADPTGLSDVGNPAIST TENVLHKAQGRGAKGDNVYEFHLEFLDLVKPEPVVLTGQVN LIVVRFCILGKESFTDTHTVAADMYFCQHUAVETINAATGVTT SPVLPSLIQLIGRRFILFIIFTTENDAVTGVALAVETINAATGVTT SPVLPSLIQLIGRRFIIFTIFTTAMMVAQHRELLYLTUGPUN STPIPHETGSFTTLPFVKIKTVRSFFTLQIVLTMIPLIGLYINF RILVXQRRRRYGQKKKKIH FRYSFWILTCLIDMKVLTWIRLYTLAFILDIYLIGCLARAVSVIQ STPIPHETGSFTTLPFVKIKTVRSFFTLQIVLTMIPLIGLYINF RILVXQRRRRYGQKKKKIH LIVRGSFSPTTPFVKIKTRGVILFMNILOYLGFSNIFVN LIVVRSCVGOWRENTKGEKFPLFLADPTDFRULDSEDABMELRAK EBERLINKLRLESEGSPETLINLRKGVILFMNILOYLGFSNIFVN LIVVRSCVGOWRENTKGEKFPLFLADPTDFRULDSEDABMELRAK EBERLINKLRLESEGSPETLINLRKGVILFMNILOYLGFSNIFVN LIVVRSCVGOWRENTKGEKFPLFLADPTDFRULDSEDABMELRAK EBERLINKLRLESEGSPETLINLRKGVILFMNILOYLGFSNIFVN LIVVRSCVGARENGVERFLYNDLROYLAVETINAATGVTT SPVLPSLIVLGESSPVDTENTAMMYTCHAMAVETINAATGVTT SPVLPSLIVLGESSPVDTENTAMMYTCHAMAVETINAATGVTT SPVLPSLIVLGESSPVDTENTAMMYTCHAMAVETINAATGVTT SPVLPSLIVLGESSPVDTENTAMMYTCHAMAVETINAATGVTT SPVLPSLIVLGESSPVDTENTAMMYTCHAMAVETINAATGVTT SPVLPSLIVLGESSPVDTENTAMMYTCHAMAVETINAATGVTT SPVLPSLIVLGESSPVDTENTAMMYTCHAMAVETINAATGVTT SPVLPSLIVLGESSPVDTENTAMMYTCHAMAVETINAATGVTT SPVLPSCHOORSTON STANTAMMYTCHAMATAGVTT SPVLPSLIVLGEGRAFTSTSGG GGGGGGTLTGNRETTGNSLIVLGVTENGLGCAGATSTSSGGAGGSTRYSAMYSSSPCKLP GRASSONDAPTG		ł	1	SAQGKTKN
SSGSRLYPDTHALVCLLENNEGPTQUESTYORATIVANIALIEANS IVYRDWYTWRQSITTQQWSQTANVKRWILLEANSH REXILLELRIPUMARQQUSTAVVKRWILLESHKALESHK REXILLELRIPUMARQQUSALTQTOTRKLEFEVAGKTMLESHK LDNIKYLAGSIFTCLTVALGFYRLWI 11280 AGSLSRKRELBIDNIDTERPVQKRARSGPQRDJPCLLDLSPJP TAPDRATAVATASRLGFYVLLSPEBGGRAYQALPCPTGTEYTCR VYPVQGALAVLEFYARLPFHKIVARPTEVLAGTQLLYAFFTRTH GDMHSLVRSRRIFIPEDEAVLFRQMATALAHCHGGETYTCR VYPVQGALAVLEFYARLPFHKIVARPTEVLAGTQLLYAFFTRTH GDMHSLVRSRRRIFIPEDEAVLFRQMATALAHCHGGETYTCR VYPVQGALAVLEFYARLPFHKIVARPTEVLAGTQLLYAFFTRTH GDMHSLVRSRRRIFIPEDEAVLFRQMATALAHCHGGETURDLKI CRFVFADREKKLVLENDEDSCVLTGFGDSLKDKHACFAYVGPE LISSRAYSGKAADVUSLGVALFTHLAGHYPFQDSEPVLLFGKI REGAYALPAGLSAPARCLURCLLREPEABRAITATGILLHFMLRQ DPMLAFTSHLWRAAQVVDPOLLDDAREBEGDREVVLVG PPFALGSVAMENQVLTHVAVQCHRERLVESDVQNPAIST TENVLHKAQGRGAKGDNVYEFHLEFLDLVKPEPVVLTGQVN ITVQKKVGQWBELTKQBER PLFLADPTGLSDVGNPAIST TENVLHKAQGRGAKGDNVYEFHLEFLDLVKPEPVVLTGQVN LIVVRFCILGKESFTDTHTVAADMYFCQHUAVETINAATGVTT SPVLPSLIQLIGRRFILFIIFTTENDAVTGVALAVETINAATGVTT SPVLPSLIQLIGRRFIIFTIFTTAMMVAQHRELLYLTUGPUN STPIPHETGSFTTLPFVKIKTVRSFFTLQIVLTMIPLIGLYINF RILVXQRRRRYGQKKKKIH FRYSFWILTCLIDMKVLTWIRLYTLAFILDIYLIGCLARAVSVIQ STPIPHETGSFTTLPFVKIKTVRSFFTLQIVLTMIPLIGLYINF RILVXQRRRRYGQKKKKIH LIVRGSFSPTTPFVKIKTRGVILFMNILOYLGFSNIFVN LIVVRSCVGOWRENTKGEKFPLFLADPTDFRULDSEDABMELRAK EBERLINKLRLESEGSPETLINLRKGVILFMNILOYLGFSNIFVN LIVVRSCVGOWRENTKGEKFPLFLADPTDFRULDSEDABMELRAK EBERLINKLRLESEGSPETLINLRKGVILFMNILOYLGFSNIFVN LIVVRSCVGOWRENTKGEKFPLFLADPTDFRULDSEDABMELRAK EBERLINKLRLESEGSPETLINLRKGVILFMNILOYLGFSNIFVN LIVVRSCVGARENGVERFLYNDLROYLAVETINAATGVTT SPVLPSLIVLGESSPVDTENTAMMYTCHAMAVETINAATGVTT SPVLPSLIVLGESSPVDTENTAMMYTCHAMAVETINAATGVTT SPVLPSLIVLGESSPVDTENTAMMYTCHAMAVETINAATGVTT SPVLPSLIVLGESSPVDTENTAMMYTCHAMAVETINAATGVTT SPVLPSLIVLGESSPVDTENTAMMYTCHAMAVETINAATGVTT SPVLPSLIVLGESSPVDTENTAMMYTCHAMAVETINAATGVTT SPVLPSLIVLGESSPVDTENTAMMYTCHAMAVETINAATGVTT SPVLPSLIVLGESSPVDTENTAMMYTCHAMAVETINAATGVTT SPVLPSCHOORSTON STANTAMMYTCHAMATAGVTT SPVLPSLIVLGEGRAFTSTSGG GGGGGGTLTGNRETTGNSLIVLGVTENGLGCAGATSTSSGGAGGSTRYSAMYSSSPCKLP GRASSONDAPTG		1 750	898	PGVAAAAGALPQYHGPAPALVSCRRELSLSAGSLQLERKRRDFT
I TVYKDMYTMOGETTGOWNSGIANVKKOMI ILESESSALRAN BEKIKLELBIOKKOQVMOBUT KYRTDTKLDFIDEKSRVKELYSIN BEKKLLELRIEIVALHAGODRALTGTDKRIETEVAGLKTMLESIK LIDNIKYLAGSITTCLIVAGFYRLIH TIPSSAAGGRAGPPAGALEALSPGGARAHAERGERGERMATDFLAS AGSLSKKKRLELDDILDTERFVÇKRARSGPORDFALPFLLSPB AGSLSKKKRLELDDILDTERFVÇKRARSGPORDFALPFLLSPB TADDRATAVATASKIGPYVLLEBEBGGRATQALHCPTGTEYTCR VYPVQEALAVLEPYARLPPHKHVARPTEVLAGTGTEYTCR VYPVQEALAVLEPYARLPPHKHVARPTEVLAGTGLLYBFFTKTH GDMISLJVERSRHRIEPERAVLERGHSOVLJYSFFTKTH GDMISLJVERSRHRIEPERAVLERGHSOVLJYBFTKTH GDMISLJVERSHRIEPERAVLERGHSOVLJOHLISKE RRGYALPAGLSAPARCIJVECLLEREPAERLITATGILLHPMLRQ DPMPLATTESHLWBRADVUPDGIGLDEAREEEGDREVVLYG TENVLHFKAGGIGAKGINNYEFHLEFLDLVVEPERVKLTCRGVN THVOKKVSQMWERLKVGKEKRPLFLAPDFDRHLDESDAEMELRAK EEERINKLRLESEGSPETLITILKKGYLEPBTVKLTCRGVN THVOKKVSQMWERLKVGKEKRPLFLAPDFDRHLDESDAEMELRAK EEERINKLRLESEGSPETLITILKKGYLEPHVYLNGFLGFSHIFVN LTVRFCLIGKESFYDTFTTVADMMYSCMHLAVVETINAALGVTT SPULPSLIGLLGREFSTIPTYVKLKVRFSFFLQIYLTMIFLGIYINF GSPULPSLIGLLGREFSTIPTYVKLKVRFSFFLQIYLTMIFLGIYINF TENVLHFKAGGHAAKGNVYLFPHVYAAGRHEELYLEVELSDVONPAISI TENVLHFKAGGHAAKGNVYLFPHLYAAGRHEELYLEVELSDVONPAISI TENVLHFKAGGHAAKGNVYLFPHLYAAGRHEELYLEVELSDVONPAISI TENVLHFKAGGHAAKGNVYLFPHLYAAGRHEELYLEVELSDVONPAISI TENVLHFKAGGHAAKGNVYLFPHLEFLDLVKFEDVYNLTORGVN TIVOKKVSQMWERLITKGEKKPIPTALDLVKFEDVYNLTORGVN TIVOKKVSQMWERLITKGEKRPLELDLVKFEDVYNLTORGVN TIVOKKVSQMWERLITKGEKRPLELDLVKFEDVYNLTAGGVT SPULPSLIGLIGNSFITLFITEGTMEEMQNKAVVFFYFYLMSAIE TRYSSFYNLTCHIDMUKVLITKHRYTHMIPLAYFLGALARAVSIVQ SIPINMSTGRSFTLLFYDVKLKVRFSFFLQIYLLMIFLGLYINF SPULPSLIGLIGNSFITLFYDVKLKVRFSFFLQIYLLMIFLGLYINF TRAGATAGATAGATAGATAGATAGATAGATAGATAGATAG	5624	123		SSGSRKLYFDTHALVCLLEDNGFATQQAEIIVSALVKILEANMD
NEKKLELHOLKOQVMDEVIKVRTDTK.DDRNEKSRVKELTSEN EKKLLELREIVALHAGOPRATIOTRETEVAGLKTMLESIK LDNIKYLAGSIFTCLTVALGFYRLMI 1180 TIPSSAAGGRAGPPGALEALSPGGARAHAERRGEMRATPLAAP AGSLSKKKRLELDDNLDTERFVQKRARSGPQPRLPPCLLPLSPP TAPDRATAVATASRLGFYVLLSPEBGGGRYQHLPPCLLPLSPP TAPDRATAVATASRLGFYVLLSPEBGGGRYQHLPPCTLPLSPP TAPDRATAVATASRLGFYVLLSPEBGGRYQHLPPCTLPLSPP TAPDRATAVATASRLGFYVLLSPEBGGRYQHLPPCTLPLSPP TAPDRATAVATASRLGFYVLLSPEBGGRYQHLPPCTLPLSPP TAPDRATAVATASRLGFYVLLSPEBGGRYQHLPPCTLPLSPP TAPDRATAVATASRLGFYVLLSPEBGGRYQHLPPCTLPCT VPYQEALAVLEPYARDFPEKVLAGFQDELVTGKT. GDMMSLVRSRHRIPPERAVLRGVGTDLSKKHACPTYVEPT CRPYPARGEKKLVLEHLBESCVLTGPDDSLMKHACPATYVEP LISSRASYSGKAADVWSLGVALFTMLAGHYPFQDSPVLLFGKT. RRGAYALPAGLSAPARCLVVCLLRREPAERLTAGLLLHBWLRQ DMPLLAPAGLSAPAGCIVECLLRREPAERLTAGLLHBWLRQ DMPLLAPAGLSAPAGCIVECLLRREPAERLTAGLLHBWLRQ DMPLLAPAGLSPAGNACVETHVYWAQRHRELTAGVELHBWLRQ TENVLHFKAQGGGAGGONVEFHLEFLDLVREPEVYKLTQQVN TTVQKKVSQWMBRLTKQEKRPLFLAPDFDRAILDSDAEMELRAK EEERINKIKLESGSSPTLTUNLKSVTHYNLQVGLGFSWIFVN LLVRRCLLGRESFYDTHTVANDMYSCQMLAVVETINAALGVTT SPVLPSLLOLLGRRIFLSTLFTFTGTYTWAKVELSDVQNPAIST TENVLHFKAQGGASKGNVEFHLEFLDLVKREPVYKLUTQOVN TTVQKKVSQWMBRLTKQEKRPLFLAPDFDRMLDSDAEMELRAK EEERINKIKLRESGSSPETLINLRKGTHYNLOVGLGFSWIFVN TENVLHFKAQGGASKGNVYFFHLYBLOVGLGFSNIFVN TENVLHFKAQGGASKGNVYFFHLYBLOVGLGFSNIFVN SPVLPSLLQLLGRRFILFTIFGTMEMQMKAVVFFYYLMSAIE EERINKIKLRESGSSPETLINLRKGTHYNLOVGLGFSNIFVN SPVLPSLLQLLGRRFILFTIFGTMEMQMKAVVFFYYLMSAIE TRYSFYMLTCIMDMKVLIVALBYTLMIPLLYNLAGAG TRYSSFYMLTCIMDMKVLIVALBYTLMIPLLYNLAGAG TRYSSFYMLTCIMDMKVLIVALBYTLMIPLLYLAGAGAGS GGWFGGGILTGNEKETMQSLAGGSSTRVSAMYSSSFCKLP LPRAGFSSGSLKSPGGASGGSTRVSAMYSSSFCKLP TRYSFYMLTCIMDMKVLIVALBYTLMIPLLYLLAGAGAGAGG GGWFGGGILTGNEKETMQSLAGGLRSTRATSCLPALCLPAGAGAGAGAG TRYSSSFOLKFLERERGGISSANVTENERLOLDRANSVCLAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG		1		TUVKDMUTKMOOEITFOOVMSQIANVKKDMIILEKSEFSALRAE
EKKLLELRIETVALHAGODRALTOTDEKIETEVAGLKTMLESIA LDNIKYLAGSIFTCLIVAGIGFRUM TPPSSAAAGRAGPAGALEALSPGGARAHAEREGEMRATPLASA AGSLSRKKRLELDDNLDTERPVOKRARSGPOPELPFCLIPLSPP TAPDRATAVATASKLGPVYLLEPEGGRAVQALHCPTGTEYTCR VYPVQGALAVLEPVARLPPHKIVARPTEVLLGTQLLYAFFTETH GDMMSLIVARSRHRIETEPBAVLRROWATALARCGHGLVLRDLKL CRFVFADRERKKLVLENLEDSCVLTGPDDSLUMKACRAYVOPE LISSRASYSGKADVMSLGVALFTHLAGHYPFQDSSPVLLFGKI RRGAYALPAGLSAPARCLVECLLRREPAERLTATGLLHIPMLRQ DPMPLATTSHLMEAAGVVPDGLGLDEAREEGGREVVLTG FPRALGSVAMEMQVLTPHVVWAQRHRELYLEVELSDVQNPAIST TENVLHFKAQCHGAKGDNVYEPHLERPLOKPEVRLYCRGVN LTVQRKCLLGRESFYDTFHTVADMMYELVERPEVKLYCRGVN LTVQRKCLLGRESFYDTFHTVADMMYECQMLAVVETTINAAIGVTT SPVLPSLLQLLGRESFYDTFHTVADMMYECQMLAVVETTINAAIGVTT SPVLPSLLQLLGRESFYDTFHTVADMMYECQMLAVVETTINAAIGVTT SPVLPSLLQLLGRESFYDTFHTVADMMYECQMLAVVETTINAAIGVTT SPVLPSLTGLEFSFTLPVPVKLKVRFSFFLQIYLLMTFLGLYINF RILMYRGRRYRGGKKKHH FPRALGSVAMEMQVLTPHVVWAQRHREINLARVELSDVQNPAIST TRNVHHFKAQGHGAKGDNVYEFHLEFILDLVKPEPVYKLTGRGVN TRNVHRFKAQGHGAKGDNVYEFHLEFILDLVKPEPVYKLTGRGVN TRNVHRFKAQGHGAKGDNVYEFHLEFILDLVKPEPVYKLTGRGVN TRNVHRFKAQGHGAKGDNVYEFHLEFILDLVKPEPVYKLTGRGVN TRNVHRFKAQGHGAKGDNVYEFHLEFILDLVKPEPVYKLTGRGVN TRNVHRFKAQGHGAKGDNVYEFHLEFILDLVKPEPVYKLTGRGVN TRNVHRFKAQGHGAKGDNVYEFHLEFILDLVKPEPVYKLTGRGVN TRNVHRFKAQGHGAKGDNVYEFHLEFILDLVKPEPVYKLTGRGVN TRVGKVSQMWERLITGEKRPLFLAPDFDRWLDSDAEMSLRAK EEERLINLKRLESSGSPETLITILERGLLPALCLPAGGFRIFVN LTVRRCLIGKSSYDTFHTVADMMYPCONLAVVETTINAAIGVTT SPVLPSLIQLLGRNFILDFILGFTHEADAVVETTINAAIGVTT SPVLPSLIQLLGRNFILDFILGFTHEADAVVETTINAAIGVTT SPVLPSLIQLLGRNFILDFILGFTHEADAVVETTINAAIGVTT SPVLPSLIQLLGRNFILDFILGFTHEADAVVETTINAAIGVTT SPVLPSLTGLGRSFTTLFVPVKLKVRFSFFLQIYLLMTPLGLYLNFT SPVLPSLTGLGRSFTTLFVPVKLKVRFSFFLQIYLLMTPLGLYLNFT SPVLPSLTGLGRSFTTLFVPVKLKVRFSFFLQIYLLMTPLGLYLNFT SPVLPSLTGLGRSFTTLFVPVKLKVRFSFFLQIYLLMTPLGLYLNFT SPVLPSLTGLGRSFTTLFVPVKLKVRFSFFLQIYLLMTPLGLYLNFT SPVLPSLTGLGRSFTTLFVPVKLKVRFSFFLQIYLLMTPLGLYLNFT SPVLPSLTGLGRSFTTLFTNAAIGTLGCAGGAGGSTRVSAMYSSISCAL GGMFGGETLTGNNERTMSLINGCLYGFTGSTALSAGGAGGTNAVVSCAAAVASAVAAAAA ARTNCSARPICVPCGGGR OFFICER SSSINNRFILERERAGLSSAAVVTRIGNKSASCLPC		1		NEKIKLELHOLKOOVMDEVIKVRTDTKLDFNLEKSRVKELYSLN
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ILSSRASYSGKADUWSLGVALFIKLGKYPFQDSEPVLLIFGKI RRGAYALPAGLSAPARCLIKREPABERLTAGGILLHFPURQ DPMPLAPTESILWEAQUVPDGLGLDEAREBEGDREVVLYG DPMPLAPTESILWEAQUVPDGLGLDEAREBEGDREVVLYG FRAUGHAPTCSILWEAQUVPDGLGLDEAREBEGDREVVLYG PPRALGSVAMENQVLTPHVVWAQRHRELYLRVELSDVQNPAISI TENVLHFKAÇGKGKGNUVYFFHLEFLDLUKPEPVYKLTCRQVN ITVQKKVSQWWERLTKQEKRPLFLAPDFDRHLDESDAEMELRAK EEERINKURLESEGSPETLTHIKKGYLFWYHVUQFLGFSWIFVN LTVRFCILGKESFYDTFHTVADMWYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRWFILFIIFGTMEEMQNKAVVFFVFLWSAIE IFRYSFYMLTCIDMDWKVLTHLRYTLWIDLPYLGCLABAVSVIQ STPIPNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRVQCKKKLH PPRALGSVAMENQVLTPHYVWAQRHRELYLRVELSDVQNPAISI TENVLHPKAQGGGAKGDNYYSFHLEFIDLVKPEPVYKLTORQVN ITVQKKVSQWMERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERINKURLESEGSPETITHIRKGYLFWYNLUQPLGFSWIFVN LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFIITHIRKGYLFWYNLUQPLGFSWIFVN LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFITHIRKGYLFWYNLUQPLGFSWIFVN LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFITHIRKGYLFWYNLUQPLGFSWIFVN LTVRFGILGKSFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILTHIRKGYLFWYNLUQPLGFASTSYGG GGFGGGILTGMSKETMGGKKAVVFFFTLEGLARTCLAAGGFATSYSGG GGFGGGILTGMSKETMGSKAVFFFFTLEGVFTLGAGFARSSPCKLF SSLSPVARSFSACSVGIGRSSYRATSCLPALCLFAGGFATSYSGG GGFGGGILTGNEKETMGSLNDRLAGYLEKVRQLEGENASLESR IRBMCSQQVYMCPDYQSYFFTIELQKKTLCSKABNARLUVGI DNAKLAADDFRTKYFETEVSLRQLVSSDINGKRILDDITLCKSD LEAQVESLKEELLCLKKNHEEBEVNSLRCQLGBRINGVENAAPPV DLMRVLEEMECQYSTLVENNRRDABGMLTTQSEEDMQQVVSSLD LEAQVESLKEELLCKKHNEEBEVNSLRCQLGBRINGVENAAPPV SSQLAQMQCMITNVEAQLAEIRADLERQNGCYGVLLDVRARLEC EINTYRGLLESEDSKLPCUPCAPDYSPKSCLPCLPAASCGPSA ARTNCSARPICTUPCGGGR GRPGSSDNNFFLEERGGLSSAAVOTRIGNSAASRRSPAARPPV SSQLAQMQCMITNVEAQLAEIRADLEGVGNTSGNSAASRRSPAARPPV PAPPALBERGRFGTEGSTSLSAPAVLVVAVAVVVVVSAVANAMAM NYINPPGSSPEVPCIANTUQDGEBRCREGALSLLQHRPWDD QEVILGLFTOGITNKLIGCYVGNTMEDVULVIRTIGKKELLDUR PAPPALBERGRFGTEGSTSLSAPAVLVVAVAVVVVVSAVANAMAM NYINPPGSSPEVPCIANTUQDGEBRCREGGALSLLQHRLPWDD QEVILGLFTOGITNKLIGCYVGNTMEDVULVRITIGKKELLDUR	1			COMMS DEED VILLE IN ENT. EDS CVI. TGPDDSLWDKHACPAYVGPE
RRGAYALPAGLSAPARCLVRCLLEREPAGRITATGILLHWILD DPMPLAPTRSHLWEAQUVUPDGLGLDEAREPEGDREVULYG SPEALGSVAMENQVLTPHVVWAQRHRELYLRVELSDVQNPAISI TENVLHFKAQCHGAKGDNVYEFHLEFIDLVKPEPVYKLTCRQVN ITVQKKVSGWBERITKGBKRPLFLAPPDFRAIDESDAEMELRAK EEERINKLRLESEGSPETLTNLRKGYLFMYNLVOPLGFSWIFVN LTVRCILGKESFYDTFHTVADMWYLCOMLAVVETINAAIGVTT SPVLPSLIQLLGRNPILFI IF GTMEEMQNKAVVFFVFYLWSAIE IFRYSFYMLTCIDMDKVLTWLRYTLWIPLVPLGGLAEAVSVIQ SIPIENETGRSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRRYQKKKKI PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTORQVN ITVQKKVSQWMERLTKGEKPLFLAPDFDRWLDESDAEMELRAK EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQPLGFSWIFVN LTVRFCILGKESFYDTFHTVAMMYFCOMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVPYLWSAIE IFRYSFYMLTCIDMDKVLTTMLRYTHANFLYPLGCLAEAVSVIQ SIPIFMETGRSFTLPYVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRYGQKKKKH SEVERSLIKKRLESEGSPETLTNLRKGYLMINFUGLAEAVSIQ SIPIFMETGRSFSTLPYVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRYGQKKKKH SPVLPSLIGLLGRNFILFIIFGTMEEMQNKAVVFFVPYLWSAIE IFRYSFYMLTCIDMDKVLTTMLRYTHANFLYPLGCLAEAVSVIQ SIPIFMETGRSFSTLPYVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRYGQKKKKH SLEPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG GGWFGGILTGNEKETMQSLNDRLAGYLEKVRQLEGENASLESR IRBWCSQQVYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI DNAKLAADDFRTKYFTEVELRQLVESDINGLRRILDDLTLCKSD LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLAWVDAAPPV DLMRVLEEMRCQYETLVENNRTABAEDWLDTQSEELMQQVYSSES QLQSCQABITELRRTVNALEIELQACHSRRDALESTLAETEARY SSQLAQMQCMITNVERQLAEIELQDAGHSRRDALESTLAETEARY SSQLAQMQCMITNVERQLAEIELQDAGHSRRDALESTLAETEARY SSQLAQMQCMITNVERQLAEIELQDAGHSRRDALESTLAETEARY SSQLAQMQCMITNVERQLAEIELGLAGAHSRRSPAARPFV SSQLAQMQCMITNVERQLAEIELGLAGAHSRRSPAARPFV SSQLAQMQCMITNVERQLAEIELGLAGAHSRRSPAARPFV PAPPALPRRPREPGTEGSTSLSAPAVLVVAVVVVVVSAVANAMA NYINPPGSSEVRENNTVQDGEERRCREGALSLLQHLRPHWDE PREPKYSBRUICHASHGGVGTTNNGLCYGFTGGALSLLQDRHVDR	l		1	CREVEADRERALLY DENIES CHALFTML AGHYPEODSEPVILLEGKI
DEMPLAPTESHLMERAQVVPDGLIGLAREEEGDREVVLTS 5626 3123 2011 PPRALGSVAMENQVLTPHVYWAQRHRELYRVELSDVQNPAIST TENVLHFKAQGHGAKGDNYYEFHLEFLDLVKPEPVYKLTQRQVN TENVLHFKAQGHGAKGDNYYEFHLEFLDLVKPEPVYKLTQRQVN TENVLHFKAQGHGAKGDNYYEFHLEFLDLVKPEPVYKLTQRQVN LTVRCILGKESFYDITHIVADMMYFCQMLAVVETINAAIGVTT SPVLBSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVYLMSAIE IFRYSFYMLTCIMDMKVLTWLRYTLWIPLYPLGCLAEAVSVIQ SIPIPMETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRYRGGKKKKIH PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI TENVLHFKAQGHGAKGDNYYEFHLEFLDLVKPEPVYKLTQRQVN ITVQKKVSQMWERLTRQEKRPLFLAPPTDRWHDLESDAEMELRAK EEERLNKLRLESEGSPETLINLRKGYLFMYMLVQFLGFSWIFVN LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLIGRNFILFIIFGTMEEMQNKAVVFVFYLWSAIE IFRYSFYMLTCIDMDWXTUMLRYTLMIPLYPLGCLAEAVSVIQ SIPIFMETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRRYGGKKKIH TRHLYKQRRRRYGGKKKKIH VAGAMASKCLKAGFSSGLKSPGGASGGSTRVSAMYSSSPCKLP SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG GGMFGGILTGNREETMQSLINDELAGYLEKVRQLEQERASLESR IREWCEQQVPYMCDPQGKKKTLCSKAENARLVVEI DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD LEAQVESLKEELLCLKKNHEEEVWSLRCQLGBRLNVEVDAAPPV DLNRVLEEMRCQYSTEVRTIELQKKTLCSKAENARLVVEI DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD LEAQVESLKEELLCLKKNHEEEVWSLRCQLGBRLNVEVDAAPPV DLNRVLEEMRCQYSTEVRTIELQAQHSMRDALESTLAETEARY SGOLAOMQCMITNNERQLAETRAALLERGNQEVQVULSDVARLECC EINTYRGLLESEDSKLPCNCAPDYSPSKSCLPCLPAASCGESA ARTNCSARPICVPCPGGRF 6RPRSSSDNRNFLRERAGLESSAAVQTRIGNSAASRRSPAARPPV PAPPALPRGRPGTEGSTSLSAAPAVLVVAVAVVVVVSAVAMAMA NYIHVPGSPEVPKLNVTVQDGEERCREGALSLLQHLRPHWDE QEVTLQLFTDGITNALIGCYVGRITMEDVVLVALYGNKTELLUDR	1	}	ļ	ILSSKASYSGAADVWSLGVADI IMDEDAFRITATGILLHPWLRO
5626 3123 2011 PPRAJGSVAMENQV.TPHYVNAQRHRELYLRVELSDVQNPAISI TENVLHFKAQGGGAKGDNVYEFHLEFIDLUKPEPVYKLTCRQVN ITVQKKVSQWBELTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERINKLRLESEGSFETTITINKRGVIFMYNLVQFLGFSWIFVN LTVRFCILGKESFYDTFHTVADMMYFCOMLAVVETIWALIGVTT SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE IRYSFYMLTCIDMDKVLTWLRYTLWIPLYPLGCLAEVSVIQ SIPIMETGFFSFTLEPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRRYGQKKKKIH PPRALGSVANENQVLTPHYVWAQRHRELYLRVELSDVQNPAISI TENVLHFKAQGGAKGNONYEFHLEFIDLUKPEPVYKLTORQVN ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERINKLRLESEGSFETLTITIKRYLFMYNLVQPLGFSWIFVN LTVTRFCILGKESFYDTFHTVADMMYFCOMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFIIFGTWEEMQNKAVVFFVFYLWSAIE IRFYSFYMLTCIDMDKVLTWLRYTLWIPLYPLGCLAEAVSVIQ SIPIFMETGFFSTTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRRYGGKKKIH 5628 75 1455 VAGAMASKCKKAGFSSGSLKSPGASGGSTRVSAWYSSSPCKLP SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG GGWFGGGILTGNRKETMQSLNDRILAGVILEKVRQLEQENASLESR IRBWCRQVPYMCPDYQYSFRTIELQKKTLCSKAENARLVVEI DNAKLAADDFRTKYETEVSLRQLVESDINGERRILDDLTLCKSD LEAQVESLKEELLCLKKNHEEEVSLRQLGGSLAVEUROQVVSSSE QLQSCQAEIIELRRTVWALEIELQAQHSMRDALESTLAETEARY SQLAQWGCMITNVEAQLAEITRADLERQNQEVQULLDWARALEC EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASGGPSA ARTNCSARPICVPCGGRF 6RPRSSSDNRNFLRERAGLESSAAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTEGSTSLSAPAVLIVAVAVVVVVSAVAWAMA NYIHVPGSPSPVPKLNVTVQDGEERCREGALSLLQHLRPHWDE QEVTLQLETDGITNTLGCYVGTTMEDVVLVAY YGKKTELLUDR	İ			RRGAYALPAGLSAPARCHVRCHLRREFARCHVIAG
TENULHFKAQGHGAKGDNVEFHLEFLDLVKEFPYKLTQROWN ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERLINKLRLESEGSPETLTINLRKGYLFMYNLVQFLGFSWIFVN LTVRFCILGKESFYDTFHTVADMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFI IFGTMEEMQMKAVVFFVFYLWSAIE IRYSFYMLTCIDMDWCULTWLRYTLWIPLYPLGCLAEAVSVIQ SIPLFMETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRRYSQKKKKIH PPRALGSVAMENQVLTFHVYWAQRHRELYLRVELSDVQNPAIST TENVLHFKAQGHGAKGDNVYSFHLEFIDLUKPEPVYKLITQRQVN ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERLMKLRLESEGSPETLTTALRKGYLFMYNLVQPLGFSWIFVN LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFIFFTMEEMQMKAVVFPYFYLWSAIE IFRYSFYMLTCIDMDWKVLTHLRYTLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRYGQKKKKIH 5628 75 1455 VAGSMASACLKAGFSGSLKSPGGASGGSTRVSAMYSSSPCKLP SLSPVARSFSACSVGLGRSYRATSCLPALCLPAGGFATSYSGG GGMFGGGILTCDEKTTMGSLNDRLAGYLEKVRQLEQENASLESR IRENCEQQVPYMCDPYQSYFRTIEELQKKTLCSKAENARLVVEI DNAKLAADDFRTKYETEVSLRQLVESDINGJRRILDDLTLCKSD LERQCESLKEBLLCLKKHHEEVNSLRCQLGDRLINVEVDAAPPV DLINKVLEBMRCQVFTLVENNRDAEDWLDTQSEELINQQVVSSE QLQSCQABIIELRRTVNALEIELQAGHSMRDALESTLAETEARY SSOLAQMCCMTTNVBAQLAEIRADLERQNGEYQVLLDVRARLEC EINTYRGLLESEDSKIPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCGGGF GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSASRRSPAARPPV PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVSAVAMAMA NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLLQHLRPHWDP OBVILQLFTDGITNKLIGCYVGNTMEDVULTRIYGNKRELLVDR DEBLIGGRADDJYCTFNINGLCYBEIQGGBADDKHVCN	1			DPMPLAPTRSHLWEAAQVVPDGLGBBBLACERDVONPATST
TTVQKKVSQMWBRLTKQEKRPLFLAPDFDWILDESDAEMLRAK EEERLNKLRLESEGSPETLTNLRKGYLFWINLVGTGFSWIFVN LTVRFCILGGESTYDTHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLIGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE IFRYSFYMLTCIDMDKVLTWLRYTLWIPLYPLGCLAEAVSVIQ STPIFMETGRFSFTLPYPVKKKVRSFFFLQIYLIMIFLGLYINF RHLYKQRRRYGQKKKKIH 5627 3123 2011 PPRALGSVAMENCVLTPHVYWAQRHRELYLRVELSDVQNPAIST TENVLHFKAQGHGAKGNVYEFHLEFLDLVKPEPVYKLTQRQVN ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERLNKLRLESEGSPETLTHLIKGYLFWNLVQFLGFSWIFVN LTVFFCILGKESFYDTFHTVADMMYFCOMLAVVETINAAIGVTT SPVLPSLIQLIGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE IFRYSFYMLTCIDMDWKVLTVLRYTLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRNYGQKKKKH VAGAMASKCLKAGFSSGSLKSFGGASGSTRVSAMYSSSPCKLP RHLYKQRRRNYGGKKKKH VAGAMASKCLKAGFSSGSLKSFGGASGSTRVSAMYSSSPCKLP SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGPATSYSGG GGWFGGGITTGNEKETMQSLNDRLAGYLEKVRQLEQRMASLESR IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD LEAQVESLKEELLCLKKHHEEEVNSLRCQLGBRINVEVDAAPFV DLNRVLEEMRQQYETLVENNRRDAEDWLDTQSEELNQQVSSSE QLQSCQABIIELRRTVNALEIELQACHSMRDALESTLAETEAVY SSQLAQMQCMITNVEAQLAEIRADLERQNQEYQVLDURARLEC EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCPGGRF SSDINNFLRERRAGLSSAAVQTRIGNSAASRRSPAARPPV BAPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVSAVAMMA NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLLQHLRPHWDP QEVTLQLETDGITNKLIGCTVETTMEDVULTRIYGNKTELLVDR DEBLING SPRINGLYFETTOGLEGDLINCTTVNINGLCYFETTOGLEADLFRUKDVA	5626	3123	2011	PPRALGSVAMENQVATPHVYWAQARAEBIBAVEBBDVQATAIDA
EERIMKLRLESEGSPETLTNIRKGYLFMYNLOFILGFSWITVT LTVRFCILGKESFYDTFHTVADMMYFCOMLAVVETINAAIGVTT SPULPSLIQLIGRHFILFIIFGTMEEMQNKAVVFFVFYLWSAIE IFRYSFYMLTCIDMDWKULTWLRYTLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRRYGGKKKKH PPRALGSVAMENQVLTPHYVMAQRHRELYLRVELSDVQNPAISI TENVLHFKAQCHGAKGDUVYEFHLEFLDLVKPEPVYKLTORQVN ITVQKKVSOWMERLTKQEKFPLFLAPDFDRWLDESDAEMELRAK EEERLNKLRLESEGSPETLTNIRKGYLFMYNLVOPLGFSWIFVN LTVRFCTLGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPULPSLIQLLIGNFILFIIFGTWEEMQNKAVVFFVFYLWSAIE IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRYSGYKKKKIH VAGAMASKCLKRGFSSGSLKSPGGASGGSTRVSAMYSSSPCKLP SLSPVARSFSACSVGLGRSSYRATSCLEALCLPAGGFATSYSGG GGWFGEGILTGNEKETMQSLNDRLAGYLEKVRQLEQENASLESR IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI DNAKLAADDFRTKYFTEVSLRQLVESDINGLRRILDDLTLCKSD LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV DLNRVLEEMRCQVSTLVENNRRDAEDWLDTQSEELNQQVVSSSE QLQSCQAEIIELRRTUNALBIELOAQHSWRDALESTLAETERAY SSQLAQWCCMITNVEAQLAEIRADLERQNQEYQVLLDWARLEC EINTYRGLLESSBSKLPCNPCAPPYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCPGGRF 5629 2287 938 GRPRSSSDNRNFLERRAGLSSAAVQTRIGNSAASRRSPAARPPV BAPPALBRGRPGFGGSTSLSAPAVLVVAVAVVVVVSAVAWAMA NYIHVPPGSPEVKLNUTVQDQEEHRCREGALSLLOHLRPHWDB OBVILGLFTDGIINKLIGCVYGNTMEDVVLVRIIGKNTELLWDB		Į	1	TENVLHFKAQGRGAKGDNV18FHDEFDDDVKFEFV1RD1QKQV
LTVRFCILGRESFYDTFHTVADMMYFCQMLAVVETTMARIGVTT SPVLPSLIQLIGRNFILFI1FGTMEEMQNKAVVFFVYLWSAIE IRRYSFYMLTCIDMDWKVLTWLRYTLWIPLTPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRRYGQKKKKLH PPRALGSVAMERQVLTPHYVWAQRHRELYLRVELSDVQNPAISI TENVLHHKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQQVM ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERLNKLRLESEGSPETLTINLRKGYLFMYNLVQPLGFSWIFVN LTVRFCTLIGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLIGRNFILFIIFGTWEEMQNKAVVFFVYLWSAIE IFRYSFYMLTCTDMDWKVLTWLRYTLWIPPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRRYGQKKKKIH VAGAMASKCLKAGFSSGSLKSPGGASGGSTRVSAMYSSSPCKLP SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG GGMFGGGILTGMEKETMQSLNDRLAGYLEKVRQLEQENASLESR IREWCEQQVPYMCPDYQSYBRTIELQLKKTLCSKAEMARLVVEI DNAKLAADDFTKYETEVSLRQLVESDINGLRRILDDLTLCKSD LEAQVESLKEELLCLKKNHEBEVNSLRCQLGDRLNVEVDAAPPV DLNRVLEEMRCQYETLVENNRRDAEDWLDTQSEELNQQVVSSSE QLOSCOABIIELRRTVNALEIELQAQHSMRDALESTLAETEARY SSQLAQMQCMITNVEAQLAEIRADLERQNQEYQVILDVRARLEC EINTYRGLLESEDSKLPCNCCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCPGGRF GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPPV BAPPALPRGRPGGFTGSTSLSAPAVLVVAVAVVVVVSAVAWAMA NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLLOHLRPHWDF QEVTLQLFTDGITNKLIGCVGNTMEDVVLVRIYGNKTELLVDB	1			ITVQKKVSQWWBRLTKQEKRPLFLAPDFDKWLDESDALFLESWTFVN
SPVLPSLIQLIGRNFILFI IFGTMEEMQNKAVVFFVYMSAIE IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ SIPIFNETGRESFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRYGQKKKKIH S627 3123 2011 PPRALGSVAMERQVLTPHVVWAQRHRELYLRVELSDVQNPAISI TENVLHPKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTORQVN ITVQKKVSQWMERQVLTPHVVWAQRHFELYLRVELSDVQNPAISI TENVLHPKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTORQVN LTVGKVSQWMERPLTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERLNKLRLESEGSPETLTNLRKGYLFMYMLVQFLGFSNIFVN LTVRFCILGKESFYDTFHTVADMMYCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVYLMSAIE IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRRYGCKKKKIH RHLYKQRRRRYGCKKKKIH SLEPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG GGWFGEGILTGNEKETMQSLMDRLAGTLEKVRQLEQENASLESR IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV DLNRVLEEMRCQVETLVENNRRDAEDWLDTGSEELNQQVVSSE QLQSCQABIIELRRTVNALEIELQAQHSMRDALESTLAETEARY SSOLAQMQCMITNVEAQLAEIRADLERQNQEYQVLLDVRARLEC EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCPGGRF SSOLAQMCCMITNVEAQLAEIRADLERQNQEYQVLLDVRARLEC EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCPGGRF GPRSSSDNRNFLRERGGLSSAAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTEGSTSLSABAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTEGSTSLSABAVUTVAVAVVVVVVSAVAWAMA NYIHVPPGSPEVPKLNVTVQDOEHRCREGALSLLQHLRPHWDB OEVTIQLFTDGITNKLIGCYVGNTMEDVVLVRIYGNKTELLVDR	1	l	1	EEERLNKLRLESEGSPETETNERRGIEFMINDVQFEGFOWIT VI
IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ SIPIFETGRESFTLPYPVKIKVRFSPFLQIYLIMIFLGLYINF RHLYKQRRRYGQKKKKIH PRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI TENVLHPKAQGHGAKGDNYVEFHLEFIDLVKREEPYYKLTQRQVN ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMLRAK EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQPLGFSWIFVN LTVRFCILGKESFYDTFHTVADMMYFCOMLAVVETINAAISUTT SPVLPSLIQLLGRNFILFIFGTMEEMQNKAVVFFVFYLWSAIE IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ SIPIFNETGRESFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRYGQKKKKIH 75 VAGAMASKCLKAGFSSGSLKSPGGASGGSTRVSAMYSSSPCKLP SLSPVARSFSACSVGLGRSSVRATSCLPALCLPAGGFATSYSGG GGWFGEGILTGNEKETMQSLNDRLAGYLEKVRQLEGENASLESR IRENCEQQVPYMCPDYQSYFRTIELCKKTLCSKAENARLVVEI DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD DLNRVLEEMRCQYETLVENNRRDAEDWLDTQSEELNQQVVSSSE QLQSCQABIIELRRTVNALEIELQAQHSMRDALESTLAETEARY SSQLAQMQCMITNVEAQLAEIRADLERQNQEYQVLLDVRARLEC EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCPGGRF GPRESSDNRNFLRERGGISSAAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTGSTSLSABAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTGSTSLSABAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTGSTSLSABAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTGSTSLSABAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTGSTSLSABAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTGSTSLSABAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTGSTSLSABAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTGSTSLSABAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTGSTSLSABAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTGSTSLSABAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTGSTSLSABAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTGSTSLSABAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTGSTSTLSABAVLVVAVAVVVVVVSAVAWAMA NYIHVPPGSPEVPKLNVTVQDOEHRCREGALSLLQHLRPHWDP OEVTLQLFTDGITNKLIGGYVGNTMEDVVLVRIYGNKTELLVDR	1		ì	LTVRFCILGRESFYDTFHTVADMMIFCQMMAVBFUFVLWGATE
SIPIFNETGRESTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRYGQKKKKIH PPRALGSVAMERQVLTPHVYMAQRHRELYLRVELSDVQNPAISI TENVLHFKAQGHGAKGDNYEFHLEFLDLVKPEPVYKLTQRQVN ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERLINKLRLESEGSPETLTINLRKGYLFMYNLVQFLGFSWIFVN LTVRFCILGKESFYDTFHTVADDMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRRYGCKKKKH 5628 75 1455 VAGAMASKCLKAGFSSGSLKSPGGASGGSTRVSAMYSSSPCKLP SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG GGMFGEGILTGNEETMQSLNDRLAGYLEKVRQLEQENASLESR IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD LEAQVESLKEELLCLKKNHEEEVMSLRCQLGBRLINVEVDAAPFV DLINRVLEEMRCQYETLVENNRRDAEDWLDTQSEELNQQVVSSSE QLQSCQAEIIELRRTVNALEIELQAGAHMRDALESTLAETEARY SSQLAQMQCMITNVEAQLAEIRADLERQNQEYQVILDVRARLEC EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCGGGRF GRPRSSSDNRNFLRERAGLSSAAVOTRIGNSAASRRSPAARPFV PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVVSAVAMAMA NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLLCHLRPHWDP PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVVSAVAMAMA NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLLCHLRPHWDP GEVTLQLFTDGITNKLIGCTVGNTMEDVVLVRIYGNKTELLVDR	ĺ	1	1	SPVLPSLIQLIGRNFILF11FGTMEEMQNKHVVFFVF1BASA1S
RHLYKQRRRYGQKKKIH 5627 3123 2011 PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI TENVLHYKAQGHQAKGDNYYEFHLEFILDLVKPEPVYKLTQRQVN ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERLNKLRLESEGSPETLINLRKGYLFMYNLVQFLGFSWIFVN LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLIGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRYGQKKKKIH VAGAMASKCLKAGFSSGSLKSPGGASGGSTRVSAMYSSSPCKLP SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG GGWFGGGILTGNEKETMQSLNDRLAGYLEKVRQLEQENASLESR IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI DNAKLAADDFRTKYBTEVSLRQLVESDINGLRRILDDLTLCKSD DLNRYLEEMRCQYBTLVENNRRDAEDWLDTQSEELNQVVSSSE QLQSCQABIIELRRTVNALEIELQAQHSMRDALESTLAETEARY SOLAQWQCMITNVEAQLAEIRADLERQNQEYQVLLDVRARLEC EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICYPCPGGRF GRPRSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPCTEGSTSLSAPAVLVVAVAVVVVVVSAVAWAMA NYIHVPPGSPEVPKLNVTVQDGEHRCREGALSLLQHLRPHDDF DEFENSERVLOB HIGHERDVLVTRINGLCYEFIQGEALDPKHVCN			ł	IFRYSFYMLTCIDMDWKVLTWLKYTLWIPLIPLICHAEAVSV12
5627 3123 2011 PPRALGSVAMENQVLTPHVYMAQRHRELYLRVELSDVQNPAISI TENVLHFKAQGHQAKGDNYYEFHLEFLDLVKPEPVYKLTQRQVN ITVQKKVSQWMERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQPLGFSWIFVN LTVRFCILGKESFYDTFHTVADMMYFCOMLAVVETINAALGVTT SPVLPSLIQLLGRRFILFIIFGTMEEMQNKAVVFFVFYLWSAIE IFRYSFYMLTCIDMDWKVLTWLRYYTLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVXIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRYGQKKKKH 5628 75 1455 VAGAMASKCLKAGFSSGSLKSPGASGGSTRVSAMYSSSPCKLP SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG GGWFGEGILTGNEKETMQSLMDRLAGYLEKVRQLEQENASLESR IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV DLNRVLEEMCQYETLVENNRRDAEDWLDTQSEELNQVVYSSSE QLQSCQABIIELRRTVNALEIELQAQHSMRDALESTLAETEARY SSQLAQMQCMITNVEAQLAEIRADLERQNQEYQVLLDVRARLEC EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCPGGRF GRPRSSDNRWFLRERRGLSSAAVQTRIGNSAASRRSPAARPPV PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVSAVAWAMA NYIHVPPGSPEVPKLNNTVQDOEBHRCREGALSLLQHLRPHNDD DEFENS SPULDB HCCAPOLYCTTRNGLCYEFIQGEALDPKHVCN	1	ì	1	
TENVLHFKAQGHGAKGDNYEFFILEFLDLVKPEPVYKLTQRQVN ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERLNKLRLESEGSPETLTNLKGYLFMYNLVQFLGFSWIFVN LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ SIPIFNETGRESFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRYGQKKKKIH 75 1455 VAGAMASKCLKAGFSSGSLKSPGGASGGSTRVSAMYSSSPCKLP SLSFVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG GGWFGEGILTGNEKETMQSLNDRLAGYLEKVRQLEQENASLESR IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVEI DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV DLNRVLEEMCQYETLVENNRRDAEDWLDTQSEELNQQVVSSSE QLQSCQABIIELRRTVNALEIELQAQHSMRDALESTLAETEARY SSQLAQMQCMITNVEAQLAEIRADLERQNQEYQVLLDVRARLEC EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCPGGRF GPRSSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPFV PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVVSAVANAMA NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALLQHLRPHWDF QEVTLQLFTDGITNKLIGCYVGNTMEDVVLVRIYGNKTELLVDR DEFLYGERBYLOAFGCAPOLYCTFNNGLCYEFIQGEALDPKHVCN	ì		·	RHLYKQRRRYGQKKKKIH
TENVLHFKAGCHGAKGDNVYEFHLEHDVAFEVARATKAK ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK EEERLIKLRIESEGSPETLTINIRKGYLFMYNLVQPLGFSWIFVN LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLIGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE IFRYSFYMLTCIDMDWKVLITWLRYTLWIPLYPLGCLAEAVSVIQ SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRYGQKKKKIH VAGAMASKCLKAGFSSGSLKSPGGASGGSTRVSAMYSSSPCKLP VAGAMASKCLKAGFSSGSLKSPGGASGGSTRVSAMYSSSPCKLP SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG GGWFGEGILTGNEKETMQSLINDRLAGYLEVRQLEQENASLESR IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV DLNRVLEEMRCQYETLVENNRRDAEDWLDTQSEELNQQVVSSSE QLQSCQABIIELRRTVNALEIELQAQHSMRDALESTLAETEARY SSQLAQMQCMITNVEAQLAEIRADLERQNQEYQVLLDVRARLECC EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCPGGRF GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPPV PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVVSAVANAMA NYIHVPPGSPEVPKINVTVQDQEEHRCREGALSLQHLRPHWDF QEVTLQLFTDGITNKLIGCYVGNTMEDVVLVRIYGNKTELLVDR DEFLYKESTENJOAFGCAPOLYCTFNNGLCYEFIQGEALDPKHVCN	5627	3123	2011	PPRALGSVAMENOVLTPHVYWAQRHRELYLKVELSDVQNPA131
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1			ADEDINKRFLSDIPSSQILQEEMTWMKEILSNLGSPVVLCHNDL
1	1		LCKNIIYNEKQGDVQFIDYEYSGYNYLAYDIGNHFNEFAGVSDV
ĺ	· ·	1	DYSLYPDRELQSQWLRAYLEAYKEFKGFGTEVTEKEVEILFIQV
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			NQFALASHFFWGLWALIQAKYSTIEFDFLGYAIVRFNQYFKMKP EVTALKVPE
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ľ	1		TEVLKNMGYAAKAMKAAHDMMDIDKVDELMQDIADQQELAEEIS
Į	1		TAISKPVGFGEEFDEDELMAELEELEQEELDKNLLEISGPETVP
5632			LPNVPSIALPSKPAKKKEEEDDDMKELENWAGSM
3632	3	952	VVLGWSPPRPI.WWGSI.CAAODDAWWAGSM
1			VVLGWSPPRRLWWGSLGAAQRPAVPVSGLARSLHVETRRPHRRA
1	ı		SVRVARGRLGVWAQPQPLLPRPVGSRREMQPPGPPPAYAPTNGD
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5635			ALAVGGLGSIIRVLTARKTV
3033	3	943	DRGPRSTATDTGRARVSFWRFPLDPGVKNSNVQISGEKRRFRTL
i	į	i	RSLFHPFPVTPSGADBAUT VTGGUDDEVKNSNVQISGEKRRFRTL
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ļ			- COMEDCES ALISCS VIGANS TIGGT A VICA CCC PURATUR DAGGET
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1	1	- 10	QEALEACQTRISKMELQQQQQQVVQLEGLENATARNLLGKLINI
	I		LLAVMAVILLYBYCTYANGWIDLAWWWW.
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I	İ		SCREET AND CERKHONVI.SALDIIODDUIDVEED TIER TO THE TOTAL TOTA
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1		i +	MEGNADONONCVLKICDEGI.ARVERI.DEGDUMPORIERMOSES
- 1	}	g i	EILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQQLDL
			TDLLGTPSLEAMRTACEGAKAHILRGPHKQPSLPVLYTLSSQA

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
j	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
1	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	P=Proline, Q=Glucamine, K=Alginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		_nossible nucleotide insertion)
	sequence		THEAVELL CRMINEDPYKRISAKDALAHPYLDEGRLRYHTCMCK
		1	CCFSTSTGRVYTSDFEPVTNPKFDDTFEKNLSSVRQVKEIIHQF
		1	ILEQQKGNRVPLCINPQSAAFKSFISSTVAQPSEMPPSPLVWE
		<u> </u>	DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG
5638	125	1155	RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY
	i .	1	RIQMRTRRTLRGHLAKI YAMHWGIDSKUMSASQUGGUTTMOOT
	1	1	TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR
	ì	1	EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET
	1.	i i	GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM
	,	ĭ	CROTETCHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL
	1		MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA
	1	į.	LOWINGUDNEVSCI.GVTDDGMAVATGSWDSFLKIWN
	[DRKMSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVG
5639	125.	1155	RIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSY
	1	1	RIQMRTRRTLRGHLAKIYAMHWGIDSKDAVASQDGKDIITHDOI TTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTR
	}	1	TTNKVHAIPLRSSWVMTCAYAPSGNIVACGGDDNTCSIINDKIK
	}	1	EGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIET
		1	GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGM
	ł		CROTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQEL
	1	1	MTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRA
	ì	1	CULTACUDNEUSCI CUTDDGMAVATGSWDSFLKIWN
	1	1092	OCCULKTMI.SHNTMMKORKOOATAIMKEVHGNDVDGMDLGKKVS
5640	280	1092	IPRDIMLEELSHLSNRGARLFKMRQRRSDKYTFENFQYQSRAQI
		1	NHSIAMQNGKVDGSNLEGGSQQAPLTPPNTPDPRSPPNPDNIAL
	Į.		NHSIAMQNGKVDGSNLEGGSQQAFBIFFR TERRESERVER GYSGPLKEIPPEKFNTTAVPKYYQSPWEQAISNDPELLBALYPK
	1	1	GYSGPLKEIPPEKFNTTAVPKYIQSPWEQAISKDFEBBBBBBILL
	į		LFKPEGKAELPDYRSFNRVATPFGGFEKASRMVKFKVPDFELLI
	į	1	LTDPRFMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDTT
	1	1	VPESEDL
5641	27	332	CRHNCNGDVKLLSNQMDKLFAFHLFTFHGLLHFLDGSIQKLIQ
2041	1 - 2'		EIILSDNSSILVLENNFLFKVKSKQFIHLIAKKFYISITIVSAS
	1	1	NGPSEVI.SMTVTG
		1247	TTDCPMDELVLFLEYLASVLMGLVLICVCSKTHSLKGLARGGA
5642	199	1247	IFSCI TPECLQRAMHGLLHYLFHTRNHTFIVLHLVLQGMVYTE
	Į.	1	TWEVFGYCQELELSLHYLLLPYLLLGVNLFFFTLTCGTNPGII
		l l	KANBLLFLHVYEFDEVMFPKNVRCSTCDLRKPARSKHCSVCNW
	1	ı	VHRFDHHCVWVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTT
	ł	i	VHRFDHHCVWVNNCIGAWNIKIFLIIVEIHASARIVALVSII
	İ	(LVHLVVMSDLYQETYIDDLGHLHVMDTVFLIQYLFLTFPRIVF
	İ	1	LGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQRCP
	ì		VAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQE
		847	PSGGVPDVETRGPGSRAARGPRVVMERRGVGAGAIAKKKLAEA
5643	1	01,	VVERGTVI.AEDOLAOMSKOLDMFKTNLEEFASKHKQEIRKNPE
		1	DITORODMONTICUDDI NSCKCEWSEMI GVGDFYYELGVQI LEV
	1		LALKHRNGGLITLEELHQQVLKGRGKFAQDVSQDDLIRAIKKL
			ALGTGFGIIPVGGTYLIQSVPAELNMDHTVVLQLAEKNGYVTV
			EIKASLKWETERARQVLEHLLKEGLAWLDLQAPGEAHYWLPAL
	1		ETKASTKWETEKARQVEEHDDKEGDAWDDDQAFGBAITWDFAD
			TOLYSQEITAEEAREALP
5644	B3	1138	PRRMGSWVQLITSVGVQQNHPGWTVAGQFQEKKRFTEEVIEYF
~J = I	1		KKVSPVHLKILLTSDEAWKRFVRVAELPREEADALYEALKNLT
			VVATEDEDMOOKEOOFREWFLKEFPCIRWKIQESIERLRVIAN
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	1		CICIACATACIASSIVENTYTRSAELTASRLTATSIDQLEALS
	1		TLUDTTPNVLSFALDFDEATKMIANDVHTLRRSKATVGRPLIA
	l		RYVPINVVETLRTRGAPTRIVRKVARNLGKATSGVLVVLDVVN
			VQDSLDLHKGEKSESAELLRQWAQELEENLNELTHIHQSLKAG
1	}		VQSVRDLKRLSPTDPPGDSGNRDVTREDPVTGPLNSASSQVP1
5645	537	799	VQSVRDLKRLSPTDPPGDSGMKDVIREDFVIGEDRADGGT DDI AVET
	l		YLCLQNSLLGHSSVEDARATMELYQISQRIRARRGLPRLAVSI
5646	3745	3328	AEQYGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTTAL
3040	1		AGYDADCRYTITI.RASIPATKRASFLSSFIKMFFEELEYILG
			LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTH
			PARCGAO
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		900	CVIMATSELSCEVSEENCERREAFWARWADDIDSIRFESCOI
5647	288	800	GYIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCS EEJTQRHETYHQQGQCQVLVQRSPWLMMRMGILGRGLQEYQL

SEO	Predicted		
ID	beginning	Predicted end	Amino acid segment containing signal peptid
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
		location	Glutamic Acid E-Dhamas B-Aspartic Acid, E-
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	
1	to first	amino acid	1 Leucine, Memernionine W-X
	amino acid	residue of	
	residue of	amino acid	Sectine, TeThreonine V-Valine
1	amino acid		/ "=11yptopnan, Y=Tyroeine v v-1
	sequence	sequence	
ļ——	Dequence		
1 1			QRVLPLPIFTPAKMGATKEEREDTPIQLQELLALETALGGQCVI
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1 1			VISSICGREEALREVGAEWPDDTCCDKTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT
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	020	1869	ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL
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ı	}	j e	WRAGISPELLGAAGLSDNWARCPGPGPAE*GGQPGCRTIPASA
i	Ì	ĺc	MPSPPVEGSLGLSPKGUCDLDGGGPGCRTIPASA
		_	MPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL GPRGRTGRPSSPS
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5652		1 44	HKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI
652	1	i c	TI CHROLKIOONDVIHRRIHTGEKDIACETCCETCDOXX
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			QRKHAETVAALREPCEECGKREPKBBGKAAN
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	66	1401 R	GRLQSRGRLTLGLVLLLLDILGAPOHGOPUSHCHUSGRISS
5652	66	1401 R	GRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL FPQPCQPGTRRGRRRSLKEATEDOLAMAFERUM VOLUME
	66	1401 R	GRLQSRGRITLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL FFQPCQPGTRRGRRRSLKEATEPQLAMAEEFVTLKDVGMDFTL DWEQLGLEQGDTFWDTALDNCODLFLLDRDRDRM TSUBGRDS
	66	1401 R	GRLQSRGRLTLGLVLLLLDILGAPONGOPUSHCHUSGRIST

		1 - 1	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning nucleotide	nucleotide location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
:	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
	- Doques	 	ES*IKERTQSCVHRFHGRRFHG\DNVSEKTLTPAKSKEYRGEFF
		1	SYSDHSQQDSVQEGEKPYQCSECGKSFSGSYRLTQHWITHTREK
	ļ		PTVHQECEQGFDRKASHSGYPKTHTGYKFYVCNEYGTPFSQSTY
		1	LWHQKTHAGEKPCKSQDSDHPPSHDTQSGEHQKTHTDSKSYNCN
	ļ		ECGKAFTRIFHLTRHQKIHTRKRYECSKCQATFNLRKHLIQHQK
			THAANV
5554	3	598	TLPLFPGRRFRGWRRCGAVAARKNSTGGNVSINQRRDSVRMSAL
	į		NWKPFVYGGLASITAECGTFPIDLTKTRFQIQGQTNDAKFKEII
	}		YRGMLHALVRIGREEGLKALYSG*VGLHAFLCHCSLFHMGIDFR
			PRLHRSQVKSLRCV*KEQIA**/MFSLLISTLISKYIYYAADVL
	ł		EKLFYYIQVQTDNNKKICLFKNI
5655	2	867	RPPGTRAPRQLHPAAGRRPDASARPRFRPTVLLHDPFQLSFPPP
	1		PLSYPSVFPAVARVLPQRSGDYRAAGMPQLSGGGGGGGGDPELC ATDEMIPFKDEGDPQ\REKIFAEIVNPEEEGDLADIKSSLVNES
	}		ATDEMIPFKDEGDPQ\REKIFAEIVNPEEEGDLADIKSSLUNES EIIPASNGHEVARQAQTSQEPYHDKAREHPDDGKHPDGGLYNKG
		1	PSYSSYSGYIMMPNMNNDPYMSNGSLSPPIPRTSNKVPVVQPSH
		1 -	AVHPLTPLITYSDEHFSPGSHPSHIPSDVNSKQGMSRHPPAPDI
			PTFYPLSPGGGGQITPPLGWQGQP
		1066	PRRVPPLPEFASGPGAAFFHSGRLQRSLTKDSAGCFSQCRSRAM
5656	228	1000	LVLRSGLTKALASRTLAPQVCSSFATGPRQYDGTFYEFRTYYLK
		1	PSNMNAFMENLKKNIHLRTSYSELVGFWSVEFGGRTNKVFHIWK
			YDNFPHRAEVRKALANCKEWQEQSIIPNLARIDKQETEITYLIP
			WSKLQKPPKEGVYELAVFQMKPGGPALWGDAFERAINAHVNLGY
			TKVVGVFHTEYGELNRVHVLWWNESADSRAAVRHKSHEDPISWG
			GVRESVNYL\VSQQNM
5657	105	1052	GORLOSPRVOMPVOPPSKDTEEMEAEGDSAABMNGEEEESEEER
3637	103		SGSOTESEEESSEMDDEDYERRRSECVSEMLDLEKQFSELKEKL
}		Į	PRERLSOLRLRLEEVGAERAPEYTEPLGGLQRSLKIRIQVAGIY
	\		KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQERIQR
	1	ŧ	LEEDROSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG
	1	}	PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ
1	1	1	GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL
]			ALVWTPPL
5658	2346	3541	TERRVYNPWPEPDPD\CIQEDPWNLPNSIKTLVDNIQRYVEDGK
			NOLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY
		}	RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE
		1	RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA
			LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS
		1	PGSQAAEDLOQDINAQSLEKVQQYYRKLRAFYLERSNLPTDAST TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS
			TAVKIDQLIRPINA_DELCKEMESFVEFKFOAAGSVGAGDIT-25 SELCYRLGACQMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC
1			IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN
			GDL
			WKRSGEVSPKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP
5659	2	696	GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\
!			EREGEGORGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA
1	1		AAGGREMVOKESOATLEERESELSSNPAASAGASLEPPAAPAPG
			EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL
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5000	229	853	DVTMWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL
5660	229	833	· COODLNKTSROOIPESOGVISGAVFLIILFCFIPFPFLNCFVKE
1	1	,	OPKAEPHHEEVALIGALLAICCMIFLGFADDVLNLRWRHKLLLP
1			TAASLPLLMVYFTNFGNTTIVVPKPFRPILGLHLDLGR*SYHCC
	1	[PYGTYFREPFLYLHILLOVFLFCLCVFPDPFW
5661	2	473	LNI.VPSPCGGTPKLPGLPREAAAALGASFLAEAPLPVTVRGSGL
2001	1	1 7.7	DCMDUTCDPKAFLSICFVTLVFLQLPLASICQN*GTDSCASRGK
		1	ADFDVTGPHAPILAMAGGHVELQCQLFPNISAEDMELRWYRCQP
1	1		SLAVHMHERGMDMDGEOKWQYRGRT
1	· ·		
5662	 	1318	LRKEGRCRRGSNRGVWAAPAEGLGGRGMLGVRCLLRSVRFCSSA PFPKHKPSAKLSVRDALGAQNASGERIKIQGWIRSVRSQKEVLF

SEQ	Predicted	I Brook - to the	
ID	beginning	Predicted end	
NO:	nucleotide	location	I WITH GUILLE, CELVSTEINE DENGERALIE NEIN
	location	corresponding	
1	corresponding	to first	n-nistidine, i=1solencine V-lucine
ŀ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ł	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
i			LHVNDGSSLESLQVVADSGLDSRELTFGSSVEVQGQLIKSPSKR
- 1		1	QNVEDAMERIKVIGNCDAKDFPIKVKEDUDI.EVI.DOVDIJEDODO
1		1	NVLGSILKIKSKATAAIHSFPKDSCEVUTUUDTTUGATDGDGDGDG
ŀ	1		LEQUEPSGKLKVPEENFFNVPAFI,TVCCOLULEUMCCA PROLUDE
1	ł	1	I POFIC RADINGUS REMLAE FYMTRAET CRUDCLODT MOTERNIE DE
	1		ATTIMIVES ACCEDIVE LICHKET ADGOVED DILLE AND VANIET TACKED
			AVOIDAQASQNFTFTPEWGADI.RTEHFKVT.WUCGMIDMERTAN
5663	119	698	FULUATE IMADINEDGPOELEGSVA*HSLGIMTLLGTIMITCOD
		038	PADIGRSTARTPGPPRSLEMDDPRYCMCDLYGASCCDGARDOXY
1	<u> </u>		VQSIFEKGPLTFRDVAIEFSLEEWOCI.DSIOOGI VDVIMI DAND
İ	1	1	NOVE DO LALTRIPOLITCI.EOGKEDWNTVDUEMIN VDDILL OCCUPA
			QDLWAEQDIKDSFQEAILKKYGKYGHANFQLQKGCKSVDECKVH KEHDNKLNQCLIPKKKK
5664	118	572	SI-SMESHUVECDCI COMOVED
	ł		SLSMESNHKSGDGLSGTQKEAALRALVQRTGYSLVQENGQRKYG
	•		GPPPGWDAAPPERGCEIFIGKLPRDLFEDELIPLCEKIGKIYEM RMMMDFNGNNRGYAFVTPSNKVEAKNAIKQLNNYEIRNGRLLGV
			CASVDNCRLFVGGIPKTKK
5665	347	702	VVQHLIILLHCERTSPAMITSELPVLQDSTNETTAHSDAGSELE
			DIEVEGRERGEPERTNERPERS DEFENDE TEXALD AS A DOD
5666			ANGHPQQNGEGEPVTLFEVVKLGKSAMORC
3666	213	540	VSCLPTSCKMITLINNODOPVPFNSSHDDEVKIAALVEVCOLDIX
1			GDF VNITALWVFSCTTKKRTTVTIVMMWALVDI TETMTI DEDM
5667	1		FIIAKDEWPFGEYFCOILGA
	•	695	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRARVGSP
1 1			SGDAASSTPPSTRFPGVAIYLVEPRMGRSPPAFI.TGLABEVGDD
			VLUACSSEATHVVMEETSAEEAVSWOERDMAAADDCCTDDALLD
1 1			ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR
			PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL PSPVTTLSQLQ
5668	691	894	CSPLFCIPDLFLQFLLGRKEEEAVLVGGEWSPSLDGLDPQADPQ
			VLVRTAIRCAQAQTGIDLSGCTKW
5669	407	1	DSGAPEGLSPLMSTQEGLSMHAHPQAYTPFIYLHARKRRGEIGD
1 1	i		ADSRFNDRYAHKSAQLYFLYFVCWIFQDVYYFTIKEKNHFFFPK
1 1	1		ARGAPTKYSGSPIGSPTTTPPTRPPSFNLHPAPHLLASMQLQKL
5670		· · · · · · · · · · · · · · · · · · ·	NSQ
30,0	3	373	SSECLTMAWIPLLLPLLILCTVSVASYELAQPSSVSVSPGQTAK
1 1	Í		I TICGGDVUAKKYAKWEOOKPGOADMAATTVURDDGGTDRDGG
5671	280		SISGITVILIISGAOVEDRADVECVGATOMETIME
	200	524	KFPPKKTPPHLGMESAITLWOFLLOLLLDOKHEHLTCWTCNDGB
5672	2	FFS	FAUDARANAKUMGURKNKTNMNVIIKT.CDAT.DT.T. Dawn
	- 1	557	FVPATPDPGVWLPPSRDPAMAKRSSLVIPIVECKNI DAVOTEGO
1 1	ļ		SDEICIAKADNEPIIKTATAMKTLCPFNCFFACOUT DDDDDDDDD
1			FIVMUEDALSKUDVIGKVCLTRDTIASHPKGKESI DCUTCT DCD
		İ	WPPSHSETSPLGSVWSPAQGKPFLLSPEAGATFCTPGLCSAACS QAWLLLPLP
5673	327	696	
			ITVADQISHWSAGRIKNRTRIPECIHSSAATTLAGPHTMEGESV KLSSOTLIOAGDDEKNORTYTTIPECIHSSAATTLAGPHTMEGESV
	_		KLSSQTLIQAGDDEKNQRTITVNPAHMGKAFKVMNELRSKQLLC
5674	17	984	DVMIVAEDVEIEAHRVVLAACSPYFCAMFTGDMS GGGSMEGFSTSAVISGEVICALAEGU
	İ	i	GGGSMEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGEVKGE AKNSITDSQMDDVEVVYTIDIQKYIFCYQLFSFYNSSGEVNEQA
i i	j	į	LKKII SNVKKNUJGUVVEDDUGDOTAMIDDES TANSGEVNEQA
	į	•	LKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQ DLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLG
	}		MSEQLGYKTVSGSCMSTGFSRAVQTHSSKFFEEDGSLKEVHKIN
	}		EMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
			QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKID
5675			MFLKVAVTTTTISM
5675	80		EGSRRGPTRLARLSARAGRLHFPPGFSSRLIHFRGVSECRRPPG
ł	ł		KSGVPVSAPGSDGKWWEERPGMFSLMASCCGWEKDWDDDDDGGGG
ſ	1	í	LLMVGLDNAGKTATAKGIOGEYPEDVAPTVGFSKINI.POGVERV
			TIFDLGGGIRIRGIWKNYYAESYGVIFVVDSSDEERMEETKEAM

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A-Alanine C=Cvsteine, D=Aspartic ACld, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
1	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	P=Proline, Q=Giutamine, R=Alginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		Bequeine	_noggible pucleotide insertion)
	sequence		SEMLRHPRISGKPILVLANKQDKEGALGEADVIECLSLEKLVNE
		1	HACI
		<u> </u>	FVSSPPPRPVQPARPGGFGLSGRRSLLCQVASTPAHVGVMRSPV
5676	2	930	RDLARNDGEESTDRTPLLPGAPRAEAAPVCCSARYNLAILAFFG
	1		FFIVYALRVNLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVH
	1	ł	FFIVYALRVNLSVALVDMVDSNTIDEDNRISKACPENSKI ZKVI
		ì	HNQTGKKYQWDAETQGWILGSFFYGYIITQIPGGYVASKIGGKM
]	1	LLGFGILGTAVLTLFTPIAADLGVGPLIVLRALEGLGEGVTFPA
	ł		MHAMWSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYMN
	1	1	WTYVFYFFGTIGIPWFLLWIWLVSDTPQKHKRISHYEKEYILSS
	1	1	1
	i		PPRDGFLELRRLSVPLCSGPCPLTSLSRQGERSGGHLVAAARAA
5677	1	1028	VTAETHPLPLLAPLAVCQSVKSPAACQVRPRPRAVALPAALGGP
	1	1	GRSLPGLTAATMSSFSESALEKKLSELSNSQQSVQTLSLWLIHH
	1	1	GRSLPGLTAATMSSFSESALEKKLSEDSNSQQSVQTDSLWEITH RKHAGPIVSVWHRELRKAKSNRKLTFLYLANDVIQNSKRKGPEF
			RKHAGPIVSVWHRELKKAKSNKKLTTLILANDVIQUSKKAGPET
			TREFESVLVDAFSHVAREADEGCKKPLERLLNIWQERSVYGGEF
			IQQLKLSMEDSKSFPPKATEEKKSLKRTFQQIQEEEDDDYPGSY.
			SPQDPSAGPLLTEELIKALQDLENAASGDATVRQKIASLPQEVQ
	1	,	DVSLLEKITDKEAAERLSKTVDEACLRNRGPGTS
	<u> </u>	593	COORDESTRATION OF THE CONTROL OF THE
5678	3	333	CCCPTA A PRITINGA A CSI MIMNKMKNFKRRFSLSVPRTETIEE
	}	ł	CLAFFTEOFMOLUNDENFNLOLGPLGRDPPOECSTFSPTDSGEE
	1	1	PGQLSPGVQFQRRQNQRRFSMEVRASGALPRQVAGCTHKGVHRR
	1	1	AAALQPDFDVSKRLSLPMDI
	l l	l	LNSRVDDFVAVPGAIMDEDYYGSAAEWGDEADGGQQEDDSGEGE
5679	2	623	INSRVDDFVAV-GAIMDEDIIGSAABMODELLEOQQ DDAEVQQECLHKFSTRDYIMEPSIFNTLKRYFQAGGSPENVIQL
	1	1	DDYEAOOECPHKE21KDA IMEE 21 MID WALL OVOR A TANK
	1 .	1	LSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLKSLLIKH
	1	1	FDPRKADSIFTEEGETPAWLEQMIAHTTWRDLFYKLAEAHPDCL
	1	1	MLNFTVKVGRVLELRRKVFMNVYFWLLVCFL
	258	592	RRLTSTSEKLQNRNSHTPLESLIHPQPSYKGFGIMFGKKKKKIE
5680	250		ISGPSNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMV
	1	İ	DRECTER TOTAP MET TVRGN KPC
	45	869	LLCAKTLGVRTKESQABGYNRSGINNHQAEDPRFCPSFCWMRSA
5681	1 25	1 335	POWDPODI PYPARPPTTPGSCPGGTGMDGKKCSVWMFLPLVFTL
1		· I	PTEACTWIVVETAVEDDKILPLNSAERKPGVKHAPYISIAGDDP
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1			TO A SECMENT CONFORT TWO FIRM VGTSLTFGFGTLTCW1QAAL
	Ì	- 1	TLKVNIKNEGRRVGIPRVILSASITLCVGPLLHPHGPKHPHVCS
1	1		
1	1		QGPVGPGHVL PSRSCLGTMRKWRHREVNLPEVTQQDAVCPAPIPSPGLSAQTGL
5682	3.9	622	PSRSCLGTMRKWRHREVNLPEVIQQDAVCFAFIFSTOLDAQTOL QKIWGTIHCQVCPGAPAWPGSPWHEEMGLLLLVPLLLPGSYGL
			QKIWGTIHCQVCPGAPAWPGSPWILEFIGHERD F BELLE GOTGE
1	1		PFYNGFYYSNSANDONLGNGHGKDLLNGVKLVVETPEETLFTYQ
i	1	1	GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIG
1		1	t pupe PCDVOCRVHI ROD
	.1		
		778	GOCCATAL TTPCLAWSVLTSRLAMATYTCITCRVAFRDADMQRA
5683	. 89	778	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMQRA
5683	. 89	778	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMQRA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS
5683	. 89	778	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMQRA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEESKGS ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM ATYCTVCSKKFASFNAYENDANJAIOOAIKAQPSMSPKKAPPAPAK
5683	89	778	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMQRA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEESKGS ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM ATYCTVCSKKFASFNAYENDANJAIOOAIKAQPSMSPKKAPPAPAK
5683	89	778	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMQRA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD
5683	89		GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMQRA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM NEKNLEKGLGVDSVDKDANNAAIQQAIKAQPSMSPKKAPPAPAK EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD
		778	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMQRA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM NEKNLEKGLGVDSVDKDANNAAIQQAIKAQPSMSPKKAPPAPAK EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD SEDEEHDLC SECTION GDDVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT
5683			GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMQRA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD SEDEEHDLC TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT
			GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMQRA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM NEKNLEKGLGVDSVDKDANNAAIQQAIKAQPSMSPKKAPPAPAK EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD SEDEEHDLC TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY OSAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERHFAESET
			GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMORA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEESKGS ATYCTVCSKKFASFNAYSHNLKSRRHVELEKKAVQAVNRKVEMM NEKNLEKGLGVDSVJKDAMNAAIQQAIKAQPSMSPKKAPPAPAK EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD SEDEEHDLC TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY QEAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERHFAESET
5684	195	677	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMORA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEESKGS ATYCTVCSKKFASFNAYSHNLKSRRHVELEKKAVQAVNRKVEMM NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQAKKLAKHSEDD SEDEEHDLC TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY QEAVINKLTDASWYTVVDDGDEKTLRRSSLCLKGERHFAESET LDQLPLTNPEHFGTPVIGKKTNRGRRYE
	195		GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMORA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS ATYCTVCSKKFASFNAYSHNLKSRRHVELEKKAVQAVNRKVEMM NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSFKKAPPAPAK EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD SEDEEHDLC TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY QEAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERHFAESET LDQLPLTNPEHFGTPVIGKKTNRGRRYE LLLQQFVVHCFLLFPFFRFSHHMIPGPPGPHTTGIPHPAIVTPQ
5684	195	677	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMORA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS ATYCTVCSKKFASFNAYSHNLKSRRHVELEKKAVQAVNRKVEMM NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSFKKAPPAPAK EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD SEDEEHDLC TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY QEAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERHFAESET LDQLPLTNPEHFGTPVIGKKTNRGRRYE LLLQQFVVHCFLLFPFFRFSHHMIPGPPGPHTTGIPHPAIVTPQ
5684	195	677	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMORA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK EARNVVAVGTGGRGTHDRDFSEKPPRLQWFEQQAKKLAKHSEDD SEDEHDLC TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY QEAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERHFAESET LDQLPLTNPEHFGTPVIGKKTNRGRRYE LLLQQPVVHCFLLFPPFRFSHHMIPGPPGPHTTGIPHPAIVTPQ VKQEHPHTDSDLMHVKPQHEQRKEQEPKRPHIKKPLNAFMLYMK EMRANVVAECTLKESAAINQILGRWHALSREEQAKYYELARKE
5684	195	1262	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMORA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK EARNVVAVGTGGRGTHDRDFSEKPPRLQWFEQQAKKLAKHSEDD SEDEHDLC TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY QEAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERHFAESET LDQLPLTNPEHFGTPVIGKKTNRGRRYE LLLQQPVVHCFLLFPPFRFSHHMIPGPPGPHTTGIPHPAIVTPQ VKQEHPHTDSDLMHVKPQHEQRKEQEPKRPHIKKPLNAFMLYMK EMRANVVAECTLKESAAINQILGRWHALSREEQAKYYELARKE
5684	195 5 779	677	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMORA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD SEDEHDLC TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY QEAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERHFAESET LDQLPLTNPEHFGTPVIGKKTNRGRRYE LLLQQPVVHCFLLFPPFRFSHHMIPGPPGPHTTGIPHPAIVTPQ VKQEHPHTDSDLMHVKPQHEQRKGEPKRPHIKKPLNAFMLYMK EMRANVVAECTLKESAAINQILGRRWHALSREEQAKYYELARKE RQLHMQLYPGWSARDNYVSPSSIPVALHS
5684	195 5 779	1262	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMORA HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK EARNVVAVGTGGRGTHDRDFSEKPPRLQWFEQQAKKLAKHSEDD SEDEHDLC TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY QEAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERHFAESET LDQLPLTNPEHFGTPVIGKKTNRGRRYE LLLQQPVVHCFLLFPPFRFSHHMIPGPPGPHTTGIPHPAIVTPQ VKQEHPHTDSDLMHVKPQHEQRKEQEPKRPHIKKPLNAFMLYMK EMRANVVAECTLKESAAINQILGRWHALSREEQAKYYELARKE

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	
1	location		
]	corresponding	corresponding	
1	to first	to first	D-Deuclie, Memorbioning N x
1		amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Sering Tombers, R=Arginine,
Į.	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ļ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	sequence	acquence	1 TOWN / TOUSSIDIE MICIACHIAG ASIAL
	1		'-Possible nucleotide incertion'
	İ		UNLIPF VAEVLEGIPAGVS I YOUVAIDI DEGI NOLLYGUE
j		1	RMDFLINSSSGVVVTTTELDRBRIAEYQLRVVASDAGTPTKSS:
	1	Į.	STLTINU DVNDETDTERDAMERIAE YQLRVVASDAGTPTKSS
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			SGCPMPSTSAGE /AAGGGGAGTTSAGE PDPPPLTVP/ADA/PMPVT
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DITOCI SEPARSLHRZGGHKSSAGKWGSVILSTAGALG*KQLHQ*WT GSKEPARSLHRZGGHKSSAGKWGSVILSTAGALG*KQLHQ*WT GRCL\NNLSSEEPRASSLASLPSTPTAGRRSSTIVLRTDSEKR SLAESCLEWFSESEEKAPKKLEYDGGLKWEPGTSKKWRERPESE CDSSKGGELKKPILSHGHGSLKKWRERPESE LAPSTSGGFKKKPILSHGHGSLKKWRERPESE LAPSTSGGFKKKPETPESAGRRSTAGKKSSAD KVAGKPEGKATTKGKLAVKNTGLQRSSDAGBRISDAKKPPSG LAPSTSGGFKKKPEPATGTATVMOTGGGATLSKLOKSGSIPV KPVNGRKTSLDVSNABEPGFLAPCARSNIQYSLPPAKSSSMS VTGGRGPRPVSSSIDPSLISTKGGLTPSRLKEPTVANSGRTT PAPVNOTDREKEKARKAKAVALDSDNISLKSIGSPBSTPKNOASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS DITOCI SPERLASPPACPSAPARRSIISRLFGTSPATEAAPPPPEPVPAA GGPATVOSVEDVYPDDRLDRSFLEDTTPARDEKKVGAKAQODS DSDGEALGGNPWVAGFQDDVDLEDQPRGSPPDAGPVPSQDITL SSBEEAEVAAP*KGPAPAPQCSSPPTKWSSIPASKPRGTAPT RTAAPPWPGGVSVRTQPEKKRSTRPPAEMEPGGEGASSSEDP EGPIAAQMLSFVMDDPPESSGSPPTKWSSIPASKPRGTAPT RTAAPPWPGGVSVRTQPEKRSSTPPAEMEPGGEGASSSEDB EGPIAAQMLSFVMDDPPESSGSPPTKWSSIPASKPRGTAPT RTAAPPWPGGVSVRTQPEKRSSTRPPAEMEPGGEGASSSEBGK EGKTPSKEMKKKKKGKEEEEKAAKKKSKKHKEKSKDKEEGKEERR RRQQRPPRGREETAAS FRQGRPPRGREETAAS FRQGRPPRGREETAAS FRGGDVBGNUTGDUTLERIQGERNKPSRQTVFI FETL*#, PEGNUNGMTFDVETNIPVSNLVSVGHIIKPDVISKLEG GEEPWIVEGFFLLQSYDEVWQTDDLIERIQGEENKPSRQTVFI FETL*#, PEGNUNGMTFDVETNIPVSRLVSVGHIIKPDVISKLEG GEEPWIVEGFFLLQSYDEVWQTDDLIERIQGEENKPSRQTVFI FIL*#, PEGNUNGMTFDVETNIPVSRLVSVGHIIKPDVISKLEG GERMIVEGGFLAGGRAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA			1	PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
S696 3 1338 GSKEPARSLHRSGSCHKSSAGKWGSVTLSTAGALG*KQLL*WCQCCL\NNLSSEFTNASSSLANLSPTPTAGRNSTTYLTRIDEKK SLAESCLEWFESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES CDDSSKGGELKKPISCHKPGTSKWRRERPES CDDSSKGGELKKPISCHSKGKTPFVATSPITHTAQSAL KVAGKVEPGKATTKGKLAVKNTGLQRSSSDAGKDRLSDAKKPPSG LARPSTSGSFGYKKPPATGTATVMOTGGSATLSKLOKSGSLDY KPVMGRKTSLDVNSABAPGFLAPGATSLSKOKSGSLDY KPVMGRKTSLDVNSABAPGFLAPGANIQYRSLPPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKGGGLTPSRLKEPTKVASGRTT PAPVNQTDREKEKAKAKAVALIDSHLSSLSGSPSTFNAQSH PTATKLAELPPTPLRATAKSPVKPPSLANLDKVNSNSLDLPSSS DTTQCI SEBLASPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEBFVPDDRLDRSFLEDTTPARDEKKVCAKAAQODS DSIGGALGGNPWNAGFDDVLLEDGSSPLPLAPGPVSGDITL SSEEABVAAP*KGPAPAPQCSSPETKWSSIPASKPRGTAPT RTAAPPNPGGVSVRTGPEKRSSTRPDAEMEPGKGGASSSESDY BCGPLAAQMLSFVWDDPPDESSGSTDTQRADDFPVRDDPSDVTDE DEGGARPPPPPKLPLPAFRLKNDSDLFGLGLBGAPKRSSEEGK EGKTPSKENKKKKKKKKEEEKKAAKKKSKKKEKEKEKAKKKSEEKEKAKKKSKEEKEKAKKKSKEEKEKAKKKSKEEKEKAKKKSEEKEKAKKKSEEKEKAKKKSEEKEKAKKKSEEGK GERWIVEGFFLQSYDDEWQTTDLIERIQEENKPSRQTVPI ETLI*#, PRINTPEPTENTPVTNPVPSKKIAYTHSLCNSCERGF NASSEYISSDGYARMKADECSGCGKSLLHIKKEKTHFGLOAYE PNO SETTL*#, PRINTPEPTENTPVPSKKIAYTHSLCNSCERGF NASSEYISSDGYARMKADECSGCGKSLLHIKKEKTHFGLOAYE PNO SERSESKGSGWBTDVPWSTAQPPLPRVSTOVAL**DEKPLA RPS/GRTNAPFGGGRPAGKAAPGPAAAGRVAMR\PGHPGLLAS DSQRSSSKGSGWBTDVPMS*AQPGWVSGLLIDDFSGGSS*RS TWLVGGARGFGEGSVGRSGWBFGCDTGWALAGMNIS*HLDDNT WTOKWTGE/SPAPGEGCVAPAPRGPTAHEHHGELTTESGYSNN VPILFQMPSGALBRRTEFBGAWYARAPRGPTAHEHHGELTTESGYSNN VPILFQMPSGALBRRTEFBGAWYARAPARGSTAAA GGSIGCG/SIGLIGPGW*TLLDEPSGARGYNN VPILFQMPSGALBRRTEFBGAWPAPRGPTAHEHHGELTTESGYSNN VPILFQMPSGARBRTEFBGAWPAPRGPTAHEHHGELTTESGYSNN VPILFQMPSGARBRTEFBGAWPAPRGPTAHEHHGELTTESGYSNN VPILFQMPSGARBRTEFBGAWPAPRGPTAHEHHGELTTESGYSNN VPILFQMPSGARBRTEFBGAWPAPRGPTAHEHHGELTTESGYSNN VPILFQMPSGARBRTEFBGAWPAPRGPTAHEHHGELTTESGYSNN VPILFQMPSGARBARAFASARCPPAAAA GGSIGCG/SIGLIAHAGAHTSABARCPPAAAA GGSIGCG/SIGLIAHAGAHTSABARCPPAAAA GGSIGCG/SIGLIAHAGAHTSABARCPPAAAA GGSIGCG/SIGLIAHAGAHTSABARCPPAAAA GGSIGCG/SIGLIAHAGAHTSABARCPPAAAA GGSIGCG/SIGLIAHAGAHTSABARCPPAAAA GGSIGCG/SIGLIAH		1		DTTOCI
QRCL\NNLSSEFNASSLINSLPSTFAGRRNSTIVLETDSEKR SLAESCLEWFSESGEKAPKKLEXPEKAPKKLEYDAGAL KVAGKFEGKATDKGKLAVKNTGLQRSSDAGRDRLSDAKKPPS LAPSTSGFGYKKPPATGTATVMOTGGSATLSKIQKSSGIPV KPVNGRKTSLDVSNABEGGIAPGARSNIQYSLPRPAKSSSMS VTGRGGRPPVSSSIDPSLTSTKGGGLTPSRIKEPTVASGRIT PAPVNQTDREKEKAXAKAVALDSDNISLKSIGSPBSTPKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS DTTQCI SFORT 1147 47 PSEALSPPACPSAPAPRES IISRLFGTSPATEAAPPPPEPVPAA QCPATVQSVEDVPYDDRLDRSFLEDTTPARDEKKVGAKAAQQDS DSDGEALGGNPWAGFQDDVDLEDOPRGSPDLPAGFVPSQDITL SSEELAEVVAAP*KGPAPPAPQQCSEPETKWSSIPASVERRGTAPT RTAAPPNPGGVSVRTGPEKRSSTEPPAEMEPGKGEQASSSESDP EGPIAAQMLSFVMDDPDFESEGSDTQRAADFVRDDBDVTDE DGGPABPPPPKINLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKGKEEEKAAKKKSKKKKKKKKEKEECKERR RQRPPPRSRERTAA 5698 2 666 GABAABFQEDLPPLSQSSRFFQEQQKMNKSLGPVSFVDAVDFT QEEKQOLDPEGKITYRDVMLENYSNLVSVGYHIIKDDVISKLEQ GEEWU TUGEFLLGSTPDEVGTDDLIERTQEEENHRSRQTVFI ETLI*R/ERGNVGSMFFDVETNPVPSKRIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKHLKLEKTHFDGQAYE NASSEYISSDGRYARMKADECSGCGKHLKLEKTHFDGQAYE PNQ 5699 2 1448 RVRQPFGLWVRRTVFBMQCPAGLSRVFGVAG/DPSLPSFRGPRD SAAHGFIOTARTTRLVYQGPASGPPLPRVSTQVAIT*DEKELA RPS/GRTNAPPPGGKPAGKAAAGRAAAGRAAAGRAAAGRAAAGRAAAG	5606	 	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
SIABSGLSMYSESEEKAPKKLEYDSGSLKMRPGTSKWRREPES CDDSSKGGELKKY EIGHIPGSLKKGKTPVANTSPITHTAQSAL KVAGKPEGKATDKGKLAVKNTCLQRSSDAGRDRLSDAKKPPSG IARPSTSGSFGYKKEPPATGTATVMQTGGSATLSKLQKSSGIPV KPVNGKKTSLDVSNSAEPGFLAPGARSNIQVRSLPPAKSSMS VTGGRGPRPVSSSIDPSLLSTKQGGLTPSRIKEPTKVASGRIT PAPVNQTDREKEKAKKAKAUALDSDNISLKSIGSPSTKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS DTTQI 5697 1147 47 PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRALDSTLEDTTRADEKKVGAKAQAQOS DSDGEALGGMPWAGFQDDVLDLEDQPRGSPPLPAGPVPSQDITL SSEBEASVAAPTKGPAPAPQCCSEPSTKMSIPASKPRGTAPT RTAAPPPPGGUSVRTOTERESSTRPPAEMEPGKGQASSSEDD EGPIAAQMLSFVNDDDDPSSEGSDTQRRADDFPVRDDPSDVTDE DEGPAEPPPPKLPLPAFRLKNDSDLFGLGLEAGPKSSSEBG EGKTSFSKENKKKKKKKEEEEKAAKKKSKHKKSKNKEEGKEERR RRQQRPPRSRERTAA 5698 2 666 GABAAFPGEDLPPLSGSSRFFQEQOKMNKSLGPVSFKDVAVDFT GEENQULDPBGKTTYRDVMLENYSNLVSGYHITRPDVISKLEQ GEEPWIVEGRFLLQSYPDEVWQTDDLIERIQEERNFSRGTVDF ETLL*R/ERGNVBGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLBKTH-GDQAYE ETLL*R/ERGNVBGNTFDVETNPVPSRKIAYTHSLCNSCER\GF NASSEYISSDGRYARMKADECSGCGKSLLHIKLBKTH-GDQAYE PNQ 5699 2 1448 RVRQOPGLMVRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD SAAHRGTIOTARHTYRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPFPQQKPAGKAAPGPAAAGRVAMR\PGHBGLLAS DSRSSKGSGWETPVPNS*APPGRAGRAMFSHLLDBNT WTQKWTGE/SFAQCEGO\VAPARGFPCALPKPAGEGSSA* GGSLGCZ/SMLPASSGPPAPGPPRALAGAMTSSARGPPASGAP VSTPTWAGTP/LNASLGPTDPQGKPGCCPPCALPKPAGERSA* GGSLGCZ/SMLPASSGPPPAPGPRRLAAGAMTSSARGPPASARG VSTPTWAGTP/LNASLGPTDPQGKPGCCPPCALPKPAGERSA* GGSLGCZ/SMLPASSGPPPAPGPRRLAAGAMTSASARCPPASAR GGSLGCZ/SMLPASSGPPAPGPRRLAAGAMTSSARCPPASAR GGSLGCZ/SMLPASSGPPAPGPRRLAAGAMTSSARCPPASAR GGSLGCZ/SMLPASSGPPAPGPRRLAAGAMTSSARCPPASAR GGSLGCZ/SMLPASSGPPAPGRRAAGRSSSCLCSGFSCLCAPLD HPAHPPGGSAPPWGALGGWAAARASLEWSPSLCLSFPAVTPVAGL FPPGRG 5700 923 597 NGHKGVWEINIY*RRSNTHKNSKSESHLNDGHSFPPFTNSARS KLHSTGTAKNTGLPLSGAPRQRAVFSGRTICQEFSSCLQCAYLD E*CSIASSLIKALRVSVISE 5701 594 410 1FEKLCSDTQFFISPEINPQICSWLIFDYKKJKYKJK/DANIRGSLFTVK	2026)	1000	ORCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
CDDSSKGGELKKPISLGIRPGSLKKCKTPPVAVTSPITHTAGSAL KVAGKPEGKATDKGKLAVKNTLGSSSDAGRDRISDAKKPES IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKICKSGIPV KPVNGRKTSLDVSNSSAEPGFLAPGARSNIQYRSLPPRAKSSMS VTGGGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRIT PAPVNQTDREKERAKAKAVALDSDNISLKSIGSPBSTFKNQASH PTATKLAELPPTPLRATAKSFVKPSPSLANLDKVNSNSLDLPSSS DTTQCI 5697 1147 47 PSEALSPPACPSAPARRSITSRLFGTSPATEAAPPPPEPVPAA GGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAQQOS DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL SSEEBAEVAAPT KOPAPAPQCGPSPTKWSSIPASKPRGTAPT RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPCKGGASSGSDP EGFIAAQMLSFVNDDPDFESEGSDTQRADDFPVRDDPSDVTDE DEGGARPPPPSKELPLAFFLKNDSDLFGLGLEBAGPKESSEEGK EGKTFSKENKKKKKKKEEEKAAKKKSKHKESKEKEERR RQQQPPPRSRETTAA 5698 2 666 GABAAEPQEDLPPLSQSSRFFQBOQKNNSLGMPVSFKDVAVDFT GEKQQLDPBQKLTYRDVMLENYSNLVSVGYHIIKPDVISKLEQ GEBPWIVEGFLLQSYDDEVMQTDDLIERIQEBENKPRRQTVFI ETLL*R/ERGNVPGNTFDVETNFVPSRKLAYTHSLCNSCER\GF NASSBYISSDGRYARMKADECSGCKSLLHIKLEKTHPGDQAYE FNQ 5699 2 1448 RVRQPFGLMVRRTVPAMQCFAGLSRVFGVAG/DPSLFSFRGPRD EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPPPQGQRPAGKAAPGPAAAARGVAMR\SHLDPNT WTOKMTGE\SPACEGEQ\APARRGPAARAGRAAMARSHLUPNT WTOKMTGE\SPACEGEQ\APARRGPAARAGRAAMARSHLUPNT WTOKMTGE\SPACEGEQ\APARRGPAARAGRAAMARSHLUPNT WTOKMTGE\SPACEGEQ\APARRGPAARAGRAAMARSHLUPNT WTOKMTGE\SPACEGEQ\APARRGPARAGRAAMARSHLUPNT WTOKMTGE\SPACEGEQ\APARRGPARAGRAAMARSHLUPNT WTOKMTGE\SPACEGEQ\APARRGPARAGRAAMARSHLUPNT WTOKMTGE\SPACEGEQ\APARRGPARAGRAAMARSHLUPNT WTOKMTGE\SPACEGARAGRAARAGRAAMARSHLUPNT WTOKMTGE\SPACEGARAGRAARAGRAAMARSHLUPNT WTOKMTGE\SPACEGARAGRAARAGRAAMARSHLUPNT WTOKMTGE\SPACEGARAGRAARAGRAAMARSHLUPNT WTOKMTGE\SPACEGARAGRAARAGRAARAGRAAMARSHLUPNT WTOKMTGE\SPACEGARAGRAARAGRAARAGRAAMARSHLUPNT WTOKMTGE\SPACEGARAGRAARAGRAARAGRAAMARSHLUPNT WTOKMTGE\SPACEGARAGRAARAGRAARAGRAAMARSHLUPNT WTOKMTGE\SPACEGARAGRAARAGRAARAGRAARAGRAAMARAGRAARAGRAAMARSHLUPNT WTOKMTGE\SPACEGARAGRAARAGRAARAGRAARAGRAAMARAGRAARAGRAAMARAGRAARAGRAAMARAGRAARAGRAAMARAGRAARAGRAARAGRAARAGRAARAGRAARAGRAARAGRAARAGRAARAGRAARAGRAARAGRAARAGRAARAGRAARAGR	Ī	i .	1	CT A POCT CWECKERVAPKKI. PVDSGSLKMEPGTSKWRRERPES
KVAGKPEGKATDKGKLAVKNITGLQRESSDAGRDELISDAKKPPSG IARPSTSGSFGYKKPPPATGTATVMOTGGSATLSKIQKSGIPV KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSELKEPTKVASGRIT PAPVNOTDREKEKAKKAKAUALISDNISLKSIGSPSTFKNQASH PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS DTTQCI 5697 1147 47 PSERLSPPACPSAPAPRRSITSRLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFYPDDRALDRSFLEDTTFADEKKVGAKAQQDS DSDGEALGGNPWAMGRODDVIDLEDQPRGSPPLPAGPVPSQDITL SSEEABVAAPTRGPARPAPQQCSEPSTKNSSIPPAGKPGKAPGCSSCIPP RTAAPPNPGGUSVRTQPEKRSSTRPAEMEPGKGEQASSSESDP RTAAPPNPGGUSVRTQPEKRSSTRPAEMEPGKGEQASSSESDP RTAAPPNPGGUSVRTQPEKRSSTRPAEMEPGKGEQASSSESDP BGGPAEPPPPKLDLPAFRLKNDSDLFGLGLEEAGPKESSEEGK EGKTPSKENKKKKKKEEEEKAAKKKSKHEEGKEERR RRQQPPPRSRETTAA 5698 2 666 GABAAFPGEDLPPLSGSSRFFQEQQKMNKSLGPVSFKDVAVDFT GEEMGULDPSGKKTYRDVMLENYSNLVSVGYHIIRDDVISKLEQ GEBPWIVEGEFLLQSYDBEWQTDDLIERIQEEBNEPRGTYPFI ETLI*R/ERGNVPGNTFDVETNPVPSRKLAYTHSLCNSCER\GF NASSBYISSDSRYARKKADECSGCGKSLLHIKLEKTHPGDQAYE FNQ 5699 2 1448 RVRQDPFGLMVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPND EAAHRGTIQTARHTRKLYVQFPASGPPLPRVSTQVAI*DEKPLAA PS/GRTNAPPPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS PS/GRTNAPPPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS PS/GRTNAPPPQGRAGKAAPGPAAAGRWAMR\PGHPGLLAS PS/GRTNAPPPQGRAGKAAPGPAAAGRWAMR\PGHPGLLAS PS/GRTNAPPPQGRAGKAAPGPAAAGRWAMR\PGHPGLLAS VSTETWAGTFP/LANSLCPTDPQGKPGCRPCALPKPAGPERSA-V VFILFQMPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP VSTETWAGTFP/LANSLCPTDPQGKPGCRPCALPKPAGPERSA-V VSTETWAGTFP/LANSLCPTDPQGKPGCRPCALPKPAGPERSA-V VSTETWAGTFP/LANSLCPTDPQGKPGCRPCALPKPAGPERSA-V GGSLGCK/SMLPASGGPPPAPGPRRLAAGAHTSASARCPPAAAA GNQPRRDSFAGRAALPGPPRRLAAGAHTSASARCPPAAAA GNQPRRDSFAGRAALPGPPRRLAAGAHTSASARCPPAAAA GNQPRRDSFAGRAALPGPPRRLAAGAHTSASARCPPAAAA GNQPRRDSFAGRAALPGPPRRLAAGAHTSASARCPPAAAA GNQPRRDSFAGRAALPGPPRRLAAGAHTSASARCPPAAAA GNQPRRDSFAGRAALPGPPRRLAAGAHTSASARCPPAAAA GNQPRRDSFAGRAALPGPPRRLAAGAHTSASARCPPAAAA CNQPRRDSFAGRAALPGPPRRLAAGAHTSASARCPPAAAA GNGPRDSFAGRAALPGPRRLAAGAHTSASARCPPAAAA GNGPRDSFAGRAALPGPRRLAAGAHTSASARCPPAAAA GNGPRDSFAGRAALPGPRRLAAGAHTSASARCPPAAAA GNGPRDSFAGRAALPGPRRLAAGAHTSASARCPPAAAA GNGPRDSFAGRAALP		ł		CDRCCYCCEL WYDTCI CUDGGI, KYGYTPPVAVTSPITHTAOSAL
IARPSTSGSFGYKKPPPATGTATVMGTGGSATLSKIQKSGSIPV KPVMGRRTSLDVSNNSAEPGELAPGARSNIQYSLSPRAKSSSMS VTGGRGGPRPVSSIDPSLLSTKQGGLTPSELKEPTKVASGRIT PAPVNGTDERKEKAKAKAVALDSDIJSLKSIGSPBSTPKNQASH PTATKLAELPPTLRATAKSFYKPPSLANLDKVMSNSLDLPSSS DTTQCI 5697 1147 47 47 FSEALSPPACPSAPAPRSIISKLFGTSPATEAAPPPPEPVPAA QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQOS DSDGEALGGMPWVAGFQDDVDLEDGPRSPPLPAGPVPSQDITL SSEESAEVAAPTKGPAPAPQQCSEPETKWSIPASKPRGTAPT RTAAPPMPGGVSVKTGPEKRSTTRPJAEMEGKGGASSESDP EGPLAAQMLSPWDDDPPESEGSDTQRRADDFVRDDPSDVTDE DEGPAEPPPPPKLPLAFRLKNDSDLFGLGLEBAGPKESSESGK EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKERR RQQPPPRSRERTAA 5698 2 666 GABAABFQEDLPPLSGSSRFFOEQOKMNKSLGPVSFKDVAVDFT ETLL*R, ERGNVPGNTFDVETTNPVPSKRIATTHSLCNSCER\GF NASSSYISSGRYARMKADECSGCGKSLLHKLERTHSQDAYE FNQ FNQ FVQPFGLMVRRTVPSMGCPAGLSRVPGVAG/DPSLPSFRGPND SASSYISSGRYARMKADECSGCGKSLLHKLERTHSQDAYE FNQ FVQPFGLMVRRTVPSMGCPAGGLSRVPGVAG/DPSLPSFRGPND EAAHRGTIQTARHTKLYVGGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPPPQGGKPAGKAAPGPAAAGRVAMR\PGHFGLLAS DSQRSSKGSGWFTPVMS*AQPGMVSGLLLLGDPSGFGSSL*RS TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGMNIS*HLDPNT WTQKWTGE'SPAPGEGSQVRGSGWPSGCSDIGWALAGMNIS*HLDPNT WTQKWTGE'SPAPGEGSQVRGSGWPSGCSDIGWALAGMNIS*HLDPNT WTQKWTGE'SPAPGEGSQVRGSGWPSGCBCLLLGDPSGPGSSL*RS TWLVGGARGPEGSGRAGAGRAFAGRAGRYSAGACPAAAA GGSGCR, SMLPASGPPPAPGPRRLAAGAUTSASAACPAAAA GGSGCR, SMLPASGPPPAPGPRRLAAGAUTSASAACPAAAA GWQPRPGFAGRAALPGPPHPPS**RELGGLPGCOW*TLDFLPA HPAHPDGSAPPWGALGGWAAARARASLEWPSLCLSFPAATPAA GWQPRPGFAGRAALPGPPHPPS**RELGGLPGCOW*TLDFLPA HPAHPDGSAPPWGALGGWAAARARASLEWPSPLCLSFPAATPAAA GWQPRPGFAGRAALPGPPHPPS**RELGGLPGCOW*TLDFLPA HPAHPDGSAPPWGALGGWAAARARASLEWPSPLCLSFPAATPAAG GGSLGR, SMLPASSGPPPAPAPAPAAGRAAGRAAGAUTSASAACPPAAAA GWQPRPGFAGRAALPGPPHPPS**RELGGLPGCOW*TLDFLPA HPAHPBGSAPPWGALGGWAAARARASLEWPSPLCLSFPAATPAGG GSSLGR, SMLFASSGPPRAGPRAVYSGRTICQEFSSCLQCAYLD K-CSIASSLIKAILRVSVLSE 5700 923 597 NGHKGVWEINTY*RRSNIHKNSKSESHLNQDHSFPFTTYNSAS**IK/DANIRGETVKL KNSWMMISTCHC**C**MPRGPFYFTYTKINSK*IK/DANIRGETVKL	}	ł		CDDSS RGGEDRAF ISLGHF GODARGARIT I VITTO I STORY PORCE CONTROL OF
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LEENTGENLHDTGLGNVFLDMTPKTQPTKQK	1]		KWSWKNWLSTCR*MRPGPYFTPYTKINSK*IK/DANIKCETVKL
	1			LEENTGENLHDTGLGNVFLDMTPKTQPTKQK

SEO	Predicted	Theod: -r-3	
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	Managarine, C=CVStelne, D=lenar-ic laid =
	location	corresponding	Glutamic Acid, F=Phenylalanine C-Cleri-
Í	corresponding	to first	n-miscidine, I=Isoleucine K-Lucine
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
- }	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
Í	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
}	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence		Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5702	. 3	1517	ETFVDPSQCGGIPSDSPHPVITPSRASESSASSDGPHPVITPSR
i		ļ	ASESSASSDGPHPVITPSRASESSASSDGPHPVITPSR ASESSASSDGPHPVITPSRASESSASSDGHPVITPSRASESSA
1			SSDGPHPVITPSRASESSASSDGPHPVITPSRASESSA
			PVITPSRASESSASSDGPHPVITPSRASESSASSDGLH PVITPSRASESSASSDGPHPVITPSWSPGSDVTLLAEALVTVTN
İ			IEVINCSITEIETTTSSIPGASDTDLIPTEGVKASSTSDPPALP
			DSTEAKPHITEVTASAETLSTAGTTESAAPHATVGTPLPTNSAT
			EREVTAPGATTLSGALVTVSRNPLEETSALSVETPSYVKVSGAA
			PVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETLTMDI
1			TTKGPFPTSRDPLPSVPPTTTNSSRGTNSTLAKTTTSAKTTMKD
			PTATPTTARTRPTT\A*VOVKMEVSSSCG*VULDPVTGLTDEWO
			KG*CSSSTGNSTPTRLTSRSPYCVSGEANG/PSAAADUVDVAVD
1			GCCP*PGPPPTDCSCVTVLRGTOKVPMKGSMSKPLTPDVATCDC
5703	14		LTSTGVYVWGGASPVPRGVLGLTLAHVT.CFSVEVT
1	1 17	1117	HHKDSRSQGLPRTOECARPELRPLLCPRALWDVTDLCVPCDWO2
l l			PRAGIGTKAKPSESHLKLHPGWPSI.DROGEDATI.CTCTCUCCDC
			KIDKWHP*HTAAR*PRWRRLPSSHRWTRHIGVT.PVODVC++VCT
	1		DPSCRPRFLRTC**YGMRSVASSSNPPPGWGGDGAGUEDADDUG
1			ALPTGPRCW*APRGRTRQPCGWPRLSSPHATADWGPGCPLSPSR
1			GSWETAPGS*WCPWL*AARWTGWRTASGASAGLGRAADRPSAWA
ļ			RRVAGLLPGQGLTVRR*H*TAGAPASVRSSQGATRSPAPGGDQC
			ACGRGPGSC*HPPPWPVSPSSPVPCPSGR*HLRGPLLSAARPRA AGWPRHSPHDTQTPEP
5704	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI
			SGNAASDKNIKDGVCAQIEKNPARAKWKKAVRVTTLMKRLRAPE
1 1			USSTAAAQSASATDTATPGAAGGATAAAASGATGADEGDAADAA
1 1	1		KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE
5705			SPQP
3,03	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI
1 1			SGNAASDKNIKDGVCAOIEKNFARAKWKKAVPVTTIMKDIDADE
1 1			QSSTAAAQSASATDTATPGAAGGATAAAASGATGABECDAABA
1 1			KSUNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEAST.OPT.MGE
5706	1161	610	SPQP
1 1		010	QLGRFXAQDTVAIRKVKEVFGTGAMRHVVILFTHKED*GGQALD
			DYVANTDNCSLKDLVRECERRYCAFNNWGSVBEQRQQQAELLAV
1 1			IERLGREREGSPHSNDLFLDAQLLQRTGAGACQEDYRQYQAKVE WQVEKHKQELRENESNWAYKALLRVKHLMLLHYEIFVFLLLCSI
			LFFIIFLF
5707	28	609	GSPAPTPGFRRPGRGTPSPGTRHHQGRAEPEPDAPERAPLRR*
	1		MFAIQPGLAEGGQFLGDPPPGLCQPELQPDSNSNFMASAKDANE
1 1			NWHGMPGRVEPILRRSSSESPSDNOAFOARGSDERGURGDDEGA
1 1			E1PGAEPEKMGGAGTVCSPLEDNGVASSSISIDSBSSCSDBDAGG
5708			IPRGPGPPLPLLPSVAOA
3,00	44	1925	SFSWEETISPCFPKMPAEPWWLSPVSLGAAGWPGOPPDVLDY.DX
	ŀ	1	QASVSRPHDRA*GEAVSLSLSSGDVCGHTDGGGAGSDDOAKDKD
		ł	PKCPFTAMPSPRTKOKVRNKVCT, I TATRYSDIDSDVSKADI CDA
1 1		1	GNPHDKSSTAA*LHRRAGAGSLCLSASLLPPSRSICAPCRT
1 1	1	j	RVSPASGGPRKEGRQGSGG*AGGGGP\ARTHADI.pcvcepp
	1		LLK*SDSPVKQLPA\SGOGSGAGMPPVGSSDTLPPPDTGVCCTC
()			KAAG*CSWQPAACCTPRSO*WAVARSPSRCSRW*PAGGP*PA+6
[ļ	ļ	SKRRKGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGVABCD+
ļ i	İ	1	LEPSGPTSGSAL+TWASHSTGA++SRLCGTAGTGPLCSQSSRS+
1			AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH
			GRGRAMGSRCVCTCTGLPCPGIPLSGASPGGSGETGAGRSHTLK
į į		İ	AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS
		İ	QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP
		1	PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GEAPA PPPRPEPPPPPARRP
5709	2	2031	ITLCPLPQTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG
		į,	LHQIVVRWGAVVMRAGMGGCRCWGVMAPFAPR/NALSFLVNDCS
			LIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQGNGGGPPRKGIPE
			TOOLD THE TOOL OF THE TEE

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
l	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
ļ	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Alginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
	 		LEQYDPPELADSSGRVVREKRSADMWRLGCLIWEVFNGPLPRAA
1			ALRNPGKIPKTLVPHYCELVGANPKVRPNPARFLQNCRAPGGFM
1	1	ţ	SNRFVETNLFLEEIQIKEPAEKQKFFQELSKSLDAFPEDFCRHK
1	1	Į	VLPQLLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQQKIIPVVVK
ł)	į.	MFSSTDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVVHGFLDT
1	i	1	NPAIREQTVKSMLLLAPKLNEANLNVELMKHFARLQAKDEQGPI
Ì	ì	1	RCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPFAPSRVAGV
ì	i	1	LGFAATHNLYSMNDCAQKILPVLCGLTVDPEKSVRDQAFKAIRS.
1	1	1	FIGHT FSVSEDPTOLEEVEKDVHAASSPGMGGAAASWAGWAVTG
1	1	1	VSSLTSKLIRSHPTTAPTETNIPORPTPEGVPAPAPTPVPATPT
1	1	1	TECHWETOREDKOTAEDSSTADRWDDEDWGSLEQEAESVLAQQD
1	1	1	DWSTGGQVSRASQVS\TPTTNPPNPQSPTGAAGK\RGLLGTGLA
			CAKI.PGATS*RYTAGORV
		562	TEGETTSCEVELMARMAKTIDSFTONOTRLVVIIDGLDACEQDK
5710	1	302	W.OMI.DTVRVI.FSKGPFIAIFASDPHIIIKAINQNLNSVPSGFK
1		}	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
1	Į	1	QILQGYRKMLTEEFHRTALGR*QNLVARQPSIDG*DAIGFELYV
	l.	1	CINICENTURDDAT
		1130	DPUDEOWTTVTOEAFSHHDVAFTSTPVLFYPDSAQPFIVKSESS
5711	1526	1130	COTAKANI, SOORPSI, FHECAFHFFS*SLORHTINLDQGIF*LLM
i	1	1	LSEBROHLFESS/IWTTPHNLK*/FEIHEHLGSHEGHWTLFFLL
	1		LOTT.
			CRYL FOSLDISERI.KELI.TLDCVDDTLIVLAEEHGCLDIIKELP
5712	3	1391	ETVIDII.NKCLTFHPSKRPTPDELMKDKVFSEVSPLYTPFTKPA
1		ł	SLFSSSLRCADLTLPEDISQLCKDINNDYLAERSIEEVYYLWCL
	•	l	AGGDLEKELVNKEIIRSKPPICTLPNFLFEDGESFGQGRDRSS/
i	Į.	1	TFR*YHWDIVVMPAKK*IERCWGRSILPITLKMTSLILPYSNSN
	ļ		NELSAAATLPLIIREKDTEYQLNRIILFDRLLKAYPYKKNQIWK
İ	į.	1	EARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDTPIPTDRQI
1	\	1	EVDIPRCHQYDELLSSPEGHAKFRRVLKAWVVSHPDLVYWQGLD
1	1	1	SLCAPFLYLNFNNEALVYACMSAFIPKYLYNFFLKDNSHVIQEY
i	1	1	LTVFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL
ł	1		LTVFSQMIAFMUPELSNALNELGFIFDHIALL
1			HKIFHLW\DTLLLGEFLFPILYWE PVCAVPVDRWPVLPREDQEGQQL*AKLPRDFRR*FQILGPMEGH
5713	634	284	TACRCSRRGAQVQHLPREDIRAAE*DPHLREVWPGLPTSSATSP
į.	1		*RAVLTSPCSHLGSADAASSHWLCGVSFH
l			*RAVLTSPCSHLGSADAASSHWLCGVSFR WGLGLGPTMSSLGGGSQDAGGSSSSSTNGSGGSGSGSKAGAAD
5714	212	613	WGLGLGPTMSSLGGGSQDAGGSSSSSTNGSGGSGSGFRACKED KSAVVAAAAPASVADDTPPPERRNKSGIISEPLNKSLRRSRPLS
	ļ		KSAVVAAAAPASVADDTPPPERRNASGIISEPHARSIARUK 25 HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA
ı			
			MA ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE
5715	131	1979	ESASQQKRSKCLILTLKLELSGSAPKKISAKFGSSIMIFFINOM
		1	QTPPASKLQGGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\
1		1	GLPGP+LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVENN
- 1		!	DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS
1	1		PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS
1			QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR
ì	1		TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL
1		1	YPKTPKQRRWRRPL/LLGPSQ+GSRQSTC+EV\GALGEPVRIPG
1	1	1	T + PDT CCTT SNCSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT
i			PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP
1		1	INVENTED BY CALCULATION TRICE OF TRICE OF THE PROPERTY OF THE
1			PGDLDLDGODRGAOPCSHCPGRAAGOPEPGAGAPCRE/GG*DPT
1			GLT/GVDGTDPKRGGRKPGOSGOETQGPTVWSGPESPLQPKP*E
ì			RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL
1	}		TOLTEDOTSOH
5716	1711	1370	RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD
1 2,16	' '''		*LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC*
ŀ			DODING * CORPTITYGGYSCCMPLKT
	7 44	1489	T DEPAT EFERWISHYCKCGPRGLVPEGESTSPLPSSVDTEDSLD
5717	' ""	1	EGPGALVLESDLLLGQDLEFEEEEEEEEGDGNSDQLMGFERDSE
1	1		

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	deta segment containing giossi
NO:	nucleotide	location	1
	location	corresponding	I VINCOMIC ACIO. PEDNONVISIONING COST
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan V=T======
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	•	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
			GDSICAPPOLIPPOLICE Insertion)
	1		GDSLGARPGLPYGLSDDESGGGRALSAESEVEEPARGPGEARGI
i	ł		RPGPACQLCGGPTGEGPCCGAGGPGGGPLLPPRLLYSCRLCTFY
	ĺ	1	SHYSSHLKRHMQTHSGEKPFRCGRCPYASAQLVNLTRHTRTHTC
			EKPYRCPHCPFACSSLGNLRRHQRTHAGPPTPPCPTCGFRCCTE
			RPARPPSPTEQEGAVPRRPEDALLLPDLSLHVPPGGASFLPDCG
			Q\CGVKGRASAGLDQNHCQS\SLFPWTCRGCGQELEEGEGSRLG
			AAMCGRCMRGEAGGGASGGPQGPSDKGFACSLCPFATHYPNHLA
			RHMKTHSGEKPFRCARCPYASAHLDNLKRHQRVHTGBKPYKCPL
5718	120	284	CPYACGNLANLKRHGRIHSGDKPFRCSLCNYSCNQSMNLIRHM
			VAHALSLPAESYGNDVSMTHPQLPPTQLAWDLCRTCLPLSYNFT S**STADPLHL
5719	48	428	FLANCE FOR DI CANCELLA DE LA CANCELLA DEL CANCELLA DEL CANCELLA DE LA CANCELLA DE
I			ELNNGPFQMPLCNGGNLAVTGSWADRSPLHRAASQGRLLALRTL
			LSQGYNVNAVTLDHVTPLHEACLGDHVACARTLLEAGANVNAIT
5720	1	1051	IDGVTPLFNACSQGSPSCAELLLEYGAKAQP\ESCLPSP
J			LQAFRNASEVPMVLVGTQDAISAA\NPRVYRRTSRARKLSTDLK
ľ			RCT\YYE\TCGGTYGLQMWSVSFQDVAQKVVAL\RKKQQ\LAI
ŀ			GPCK\SLPN\SPSH\SAVSAASIPARAPINQGHE/SGGGSAFSD
j			Y\SSSVPSTPSISQRELRIETIAASSTPTPIRKQSKRRSNIFTS
1			RKGADP\DREKKAAGCKVDSIGSGRAIPIKQGILLKRSGKSLNK
1			EWKKKYVTLCDNGLLTYHPSLHDYMQNIHGKEIDLLRTTVKVPG KRLPRATPATAPGTSPRANGLSVERSNTQLGGGTGAPHSASSAS
1	1		LHSERPLSSSAWAGPRPEGLHQRSCSVSSADQWSEATTSLPPGM
5721			OHPASG OHPASG
3/21	97	192	RHSSPCCSLRRTERSSNAAVST/TTVQQFKRFIENYRRHIGCVA
1	ı		VFYAIAGGLFLERAYYYAFAAHHTGITDTTRVGIILSRGTAASI
5722			OF THE STANDING KNOWN THE RETERING VIDEOR AND THE STANDING TO COMP.
3/22	88	1043	VALLOVIAGOSPGGGMAGATI CODVIGET DAVIT DVIA DOCTION
			ODIG V STAMME PARPOGAAGS PHRCPP DECCCORCE PRRP CREE
- 1	1		ZES VENSISIARGPRRVSRRLPPOHDCDDCDDDDDDDAXCHON DDD
1	1		COARGOMGDDGROGGGGGGGGGGGGGGGAALOADDGDDDGDDDGGGGGGGGGG
- 1	j		CATACAMAPGKAPADPOPPAPRDADADADADADADADADADADADA
- 1	i		FFFFFILGALTAGSGEEROSOPRARTIDICADO DE DA DESTRA
	1		WINDARD VERRETPPARGPOSSGDPAMI POPACI POCCIA COM
5723	88		- COLUMN TEMP
1		1043	VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP
ŀ			COLG V STAMME PARPOGRACIO SPERCE DE PROPERTO DE LA COLOR DE LA COL
	1	•	VIO VERGITARGIERRVSKRI.PPOHPGPPGPDDDDDCAGUGADDD
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1			ONE RUMANAEGRAPADEOPPA PRODUCED A DA DA DA DA DA DA DA DA DA DA DA DA
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724	3		TOOTESTERM
	-		FTNEAPPAPLPDASASPLSPHRRAKSLDRRSTEPSVTPDLLNFK
l	1	- 1	AGMULAQ LEDGQWKKHWFALADOSI, DVVDDSIA DD ADA DD
			DONCTOVIBLEVORNYGEOTHTKEGEETT.CAMEGOTTON
		1 '	""TIVET LAPUVISSLPEEKNKSSCSPETCDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
			PI DE LONGRE LIKKELIKSKTEDWAERPDIOONI NORDIVOOT
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f		, .	WALLQUQUEVALGREOSAREGYVI.OATCEDCEN NADEDITOTES -
	ļ	, ,	PHYNYNYNGUSKLREEKDRIIJAFFTAATTCATDAMMAMATATTURE - I
ļ	1	1 -	ADDENSYRSYLSSYNSDVEALEROYLERI.OGUODET EUR GROUGE
	j	, ,	ENCHERALITY AUGUSTALIST AND I
1		1 -	TRUM I DU I GUGGEATGSPLAOGKDAVELEV DCG DDCL TOLO
725	3		VEFUSAANPLSYRVVGGTDLROOFSOGDGDGVCDEGGDDG
	,		MGASEETSQSPARTEPHDSDCSVDLGTSKSTZDLCDOVCGDVG
	;	j s	SVVKSHSITNMEIGGLKIYDILSDN\DLSSHLQPLK/FTSAVEG
j	ł ·		TO THE ADDITION OF THE PROPERTY OF THE PROPERT
		1 1	CNIVRSKAATLLYDQPLQVFTGSSSSSDLISGTKAIFKFDSNHN PE/GAKYNKRPHKWAHNLHLKYMVLHSIISNTVAV\RSQRHFVA

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
,	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	codon. /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence	<u> </u>	LQTKSPNRPCQFSSSAPS/VDQRAQ/INQSYAKHSANMNFSNHN
			NVRANTAYHLHQRLGPARHGEMWAISPNDRLIPAVTRSTIQRQS
		1	NVRANTAYHLHQRLGPARHGEMWAISPNDRDIPAV 1R511QRQS
	1	I.	SVSSTASVNLGDPGSTRRAQIPEGDYLSYREFHSAGRTPPMMPG
]	1	SQRPLSARTYSIDGPNASRPQSARPSINEIPERTMSVSDFNYSR
ì	1	1	TSP
		486	SPSISYWWNSGLPASSHSSKLPVTVGFSGCVKRLRLHGRPLGAP
5726	2	480	TRMAGVTPCILGPLEAGLFFPGSGGVITL/ESVGAGIPGPSRAG
1	ł	1	QGSPGGSGEGPPLSSPSQPLPADLPGATLPDVGLELEVRPLAVT
1	i	1	QGSPGGSGEGPPGSSPSQFDFADDFGATDLDVOLLETAND
1	i	}	GLIFHLGQARTPPYLQLQVTEKQVLLRADDG
5727	21	221	RPILILKETRRLPWATGYAEVINAGKSTHNEDQASCEVLTVKKK
3,2,	1	1	AGAVTSTPNRNSSKRRSSLPNGE
	2	877	GTPNGOFEPRGRAWEGSAGGLRAPGAAAGGPGVQPRGSG/LPG
5728	1 4	011	NATDAGUNDGRGPASPFWDLSLPWDLWPPPTDHAPGAPDFPAVE
1		1	GR\PWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPG/SGGLSPSQ
l		1	GR/PWAGGRPPWPVSGVLGSRVCGFB1515116167,55555555 GGPAGAGGDAG/LPGRCPSAPWRAGSRPAASCPDW1PGPQGLWL
1		1	GGPAGAGGDAG/ DPGKCPSAPWKAGSKPAASCPDHII GPQGDMD
Į.	1	1	HRNPTS/GPPSQIGEGAEQGDEGVADAPQIQCKN/GAEDPPAED
i	į.	1	EPPQVPEAGEEDAVPABEGPGGTPETQADQVRERPEAHLAEGGA
	1		KGSPRRLADPQDLPAGQMSLAPPFPPVAAVIRSNK
		1525	AGGAREVLTLOLGHFAGFVGAHWWNQQDAALGRATDSKEPPGEL
5729	1	1525	CPDVLYRTGRTLHGQETYTPRLILMDLKGSLSSLKEEGGLYRDK
ì	ł	ı	QLDAAIAWQGKLTTHKEELYPKNPYLQDFLSAEGVLSSDGVWRV
1	İ	i	KSIPNGKGSSPLPTATTPKPLIPTEASIRVWSDFLRVHLHPRSI
1		1	KSIPNGKGSSPLPTATTPKPLIPTEASIRVASDF DRVIDER NOT
İ	1	Į.	CMIQKYNHDGEAGRLEAFGQGESVLKEPKYQEELEDRLHFYVEE
1	ł		CDYLQGFQILCDLHDGFSGVGAKAAELLQDEYSGRGIITWGLLP
1	1	1	GPYHRGEAQRNIYRLLNTAFGLVHLTAHSSLVCPLSLGGSLGLR
1	1	1	DEDDVSFPYLHYDATLPFHCSALLATALDTVTCS\YRLCSSPVS
l	1	1	MULLINADMI.SECGKKVVTAGAIIPFPLAPGQSLPDSLMQFGGAT
1	}	1	PWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTPGTPPPSA
1	i	1	LHACTTGEEILAQYLQQQQPGVMSSSHLLLTPCRVAPPYPHLFS
1	1	3	LHACTTGEETEAQTEQQQQFGVH5551111111111111111111111111111111111
{	· f		SCSPPGMVLDGSPKGAAVESVPVFG
5730	1258	1713	KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK
1	\ .	ļ.	LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWAT
ł		ì	KIETEGFWERPRNFENGGRPLKSPGGEDCPSC*GGCPGSNY*AQ
Į.	1	}	GSSSREKGGQASWNPKLRVA
L			RSHRGELIPKDSCYMRKPPRRPKKRRQG/CALPQGCLTFKDVAI
5731	122	443	EFSLEEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK
ļ.			ERSTERMCTMANGETTEN INTERIOR INTERIOR
l	ł	İ	KPGRGRGKQRRQEWFFLRVY
5732	226	772	PPSRSCQSPRRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF
1 2,32			PERTCSOLOGADWAPDEGPSSEVPSWGATATGARKFLIAFNI\N
1			LICTRECARRIAI,NI.REOGRGKDOPGRLKKVQGIGWYLDEKNLA
1		į	QVSTNLLDFEVTALHTVYEETCREAQELSLPVVGSQLVGLVPLK
1		1	1
1			ALLDAA
5733	1	460	PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES
	1		MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM
1	\	ŀ	AQVQYSMWVTRKNANYFANYDPRMKREGLHYVVIERDEKYM\AS
1	1		PDRI\VP\EFTGKMDEVLSRDPM
			PUNSPESITSLLVILLTANNLEVLIPAYSKNRAYAIFFIVFTVI
5734	3	968	GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFEVLS
1			SMVGEGGAPPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY
1	1	1	SWARREREN DE CAMANDA DE L'OCA CEL EC
1	į		GSVLLSAEEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG
i	1		HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC
ţ	j		VETVYYLLEMLLKVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS
	1		TL\VCTDCHTQAGGRRWW/RLLSLWEMTRMLNMLIVFRFLRIIP
1	1		SMKPMAVVASTVLGL
			FFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL
1		540	FFTPCVARAFNFPDQATVKKAAISLFKVGGGISCGDPQAKKISL
5735	2	1	
5735	2		ATPRQLYK/SSNMTQRWQRREISNFEYLMFLNTIAGRTYNDLNQ
5735	2		VEWERWILTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE
5735	2		VEWERWILTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE
5735	2		YPVFPWVLTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIELACLWY
5735 5736		382	VEWERWILTNYESEELDLTLPGNFRDLSKPIGALNPKRAVFYAE

SEQ	Predicted	Drodict	T
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	1.12.04441100
	location	corresponding	I Gracemic Acid, Febbenylalanina C-Cli
1	corresponding	to first	n=nibtidine. = solencine v=tooi==
J	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
			TARLSVTPPNLLPTVSFPOPDLPDNDVVSTTTDVLAGDLDAVV
5737			QES**ILPUSGIFIP*T*TSYLOSTTHI, PDAKT DOLL DO
3/3/	290	1041	KACLHLLSSFLTSNFLFNPLLPDSLVSVEAPSOPANI COCCAPUS
1 1			1 LY LINKLANGE UYSSHKDPSLSAKEKETDVINGA BCDWDOWNO
1 1			RIALGSCGRGPDGAHHPGPKSSSWRASRIJ.DGI.GGGUUI DA VIIC
1 1			LANDECGTPAPLOLETPPOPRGHPAPTPTGOAGDDDCCDGAGDAG
			LIKPLINGER*PGVRPVGWTPAHPACTI.PDDCAVPDCVCACCIU
5738	8	460	APSPISQUECEGREDAVPKHRAWRTPI.CSO
1		460	DTLSLNCTLPETLPMTPSF*LSFL*FPGLARAKSIPTKTYSNEV
1 1			VILWYRPPDILLGSTDYSTOIDMW*COVEVNOCDCCVCCCC
1 1			ATYPARTURITY PSDPRGVGCT FYEMATCP DI. POCCOMPROT TOP
5739	1	1222	TRI-SEEAWALCAVETHR
		1222	SFORRGIRWNVHTLHPHPRAVWAGIGRGHGS*ALLGRARAPALC
			FPT LEF DESLEPOLPALRAMGLHI.WARGPGTUDACTODI LABOR
į f			SAEVUGPVPGYLSSPOSITDTCLYTETSCTTCT.DVAADTCUT
1 1			LQCQGFYQLCGVHQEDVIYLALPLYHMSGSLLGIVGCMGIGATV
1 1	i		VLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAERG
! !			HKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINY TGORGAVGPASHI YMILEDEGY
1 1	i		TGQRGAVGRASWLYKHIFPFSLIRYDVTTGEFIRDPQGHCMATS PGEPGLLVAPVSQQSPFLGYAGGPELAQGKLLKDVFRPGDVFFN
			TRDLLVCDDQGFLRFHDRTGDPFRWKGENVATTEVAEVFEALDF
5740			LQEVNVYGVTV
5740	265	231	PAYWLKVPTLCLESKTDLREKASHVSAQLQGEVRGLAGALWM*A
			YVYERVYN*NISRMVHALEQKRHPAGLSSMALQLNPCLGMLMA
5741			1 DOSELRALIDEETQSWVSGSACGGVP
3,41	1	650	PRKTMRRGVLMTLLOOSAMTLPLWTGKPGDPPDDLCCATDAGGE
	ľ		I VARPGDKVAARVKAVDGDEOWILAEVVSVSHATNIKVBUDATDE
i	ĺ		EGKERHTLSRRRVIPLPOWKANPETDPEALFOKEOLULAL VDOM
1			TCF TRALIHAPPORPODDYSVLFEDTSVADGVCDDIAGRACHUST
5742	2	360	ACKEPKKK*CRLADSPSPNDTGODSPGPAGTVUIDDIVVV
1	- 1	362	TOSVKEILKRNPNVNLTDKDGNTALMIAGVECUTETUOD:
	1		1 1 VM I PDROGDTVLIGAVRGGHVETVRAT.T.OKVADIDIDGODDE
5743	2	415	IALIWAVEKGNATMVRDILOCNPDTETCTRDG
	ï .	417	GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMQTDL
ļ			RAIGREISPREKTPEVIDATEEIDKDLEETGEBEIGDER
. 1		•	VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE ISPOE
5744	3	703	ISPQE
}	J		TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA
İ			VFTTANTCLSLTPSTLPEEATGLLTPEPSKEGPILTAESETVLP
	İ		SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS
			PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV
		i	QHGREDEDGLFTL
5745	1400	599	GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM
1	1	ļ	KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT
1	İ	i	VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE
- 1		}	YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR
1		į	EKSEEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE
	1		
			KLKNRKEKKSRDVVSKKEERKRTKKKKEGGGEDWEERL
F20.5		j	KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI
5746	3		KUKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF
5746	3	821	LGF SFASGRLTPSSPAFDGELDLORYSNGPAVSAWSLGMGAVSWSBO
5746	3	821	LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHOPERPRSPARALLER
5746	3	821	ALKANKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMOATPATEGLARPODASSSARDOR
5746	3	821	ALKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAPRCP YCKGKFRTSABRERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPOPOPOPPPOPERPRSPARTE
5746	3	821	ALKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAPRCP YCKGKFRTSABRERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPOPOPOPPPOPERPRSPARTE
		821	ALKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAPRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV
	3	821	ALKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAPRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV
5746		1328	ALKARKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAPRCP YCKGKFRTSABRERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAAPEEPPAPPEFRCQVCGOSFTOSWFLKGMMPKUVA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
j	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		SDNGDINYDYVHELSLEMKRQKIQRELMKLEQENMEKREEIIIK
		\	KEVSPEVVRSKLSPSPSLRKSSKSPKRKSSPKSSSASKKDRKTS
	1	1	AVSSPLLDQQRNSKTNQSKKKGPRTPSPPPPIPEDIALGKKYKE
	į.	í	KYKVKDRIEEKTRDGKDRGRDFERQREKRDKPRSTSPAGQHHSP
	ļ		ISSRHHSSSSQSGSSIQRHSPSPRRKRTPSPSYQRTLTPPLRRS
	1		ASPYPSHSLSSPQRKQSPPRHRSPMREKGRHDHERTSQSHDRRH
į		Į.	ERREDTRGKRDREKDSREEREYEQDQSSSRDHRDDREPRDGRDR
	1		\ pr
	<u> </u>	473	SECPOVEYKGLAPTLIAIFPYAGLOFSCYSSLKHLYKWAIPAEG
5748	934	4/3	VVNENI ONI I CGSGAGVISKTLTYPLDLFKKRLQVGGFEHARAA
		1	FGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFM
			FFSYEFFCNVFHCMNRTASQR
	ļ	1	GRDVDPRVRGSTLSLAERPKGMIRSGSFRDPTDDVHGSVLSLAS
5749	552	1	CASCTVSSAFERMOSEOTRKLRRELESSOEKVATLTSQLSANAN
			1 1/1A FEOSI JUNITSRI RHLAETAEEKDTELLDLRETIDFLKKKN
	Ì	1	SEAQAVIQGALNASETTPKELRIKRQNSSDSISSLNSITSHSSI
		ì	GESKDADA
5750	22	866	IFISICLWNAHLCFLLLPKDCIDQVMKLQNLFVDDSGRYLAIQF
5/50	1 22		III.EWAYUELYVYEYRKAKDOLDIAKDISQLQIDLTGALGKRTRF
	1		OFNYVAOLILIDVRREGDVLSNCEFTPAPTPQEHLTKNLELNDDT
	}		TINDIKLADCEOFOMPDLCAEEIAIILGICTNFQKNNPVHTLTE
			VELLA ETSCLISOPKEWA IOTSAL ILRTKLEKGSTRRVERAMRQ
		1	TQALADQFEDKTTSVLERLKIFYCCQVPPHWAIQRQLASLLFEL
			CCTGGALOTERKI,EMME
5751	3	751	SCGSALRAWRCGAAALATFPAPALPGLMYRALYAFRSAEPNALA
J.J.		· I	FAAGETFLVLERSSAHWWLAARARSGETGYVPPAYLRRLQGLEQ
	1		DVLQAIDRAIEAVHNTAMRDGGKYSLEQRGVLQKLIHHRKETLS
	1	i	RRGPSASSVAVMTSSTSDHHLDAAAARQPNGVCRAGFERQHSLP
	1	i	SSEHLGADGGLFQIPLPSSQIPPQPRRAAPTTPPPPVKRRDREA
	Ì		LMASGSGGHNTMPSGGNSVSSGSSVSSCI
5752	3	471	GPVCGVGLSVAWAGPWRGPVHSVGGGGRAALHGAELPCLSGAAT VEREMELRHKNEMLRVETEARARAKAERENADIIREQIRLKASE
		ı	VEREMELRHKNEMLRVETBARARARAERENADITREGIKDADO HRQTVLESIRTAGTLFGEGFRAFVTDRDKVTATVNIFIKQGWQV
	}	ł	HROTVLESIRTAGT_FGEGFRAFVIDRDRVIATINITINGONG
	,		AEROHVGASWSPRSCPCRLCTAL DDSXAIPGGVQAPFGAVRNIYTPRTGHRIRKLDQIQSGGNYVAG
5753	34	483	GQEAFKKLNYLDIGEIKKRPMEVVNTEVKPVIHSRINVSARFRK
	1	1	PLQEPCTIFLIANGDLINPASRLLIPRKTLNQWDHVLQMVTEKI
1]		TLRSGAVHRLYTLEGRLV
			TLVHVVEFAGEHAEAIASREQEVLQGWKELLSACEDARLHVSST
5754	14	331	ADALRFHSQVRDLLSWMDGIASQIGAADKPRCPSSLLGLPASPW
1		1	WPTPATPSPLTAPFSME
			I COORVEE TEHCES YNSRLCAERS VRLPFLDSQTGVAQNNCYI
5755	3	888	WMEKRHRGPGLAPGQLYTYPARCWRKKRRLHPPEDPKLRLLEIK
1			PEVELPLKKDGFTSESTTLEALLRGEGVEKKVDAREEESIQEIQ
1		ł	RVLENDENVEEGNEEEDLEEDIPKRKNRTRGRARGSAGGRRRHD
i	l	1	
			ARCORDUDY PYUCDI CGKRYKNRPGLSYHYAHTHLASEEGDEAQ
			AACOEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ
			AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ DQETRSPPNHRNENHRPQKGPDGTVIPNNYCDFCLGGSNMNKKS GPDFFLYSCADCGRSAHLGGEGRKEKEAAA
		621	AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ DQETRSPPNHRNENHRPOKGPDGTVIPNNYCDFCLGGSNMNKKS GRPEELVSCADCGRSAHLGGEGRKEKEAAA GEVENLANDELVNVPEEPPLLGAEDSLLASQEALRYYRRKVAR
5756	3	621	AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ DQETRSPPNHRNENHRPOKGPDGTVIPNNYCDFCLGGSNMNKKS GRPEELVSCADCGRSAHLGGEGRKEKAAA SSKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR
5756	3	621	AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ DQETRSPPNHRNENHRPOKGPDGTVIPNNYCDFCLGGSNMNKKS GRPELIVSCADCGRSAHLGGEGRKEKAAA SSKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR GERWAGKLODMRHFPTISADYSQDEKALLGACDCTQIVKPSGV
5756	3	621	AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ DQETRSPPNHRNENHRPOKGPDGTVIPNNYCDFCLGGSNMNKKS GRPELIVSCADCGRSAHLGGEGRKEKAAA SSKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR GERWAGKLODMRHFPTISADYSQDEKALLGACDCTQIVKPSGV
5756	3	621	AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ DQETRSPPNHRNENHRPQKGPDGTVIPNNYCDFCLGGSNMNKKS GRPEELVSCADCGRSAHLGGEGRKEKEAAA SSKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR SSPVVSKLLQDMRHFPTISADYSQDEKALLGACCTQIVKPSGV HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI AAEH DEILDERBYPPTVGRIVNVTKEIL
			AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ DQETRSPPNHRNENHRPQKGPDGTVIPNNYCDFCLGGSNMNKKS GRPEELVSCADCGRSAHLGGEGRKEKEAAA SSKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR SSPVVSKLLQDMRHFPTISADYSQDEKALLGACDCTQIVKPSGV HLKLVFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI AAFHLDRILDFRRVPPTVGRIVNVTKEIL
5756 5757	3	621	AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ DQETRSPPNHRNENHRPOKGPDGTVIPNNYCDFCLGGSNMNKKS GRPEELVSCADCGRSAHLGGEGRKEKEAAA SSKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR SSPVVSKLLQDMRHFPTISADYSQDEKALLGACDCTQIVKPSGV HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI AAFHLDRILDFRRVPPTVGRIVNVTKEIL YKDALLLPDNHRQVVFENGTLKLTDVQKGMDEGEYLCSVLIQPQ
			AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ DQETRSPPNHRNENHRPOKGPDGTVIPNNYCDFCLGGSNMNKKS GRPEELVSCADCGRSAHLGGEGRKEKEAAA SSKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR SSPVVSKLLQDMRHFPTISADYSQDEKALLGACDCTQIVKPSGV HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI AAFHLDRILDFRRVPPTVGRIVNVTKEIL YKDALLLPDNHRQVVFENGTLKLTDVQKGMDEGEYLCSVLIQPQ
			AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ DQETRSPPNHRNENHRPOKGPDGTVIPNNYCDFCLGGSNMNKKS GRPEELVSCADCGRSAHLGGEGRKEKEAAA SSKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR SSPVVSKLLQDMRHFPTISADYSQDEKALLGACDCTQIVKPSGV HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI AAFHLDRILDFRRVPPTVGRIVNVTKEIL YKDALLLPDNHRQVVFENGTLKLTDVQKGMDEGEYLCSVLIQPQ LSISQSVHVAVKVPPLQPGPFPPPASIGQLLYIPCVVSSGDMPI RITWRKDGQVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCI
5757	3	473	AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ DQETRSPPNHRNENHRPOKGPDGTVIPNNYCDFCLGGSNMNKKS GRPEELVSCADCGRSAHLGGEGRKEKAAA SSKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR SSPVVSKLLQDMRHFPTISADYSQDEKALLGACDCTQIVKPSGV HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI AAFHLDRILDFRRVPPTVGRIVNVTKEIL YKDALLLFDNHRQVVFENGTLKLTDVQKGMDEGEYLCSVLIQPQ LSISQSVHVAVKVPPLIQPFEFPPASIGQLLYIPCVVSSGDMPI RITWRKGQVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCI ASNAAATVSRERQLIVRVPPRFVV
	3		AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ DQETRSPPNHRNENHRPOKGPDGTVIPNNYCDFCLGGSNMNKKS GRPEELVSCADCGRSAHLGGEGRKEKEAAA SSKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR SSPVVSKLLQDMRHFPTISADYSQDEKALLGACDCTQIVKPSGV HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI AAFHLDRILDFRRVPPTVGRIVNVTKEIL YKDALLLPDNHRQVVFENGTLKLTDVQKGMDEGEYLCSVLIQPQ LSISQSVHVAVKVPPLIQPFEFPPASIGQLLYIPCVVSSGDMPI RITWRKDGOVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCI

Mot Motelectide location Corresponding to first Control	SEQ	Predicted beginning	Predicted end nucleotide	
corresponding to first amino acid residue of amino acid acid acid acid acid acid acid acid	NO:	nucleotide	1	In-nighting, C=CVsreine Dalamarkie Naid Dalamarkie Naid Dalamarkie Naid Dalamarkie Naid Dalamarkie Naid Dalamarkie Naid Dalamarkie Naid Dalamarkie Naid Dalamarkie Naid Dalamarkie Naid Dalamarkie Naid Dalamarkie Naid Dalamarkie Naid Dalamarkie Naid Dalamarkie Naid Dalamarkie Naid Dalamarkie Naid Dalamarkie Naid Dalamarkie Dalamar
Lofirst amino acid residue of amino acid residue of amino acid amino acid sequence and acid amino acid acid acid acid acid acid acid acid	1			H=Histidine T-Teclevation To G=Glycine,
maino acid maino acid and coid sequence and coid	1	corresponding		L=Leucine, M=Morbionine, K=Lysine,
residue of amino acid anino acid sequence Sequence 1240 1240 1240 12559 2 1240 1240 12502 1240 12503 1240 12503 12503 12503 12503 12603 127	1			P=Proline, O=Glutamine, N=Asparagine,
amino acid sequence codom, /-possible nucleotide deletion (Appossible nucleotide deletion) (Appossible nucleotide insertion) (Appossible nucleotide insertion) (Appossible nucleotide insertion) (Appossible nucleotide insertion) (Appossible nucleotide insertion) (Appossible nucleotide insertion) (Appossible nucleotide insertion) (Appossible nucleotide insertion) (Appossible nucleotide insertion) (Appossible nucleotide insertion) (Appossible nucleotide insertion) (Appossible nucleotide) (Appossible nucleotid			residue of	S=Serine, T=Threonine, V=V=1:==
Sequence Sequence Sequence Sequence Septiment Septimen			1	W=Tryptophan, Y=Tyrosine Y-Unknown +-Ob-
SSEGLIVICEDESSIVE/FITPROFITP SSSILVIVICEDESSIVE/FITPROFITP GRAFARGOGVVYETFIRISDLPSYTINGTVHUVUNNGIGETTDE RUSSSYPTDUAGNUNAD INTUNDOMA THE STATE OF			sequence	Codon, /=possible nucleotide deletion
SSGLIVGEBOSYLEFOTTPPKIEV SSGLIVGEBOSYLEFOTTPPKIEV SSGLIVGEBOSYLEFOTTPPKIEV AMASSYPTDUARVWARD I PHYNADDERAY I YUCS VAARBENTY NDUOGADLUCK PREKRIGHNENDE PHYPOLINK YN HOLVOGADLUCK PREKRIGHNENDE PHYPOLINK YN HOLVOGADLUCK PREKRIGHNENDE PHYPOLINK YN HOLVOGADLUCK PREKRIGHNENDE PHYPOLINK YN HOLVOGADLUCK PREKRIGHNENDE PHYPOLINK YN HOLVOGADLUCK PREKRIGHNENDE PHYPOLINK YN HOLVOGADLUCK PREKRIGHNENDE PHYPOLINK YN HOLVOGADUCK PROMOTO TO THE COLOR OF THE PROMOTO THE COLOR OF THE PROMOTO THE COLOR OF THE PROMOTO THE COLOR OF THE PROMOTO THE COLOR OF THE PROMOTO THE COLOR OF THE PROMOTO THE	 	sequence		\=Possible nucleotide insertion\
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FERSORARVNTENGESPOLOIPYUDSCRHILEDSCAELGESK EIMESRAVTETEETQEKKAESKEPIEEEPTGAGLINKDKETEERT DGERVABVAPERERNVATKILGESQFGNAVIDKETIDLLAFTSV AELELLGLEKLKCEIMAGLKCGGTLQ STGQYPLHSQGGGGGGGRRATPRGMPKEKYEPPDPRRMYTT MSSEEAANGKKSHWAELEISGKVRSLSASLWEITHLTALHLSDN SLSRIPSDIAKLHNLVYLDLSSNKUR LDVNDNVPTFOKDAYVGALGRETTITLARDGGGETGRVRINV LDVNDNVPTFOKDAYVGALGRENEPSVTQLVRLRATDEDSPPNNQ ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL TVMANDAGN 5764 19 441 VCARACGEMROLLRPIDRQRYDENEDLSDVERIVSVRGFSLEEK LESQLYQGDFVHAMEGKDFNYEYVQREALRVPLIPREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE TPEAQRDKL 5765 3 825 OKILRINMSHQPFTSSSNSKDCGGPASSGAGATAALADGLKFAS VQASAPQGNSHKETSKSKVKRSKTSKDANKSLJSSALYGIPBIS STGKRQBVQGRRGEATGMSALGGSVSSGGSNPNSTSTSTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHONGSGSQAPSGGHLYGPGAKSNGGGSSPFHCGGTGSGSVADA GEVSKSAPDSGIMGNSMLVKEEEEEESHRRIKKKKKKKKKKKKKLKTEKVDPLF TVPAPPPHV 5766 1608 663 GGESVDPASSQAMBLSDVTLIEGVGNEVMVVAGVVULILALVI. AWLSTYVADSGSNQLLGATVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKABEAGGGGGSTCEAGAGGGVEPSLEHLLD LGLJFKRQAGAGSSS PEARLRSEDSTCLPPSPGLITVRIKFLND TEELAVAR PEDTVGALKSKYFFGQESQMKLIYQGRLQDPARTL RSLNITIDNCVLHCHKSPPGSAVPGPSASLAPSATEPPSLGVNVG SLNWYPVVLVLIGVWWYFRINNYGFFTAPATVSLVGVTVFPSFLV FGMYGR NFRATFRPPTRPELRTGTEVILWILDWRAIMKKKRMKANIKLVG SGFPLPSSDLDDSITEEIDEKIGFRDDAMPDWONVARPERDACGG	i			GUQAASSKUVSAEISENRKROWPTKSOTDPGASAGVDDGBUY CM
EIMESRAWTETEETOEKKARSKEPIERE PTGAGLIKDKETEERT DGERVARVAPEERENVAVAKLQESQPGNAVIDKETIDLLAFTSV ARLELLGLEKLKCEIMAGLKCGGTLQ STGQTPLHSQGGGGGGGGGGGRETPERGMPKEKYEPPDPRRMYTT MSSEEAANGKKSHWAELEISGKVRSLASLWSLTHLITAHLISDN SLSRIPSDIAKLHNILVYLDLSSKKIR LDKDTGLIMLITARLDYELIGRFTHIITARDGGGETTGRVRINV LDVNDNVPTFQKDAYVGALRENEPSVTQLVRLRATDEDSPPNNQ ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDVEQISNGLIYL TYMANDAGN 5764 19 441 VCARAGGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK LRSQLYQGDFVHANEGKDFNYSVQREALRVPLIFREKDGLGIK MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSOFVRYYE TPEAQRDKL 5765 3 825 QXILRINNSHQPPTSSSNSKDCGGPASSGAGATAALADGLKFAS VQASAPQGNSHKETSKSKVKRSKTSKDAMKSLSSAALYGIPEIS STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSNSTSTSTS AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ GHQMSGSGAPSGGHLVGFGAKSNGGASPFHGGGTGSGSVAAA GEVSKSAPDSGLMGNSMLVKKEEEEESHRRIKKLKTEKUPPLF TVPAPPPHV 5766 1608 663 SGLFSUDPASSQAMBLSDVTLIEGVGNEVMVVAGVVULILALVI. AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGSGROSTGEAGAGGGVEFSLEHLLD AWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE PTELPHPSEGNDEKAEEAGSGROSTGEAGAGGGVEFSLEHLLD CQLPKRQAGASSSPEPPLRSEDSTCLPFSPGLITVRLKFLND TESLAVARPEDTVGALKSKYFFGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMPVEVVLLGVWWYFRITNYRQFFTAPATVSLVGVTVFFSFLV FGMYGR NFRATPRPPTRPELRTGTEVILWYLDWRAIMKRKMKKANIKLVG SCFPLESSDLDDSLTTEEIDEKLGFRNDANPDWONVADPEDAGGG	1	1		COLDIAEGSNSESSDDDSEEAPSTSGMGFHADVICONOUTER PARTY
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			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	H=H1SC1dine, 1=1Soleucine, R=Dysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	1	bequeine	\=possible nucleotide insertion)
	sequence	<u> </u>	HIDEFFTLNSTPSRSAYDEPHLLVNIEKQKLELEKRRLDIEAER
		1	LQVEKERLQIEKERLRHLDMEHERLQLEKERLQIEREKLRLQIV
	1	1	NSEKPSLENELGQGEKSMLQPQDIETEKLKLERERLQLEKDRLQ
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		1	FLKFESEKLQIEKERLQVEKDRLRIQKEGHLQ
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	l	1	AAMVAKDYPFYLTVKRANCSLELPPASGPAKDAEEPSNKRVKPL
		1	SRVTSLANLIPPVKATPLKRFSQTLQRSISFRSESRPDILAPRP
	1	1	WSRNAAPSSTKRRDSKLWSETFDVC
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	1		AKGGRLLLADDMGLGKTIQAICIAAFYRKEWPLLVVVPSSVRFT
	1		WEQAFLRWLPSLSPDCINVVVTGKDRLTA
		741	GLLPSACLRARSWREASEGPSSRACSNGSQUTFEACYSGTSTPS
5771	168	741	FHGSHCSGSDHSSLGLEQLQDYMVTLRSKLGPLEIQQFAMLLRE
		l .	FHGSHCSGSDMSSLGBEQLQDIMVIDGSKBGFBBTQQTFMBBKS
			YRLGLPIQDYCTGLLKLYGDRRKFLLLGMRPFIPDQDIGYFEGF
	l l		LEGVGIREGGILTDSFGRIKRSMSSTSASAVRSYDGAAQRPEAQ
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]],,2		1	ILTFSNLVTCSAIYHLPVFPEREPGCSMRDLRVA
	2	723	PRVRSKHNFCFMEMNTRLQVEHPVTEMITGTDLVEWQLRIAAGE
5773	1 2	1 /23	KIPLSQEEITLQGHAFEARIYAEDPSNNFMPVAGPLVHLSTPRA
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5777	2	949	VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSORVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV
5777	2	949	VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR
5777	2	343	VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE
5777	2	949	VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE DLLOSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP
57 77	2	949	VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE
57 77	2	949	VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKRFRTFKHAGEGDKDGKPGIGFRKEKR NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ NSZRRNV
			VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKRFRTFKHAGEGDKDGKPGIGFRKEKR NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ NSZRRNV
5777	2	1210	VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ NSERRNV OPROSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS
			VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ NSERRNV QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS GGPCWLOLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP
			VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKPRTFKHAGEDKDGKPGIGFRKEKR NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ NSERRNV QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP WAPLGAPERPEHLLNRVLERLAGGATRDSAASDILLDDIVLTHS
			VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKPRTFKHAGEGDKDGKPGIGFRKEKR NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ NSERRNV QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP WAPLGAPERPEHLLNRVLERLAGGATRDSAASDILLDDIVLTHS LFLPTEKFLOELHQYFVRAGGMEGPEGLGRKQACLAMLLHFLDT
			VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKRRTFKHAGEGDKDGKPGIGFRKEKR NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE DLLQSSSESSRVDWYAQTKLGITRTLSEENVYEDILDPPMKENP YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ NSERRNV QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP WAPLGAPERPEHLLNRVLERLAGGATRDSAASDILLDDIVLTHS LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKQACLAMLLHFLDT YOGILOEEEGAGHIKDLYLIMKDESLYGGLREDTLRLHQLVE
			VKKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKPRTFKHAEGDKNGKPGIGFRKEKR NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ NSERRNV QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP WAPLGAPERPEHLLNRVLERLAGGATRDSAASDILLDDIVLTHS LFLPTEKFLQELHQYFVRAGMEGPEGLGRKQACLAMLLHFLDT YQGLLQEEEGAGHIKDLYLLIMKDESLYQGLREDTLRLHQLVE TVELKIPEENOPPSKOVKPLFRHFRRIDSCLQTRVAFRGSDEIF
			VKKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKPRTFKHAGEGDKDGKPGIGFRKEKR NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ NSZRRNV QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP WAPLGAPERPEHLLNRVLERLAGGATRDSAASDILLDDIVLTHS LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKQACLAMLLHFLDT YQGLLQEEEGAGHIIKDLYLLIMKDESLYQGLREDTLRLHQLVE TVELKIPEENQPPSKQVKPLFRHFRRIDSCLQTRVAFFRGSDEIF CRWYMPDHSYVTIRSRLSASVQDILGSVTEKLQYSEEPAGREDS
			VKKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV YRGSEGSPTKPFINPLPKRRTFKHAGEGDKDGKPGIGFRKEKR NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE DLLQSSSESSRVDWYAQTKLGITRTLSEENVYEDILDPPMKENP YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ NSERRNV QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP WAPLGAPERPEHLLNRVLERLAGGATRDSAASDILLDDIVLTHS LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKQACLAMLLHFLDT YOGILOEEEGAGHIKDLYLIMKDESLYGGLREDTLRLHQLVE

SEQ	Predicted	Predicted end	Design of the second of the se
αī	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, P=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine
1	residue of	amino acid	W=Tryptophan, Y=Tvrosine, X-Unknown + St
1	amino acid sequence	sequence	Codon, /=possible nucleofide deletion
	aedgeuce	ļ	\=possible nucleotide insertion\
1	1	1	PLPEEIQVSPGDTEIHRVEPEDVANHLTAFHWELERCOURTERY
5779	138	 	DIVENCE
	130	1571	EAVQVLIKHSADVNARDKNWQTPLHVAAANKAVKCAEVIIPLLS
İ			SVNVSDRGGRTAUHHAALNGHVEMVNLLLAKGANTNAFDVKDDD
İ			ALHWAAYMGHLDVVALLINHGAEVTCKDKKCVTDI.UAAACNCCT
			NVVKHLLNLGVEIDEINVYGNTALHIACYNGQDAVVNELIDYGA
1	1	1	NVNQPNNNGFTPLHFAAASTHGALCLELLVNNGADVNIQSKDGK
1	}	<u> </u>	SPLHMTAVHGRFTRSQTLIQNGGEIDCVDKDGNTPLHVAARYGH
	Ì		ELLINTLITSGADTAKCGIHSMFPLHLAALNAHSDCCRKLLSSG
1	ł	l	QKYSIVSLFSNEHVLSAGFEIDTPDKFGRTCLHAAAAGGNVECI
İ			KLLQSSGADFHKKDKCGRTPLHYAAANCHFHCIETLVTTGANVN ETDDWGRTALHYAAASCMDDANKTAL
l			ETDDWGRTALHYAAASDMDRNKTILGNAHDNSEELERARELKEK EATLCLEFLLQNDANPSIRDKEGYNSIHYAAAYGHRQCLELLLE
	<u> </u>		RTNSGFEESDSGATKSPLHLAVSEMP
5780	154	624	QFFRVITCLPFKGPDYRLYKSEPELTTVAEVDESNGEEKSEPVS
ł			EIETSVVKGSHFPVGVVPPRAKSPTPESSTIASYVTLRKTKKMM
			DURTERPRESAVEQUELAESTRPRMTVEEOMERIPPHCOACLERY
5781	10-		KKGLNVIGASDQSPLOSPSNLRDNP
3,01	19	941	RGSLGGHPWRPPMRAASOGCLPVSFVTGPHOEDAVCCDCCAE
	i i		PAPPVSGTCPPDLIYAPTPEKAEGGSOKNHODDDGEDAAUDDGD
			QAPCRAGPTRKVAVAPRPPSCP*GPE\PGERDPPDT.DBCDDT.CO
1			VQPHFTSQDAKSAEDEAPSRHLGKHOPZSAOVGCDI DAY OGDVM
İ	i l		QHSIHTVTCKSPROKEDRSPKPPOAPKHPEPUGPOG\ OADDDE =
ļ			VAPSRTCGGC*TWDPALLVSP/PQGDSTPELPAP\QQPTGGPSR
			CRQALPPQG*RQQPRQRPR/PTGASRSHPAKAKGCQGPPKIRNY
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE
	1		PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV
1 1			SQPEPPVSQSEISEPSAVPTDYSVSASDPSVIVCTAAVTUDEDD
1 1	1		PEPESSITLTPVESAVVAREHEVVPRRPVTCMVQETDAMCARDO
1			VLASEPPVMSETAETFDSMRASGHVASEVSTSLI.VDAMTTDVA A
]]			ESILEPPAMAAPESSAMAVLESSAVTVI,ESSTUTVI,ESSTUTVI
1 1			ESSVVIVPEPPVVAEPDYVTIPVPVVSALEPSVDVI PPAVEIRO
			PSMIVSEPSVSVQBSTVTVSEPAVTVSEOTOVIDTEVATEGERIA
1			1DESSIMSSAVMKGINLSSGDONLADETCMOETALUCCEEDUS D
1 1	1		EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE
1			IGEEKILPTSETKORTVLDTYPGVSEADAGETLSSTGPFALEPD
1 1			ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ
1 1	1		TLAALI \SLKESSGGEKEVDDDQ+DEUT DDCGEGAATHED TOOL
			LVRPVSSPRTWNVLPSPRAGI, EGP LLASDEGRUON VGGDTER
		İ	\SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG
i i			EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESPSDADVDCGVGVC
		!	HKS \QTRSRSRS/RDRRRRSSRSRSKSRGDDGUGVEVEVEVENDOR****
1		ļ	KSKSKERKRKRSSSRDNRKTVRARSRTDSDPCDCUTDCDDDCD
			SVGRRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRPSPRSPRS
]		į	RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLPRSPTDI PRPR
1		1	RSPIRRKRSRSSERGRSPKRLTDLDKAOLLETAKANAAAMCAKA
- 1	}		GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKOTAGOVE
,	!	!	DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK
ľ		į	PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN
1		1	KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI
- 1		1	KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV
-	ľ	j	DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN
I		ļ	KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR
E202			Y
5783	1693	698	DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM
ľ	1	j '	QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDUVPGUNO
1		1	KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEVGGERGT
			NDLIEE/PI*SQ/PKILFQQP/LILKVALNMARGLKYLHQEKKL
•			

SEQ Predicted Predicted end beginning nucleotide nucleotide location corresponding to first amino acid residue of sequent containing signal product (A=Alanine, C=Cysteine, D=Aspartic Acid, F=Phenylalanine, G=Glyc H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,	d, E=
NO: nucleotide location corresponding to first amino acid project of the corresponding to first amino acid project amino acid pr	cine,
location corresponding to first amino acid personal corresponding to	1
location corresponding to first L=Leucine, M=Methionine, N=Asparagine, to first amino acid p=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,	
corresponding to first L=Leucine, M=Methionine, N=Asparagine, to first amino acid P=Proline, Q=Glutamine, R=Arginine, residue of S=Serine, T=Threonine, V=Valine,	
to first amino acid P=Proline, Q=Glutamine, R=Arginine,	
amino acid residue of S=Serine, T=Threonine, V=Valine,	
amino acid residue of S=Serine, T=Threonine, V=Valine,	ì
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknown,	t≂Stop
1 = = = = = 1	- !
amino acid sequence Codon, /=possible nucleotide deletion,	'
sequence \=possible nucleotide insertion)	
LHGDIKSSNVVIKGDFETIKICDVGVSLPLDENMTVTI	OPEACYI
GTEPWKPKEAVEENGVITDKADIFAFGLTLWEMMTLS:	PHINLS
GIBPWAR KEAVEMOVI I JOHN DELIMENT DE	PUNCTE
NDDDDEDKTFDESDFDDEAYYAALGTRPPINMEELDES	PIÓKATE
LFSVCTNEDPKDRPSAAHIVEALETDV	
5784 2669 1388 PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQME	KDKVKIH
5784 2669 1388 PRVRPRVRTDHN1115K1IGF5DSASKDLWVX1DQHSL GILSNTHRQAARVNLSFDFPYGHFLREITVATGGFI	VTGEVVH
GILSNIHRQAARVNISFDFFFIGHFIGHT	ONDIAMI.
RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVV	DMDHAHP
QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQISS'	TNHPVKV
GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITI	NISAVEM
TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFI	MUDGRAU
TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGF	occet or
VDSGCPEESKEKMCENTEPVET\FLEPPQP*ERQPPS:	2G2.TLL
E/DAVTSOFPTSLPTEDDTKIALHLKDNGASTDDSAA	EKKGGTL
HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFF	IERRPSR
INACLI VALIDILA DI VALADINA PER	
WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC	******
5785 2669 1388 PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQME	KDKAKIH
GILSNTHROAARVNLSFDFPFYGHFLREITVATGGFI	YTGEVVH
RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVV	OMDHAHP
QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQISS'	TNHPWK
QDNYNLGSFTFQATBLMDGR11FGIREIFVBV19255	774777 ATCA
GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKIT	NISAVEM
TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGF	DRHRQDW
VDSGCPEESKEKMCENTEPVET\FLEPPQP*ERQPPS	SGS*LPP
B/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAA	EKKCCTI.
K/DAVISQEPISEPIEDDIKIAHHMAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	COORDINA
FAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFF	IERRPSR
WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC	
The same of the sa	QM*SGTP
5786 2532 1674 SYKLPAAERRASSCSQPPTPTRRRWFAPGKTSKSHKP APRPPARSTVSPASPLPKPRAGRCGSRPRSACSTFRP	C*SIN*M
APRIPARS I VOFASE DE REPORTE DOCUMENTOS TIMOS	אַגשיים זמ
S+H+KRNLSQRSSSMSRRPLSCARPHR**RQGLTVAA	REPIWAR
SPPLACSFCQAAQKSQSLSSGRSTR*PERMSFRP\SP	PGNPATE
SLAPSSRP/PKGRPQCTWIPSRWPASPTAPPTTT*AP	TSSPGST
GRSMMTCPTRWTATPWSARASSRPRNWPTP+WRPSGR	LSTV*RA
TGGSTATAPPKRFPRNWNPMMAE	
TGGSTATAPPARFPRINMIPHINAE	
5787 2 1460 MASAASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HK	MECKACE
T\RYCEIP\GPD\LEESP\TCP\LCKEPFRP\GSFRF	NWQLANV
VENIERLQLVSTLGLGEEDVCQEHGEKIYFFCEDDEM	IQLCVVCR
EAGEHATHTMRFLEDAA\APYREQIHKCLKCLIKERE	RIOEIOS
ENDERALITIEST OF THE PROPERTY	7.7.707.75
RENKRMQVLLTQVSTKRQQVISEFAHLRKFLEEQQSI	
QDGDILRQRDEFDLLVAGEICRFSALIEELEEKNERE	WKRPPID
IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQQALPI	Qremkmf
LEKLCFELDYEPAHISLDPQTSHPKLLLSEDHQRAQE	SYKWQNS
PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGS	CTVGVVS
PUNPQRFDRATCVIARIGITS ACCESS TO THE PUNPQRFDRATCO	T.TT.EFOD
EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TR	THE STATE OF
RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVI	CALROTMG
RGSSFSLSS	
TOTAL STREET, TO	CHOEGDG
5788 2 6860 EHSVSGRSSAYGDATAEGHPAGPGSVSSTGATSTT	DMAGGAD
SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQI	TOTA A GO A K
AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAEI	-GWDKKDA
SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICE	ESSSLISS
ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVA	ATSOLLKP
HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMV	T.PI.PVOT
HTTSSPPDMSPFFLKQIVKGHAADVFEAIIQLILEHV	OMETAT.
KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRF	COAKKTPP
FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFI	LRASVVTA
SPQSALQYDTLISLMEHLKACAEIAAQRTINWQKFC	KDDSVLY
FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAAS	SARREBRA
FLIQVSFLVDEGVSPVLIQUISCALCGSKVBRAHAA	200000000
SSPAPVAASSQATTQSKSSTKKSKKBEKEKEKDGET	いってっておりて
I.CTALVNOLNKFADKETLIOFLRCFLLESNSSSVRWQ	DAHCLTLH
	LLGYFSLK
	W COT 1777
IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDI	
TPOTEKKIKEYSOKAVEILRTONHILTNHPNSNIYN	LUSGUVEL
TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNT	LÖÖAAKTT
TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNT DGYYLESDPCLVCNNPEVPPCYIKLSSIKVDTRYTTT GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIV	AETKNK by LÖÖAAKTT
TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNT DGYYLESDPCLVCNNPEVPPCYIKLSSIKVDTRYTTT GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIV	AETKNK by LÖÖAAKTT
TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNT	raenkoys Netknkby Löönakpi

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Transport Sequent Containing Signal Bontial
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
i			LCNACGFCKYARFDFMLYAKPCCAVDPIENEEDRKKAVSNINTL
1			LDKADRVYHQLMGHRPQLENLLCKVNEAAPEKPQDDSGTAGGIS
i		!	STSASVNRYILQLAQEYCGDCKNSFDELSKIIQKVFASRKELLE
ł			YDLQQREAATKSSRTSVQPTFTASQYRALSVLGCGHTSSTKCYG
i	l l		CASAVTEHCITLLRALATNPALRHILVSQGLIRELFDYNLRRGA
	İ		AAMREEVRQLMCLLTRDNPEATQQMNDLIIGXVSTALKGHWANP
l	1]	DLASSLQYEMLLITDSISKEDSCWELRLRCALSLFLMAVNIKTP
1	1	1	VVVENITLMCLRILOKLIKPPAPTSKKNKDVPVEALTTVKPYCN
1	Ī		EIHAQAQLWLKRDPKASYDAWKKCLPIRGIDGNGKAPSKSELRH
			LYLTEKYVWRWKQFLSRRGKRTSPLDLKLGHNNWLRQVLFTPAT
1			QAARQAACTIVEALATIPSRKQQVLDLLTSYLDELSIAGECAAE
1			YLALYQKLITSAHWKVYLAARGVLPYVGNLITKEIARLLALEEA
1	[TLSTDLQQGYALKSLTGLLSSFVEVESIKRHFKSRLVGTVLNGY
		}	LCLRKLVVQRTKLIDETQDMLLEMLEDMTTGTESETKAFMAVCT
1		l	STAKRYNLDDYRTPVFIFERLCSIIYPERNEVTEFFVTLEKDDO
· }	1		QEDFLQGRMPGNPYSSNEPGIGPLMRDIKNKTCODCDLVALLED
	1		DSGMELLVNNKIISLDLPVAEVYKKVWCTTNEGEDMDTUVDMDC
	.]		LLGDATEEFIESLDSTTDEEEDEEEVYKMAGVMAOCGGLECMLN
1	1		RLAGIRDFKQGRHLLTVLLKLFSYCVKVKVNROOLVKLEMNTLN
I	j		VMLGTLNLALVAEQESKDSGGAAVAEOVLSIMET\TOAFDNUFD
			LSEDKGNLLLTGDKDQLVMLLDQINSTFVRSNPSVLCGLLRIIP
İ]		YLSFGEVEKMQILVERFKPYCNFDKYDEDHSGDDKVFL\DCFCK
	1 1		IAAGIK\NNSNGHQL\KDL\ILQKGITQNALD\YMKKHIP/SAA
1	ĺ		RIWDADI\WKSFCLRPALPFILRLLRGLAIQHPGTQVLIGTDSI
ł	1 !		PNLHKLEQVS\SDEGIGTLA\ENL\LESLREHPDVNKKIDA\AR
			RETRAEKKRMAMAMRQKALGTLG\MTTNEKGQVVD/TRTALLEA
	1		DWEELIEEP\GLTCCICREGYKFQPTKVLGIYTFTKRVVLGGVW
1	1		ENKPRETSRATSTVSHFNIVHYDC\HLA\AVSLARGREEWESAA LQNANTKCNGLLPVWGPHVPESAPATCLARHNTYLQECTGQREP
İ	1 1		TYQLNIHDIKLLFLRFAMEQSFSADTGGGGRESNIHLIPYIIHT
	<u> -</u>		GLYVLNTTRATSREEKNLQGFLEQPKEKWVESAFEVDGPYYFTV
1	l j		LALHILPPEQWRATRVEILRRLLVTSQARAVAPGGATRLTDKAV
ŧ	l i		KDYSAYRSSLLFWALVDLIYNMFKKVPTSNTEGGWSCSLAEYIR
	1		HNDMPIYEAADKALKTFQEEFMPVETFSEFLDVAGLLSEITDPE
			SFLKDLLNSVP
5789	1	2407	LPLHAVEKTGRPGQPALKMPGKLRSDAGLESDTAMKKGETLRKQ
1			TEEKEKKEKPKSDKTEEIAEEEETVFPKAKQVKKKAEPSEVDMN
			SPKSKKAKK\KEEPSONDISPKTKSLRKKKEPTEKKIJISGUTUU
	ľ		VTKNEEPSEEEIDAPKPKKMKKEKEMNGETREKSPKLKNGFPHP
			EPDCNPSEAASEESNSEIEOEIPVEOKEG\AFSNFPTSFFTTVI
	1	Ĭ	LKGRGVTFLFPIQAKTFHHVYSGKDLIAOARTGTGKTEGENIDI
	i		1EKLHG\ELQDRKRGRAPOVLVLAPTRELANOVSKDESDITEVET
1 1	ì	ļ	SVACFYGGTPYGGQFERMRNGIDILVGTPGRIKDHTONGKLDLT
1	•	1	KLNHVVLDEVDQMLDMGFADOVEEILSVAYKKDSEDNPOTTLES
1 1			ATCPHWVFNVAKKYMKSTYEOVDLIGKKTOKTATTVEHLATKOU
1 1			WIQRAAVIGDVIRVYSGHOGRTIIFCETKKEAOFLSONSAIKOD
f			AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGIDIDEVD
j !			LVIQSSPPKDVESYIHRSGRTGRAGRTGVCICFVOHKEFVOLVO
		1	VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTATGUPV
[}	QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM
	1	1	TLQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF
1	<u> </u>	j	DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ
		i.	REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGGNKSNRSQNK
5790	3786		GQKRSFSKAFGQ
ĺ	-		ARRORDPLOALRRRNOELKOOVDSLLSESQLKEALEPNKROHIY
ļ	ļ	į .	QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD
1	i i		KLTQQLQGLAVTISRENITEVGAPTEEEBESESEDSEDSGGEEB
			DAEEEEEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEI
i	İ	1 :	LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEEGQESSEE
		;	GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN
			HVSFCYLIVLMRNRMETVEDTNGSETGFRAWNVQSRGRIFLVSK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			PVLQQINTVDVLTTMGAIPAGFRPSTLSQLLEEGNQFRANYFLQ
		ļ	PELMPSQLAFRDLMWDATEGTIRSRPSRISLILTLWSCKMIPLP
			GMSIQVLSRHVRLCLFDGNKVLSNIHTVRATWQPKKPKTWTFSP
			QVTRILPCLLDGDCFIRSNSASPDLGILFELGISYIRNSTGERG
			ELSCGWVFLKLFDASGVPIPAKTYELFLNGGTPYEKGIEVDPSI
			SRRAHGSVFYQIMTMRRQPQLLVKLRSLNRRSRNVLSLLPETLI
			GNMCSIHLLIFYRQILGDVLLKDRMSLQSTDLISHPMLATFPML
			LEQPDVMDALRSSWAGQES\TLKRSEKR\PKEFLKVPRFLLVYH
	Ī	1	\GCVLPLL/HTPTRLPPFRWAEEETETARWKVITDFLKQNQENQ
			GALQALLSPDGVHEPFDLSEQTYDFLGEMRKNAV
5791	 3	1636	LRVAEFAGTSR/IGAGLIQPLHRAPARDHGLLRGGAAPALSVSH
	ļ		GN/GKQL/AMSSQGSDDEQIKRENIRSLTMSGHVGFESLPDQLV
	1	1	NRSIOOGFCFNILCVGETGIGKSTLIDTLFNTNFEDYESSHFCP
	1		NVKLKAOTYELOESNVOLKLTIVNTVGFGDQINKEESYQPIVDY
			TDAOFEAYLOEELKIKRSLFTYHDSRIHVCLYFISPTGHSLKTL
1		1	DLLTMKNLDSKVYIIPVIAKADTVSKTELQKFKIKLMSELVSNG
1	i		VQIYQFPTDDDTIAKVNAAMNGQLPFAVVGSMDEVKVGNKMVKA
[RQYPWGVVQVENENHCDFVKLREMLICTNMEDLREQTHTRHYEL
1			YRRCKLEEMGFTDVGPENKPVSVQETYEAKRHEFHGERQRKEEE
			MKQMFVQRVKEKEAILKEAERELQAKFEHLKRLHQEERMKLEEK
İ			RRLLEEEIIAFSKKKATSEIFHSQSFLATGSNLRKDKDRKNSQF
1	İ		FVKQKVPEHRRSSSQANFIKKKLEVCFDFAVICFITSIFGEQPQ
ł			LLIFMEKYFQVQGQYISQSE
5792	2263	653	AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY
1			LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER
[TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT
	1		YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL
1	}	1	NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN
1			RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ
1		1	FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND
		\	ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP
1	Į.	Ì	AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY
1	1		DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV
ł		1	YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF
1			IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE
1			EKATRAPHTD
5793	2263	653	AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY
ł			LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER
1			TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT
			YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL
1			NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN
			RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ
			FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND
		}	ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP
	.		AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY
			DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV
1		1	YAFGPLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF
		}	IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE
l		l	EKATRAPHTD
5794	1	5016	MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV
		1	KGQKGERGLPGLQGYIGFPGMQGPEGPQGPPGQKGDTGEPGLPG
1			TKGTRGPPGASGYPGNPGLPGIPGQDGPPGPPGIPGCNGTKGER
1	1	\	GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG
1	1	1	FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGPPGEKGQM
		1	GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG
1	ì		EPGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG
1			YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT
1			PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD
1	Į.		RGFPGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP
1	1		GDOGPPGTPGOPGFTGEIGEKGOKGESCLICDIDGYRGPPGPQG
Ì			PPGEIGFPGQPGAKGDRGLPGRDGVAGVPGPQGTPGLIGQPGAK

	SEC	Dec 3:		
	ID	.	Predicted en	The dela sequent containing of med
	NO:		nucleotide	
		location	location	(ACIO, Febbonulalania - A a)
	I	corresponding	corresponding to first	
]	to first	amino acid	A-Deacine, M=Methionine M-Access
	İ	amino acid	residue of	I
]	residue of	amino acid	J-Scrine, Tathreonine Vavaline
	1	amino acid	sequence	""ITYPTOPhan, Y=Tyrogine y=time
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			 	\-Possible nucleofide incortion
		İ		GEPGEFYFDLRLKGDKGDPGFPGQPGMPGRAGSPGRDGHPGLPG PKGSPGSVGLKGPPGDDGGFPGQPGMPGRAGSPGRDGHPGLPG
				1 - MOOF OO VOLKGERGEPGGVGPPGCDCCDCCCCCCCCCCCCCCCCCCCCCCCCCCC
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		1	1	DGLPGDMGPPGTPGRPGFNGLPGNPGVQGQKGEPGVGLPGLKGL
,		1	1	PGLPGIPGTPGEKGSIGVPGVPGEHGAIGPPGLQGIRGEPGPPG LPGSVGSPGVPGIGPPGARGPPGGQGPPGLSGPPGIKGEKGFPG
ı		1		FPGLDMPGPKGDKGAQGLPGITGQSGLPGLPGQQGAPGIPGFPG SKGFMGIMGTPGCOCAPATION
			i	SKGEMGVMGTPGQPGSPGPWGAPGLPGQQGAPGIPGFPG PSI-KGDVGDVGLPGWGAPGLPGEKGD\HGFPGSSGPRGD
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		1		PGOKGEMGPAGPTGPRGFPGPPGPPGLPGSMGPPGTPSVDHGFL
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- 1				ITGENIRPFISRCAVCEAPANVMAVHSQTIQIPPCPSGWSSLWI
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- 1		1		YYANAYSFWLATIERSEMFKKPTPSTLKAGELRTHVSRCQVCMR
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	5796	2	1078	
		ì		GRVGWELWCMYISPPKDWWDAGDPSLFIRTPAMIGCSFVVNRKF FGEIGILDPGMDVYGGENIEL
- [1		FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP
- 1				GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE
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i i	j	į	į	TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG
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1		1		TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
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· ·	ĺ	1		FASAGAGNELVUVEUGPAAOPSI.GDTDFFA.DI.CDCDFDTCDD.TC
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			1.	"TECHRUF LIPPLLSVKFRYGGAPOAT.TI.KT.DVTTNTVPRODURGE
				AAQDFFQRWKQLSLPQQBAQKIFKANHPMDAEVTKAKLLGFGSA

		Predicted end	Amino acid segment containing signal pertide
SEQ	Predicted	nucleotide	/n allerine C-Cycleine D=Aspartic Acid, E=
ID	beginning	location	Clutamic Acid. F=Phenylalanine, G=Glycine,
NO:	nucleotide	corresponding	u_u;etidine. I=Isoleucine, K=Lysine,
	location	to first	Laleucine Mamethionine, NaAsparagine,
	corresponding	amino acid	Paproline, OaGlutamine, Raarginine,
I	to first	residue of	c_coming T=Threoning, V=Valing,
	amino acid	amino acid	W-Trantophan Y=Tyrosine, X=Unknown, *=Stop
	residue of		codon /=possible nucleotide deletion,
	amino acid	sequence	\occible nuclectide insertion)
	sequence	l	LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
			RTSKEPVSRHLCELLAQQF
	ì		RTSKEPVSKHLCEBHAQQF LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL
5800	2679	1435	LLSTYIKFINDFPEIRATIQGVINGSCHAKLKRKKGPGAGSAL
			DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLIGLRAAPPPAAP
		1	DDGRRDPSSNDINGGMEPTPSTVSTPSPSADSGERGATE
	1	1	PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP
	l .		EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN
	1		KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL
	t .		NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM
	1		AAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA
	1	ł .	LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
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	1		NCCHERGREDS NTPKPLHPTITCHEKVVNIQKDPGESLGMIVA
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		1	PUGD CENUALI, KDTSSSTVI, KALEVKEYEPOEDCSSPAALDSNA
	1	· I	NMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVG
	1	1	GYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSG
	1		MIHACLARLLKELKGRITLTIVSWPGTFL
			CFSLYQIMERIMDLPTLLRHAFREMFSVGGLFWMFRIRIILCLM
5802	3	290	GAFFYLISPLDFVPEALFGILGFLDDFFVIFLLIYISIMYREV
	1		
	ĺ		ITQRLTR EAQFGTTAEIYAYREEQDFGIBIVKVKAIGRQRFKVLELRTQSD
5803	2234	1299	EAQFGTTAEIYAYREEQDFGIRIVAVAAIGAQAFAVEEDOC
5000	}	ì	GIQQAKVQILPECVLPSTMSAVQLESLNKCQIFPSKPVSREDQC
	1	1	SYKWWQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLRE
	•	Ì	WDENLKDDSLPSNPIDFSYRVAACLPIDDVLRIQLLKIGSAIQR
	1	,	LRCELDIMNKCTSLCCKQCQETEITTKNEIFSLSLCGPMAAYVN
			PHGYVHETLTVYKACNLNLIGRPSTEHSWFPGYAWTVAQCKICA
			SHIGWKFTATKXDMSPOKFWGLTRSALLPTIPDTEDEISPDKVI
	1		TCT .
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l		1	TYCLYLPETFPEDGGEYMCKAVNNKGSAASTCILTIESKN
1			YISDTLGQVYKSKIRWWIEENGGNGNISVDDLIALLDLAEHAS
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l			LKNYIPYLTKLKFSLKKSFDFFDEYFVLLKPRNNIKQNEBAKT
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SEO Predicted	
Predicted end Amino acid segment contact	3 mar
nucleotide (A=Alanine, C=Cvsteine D	
NO: nucleotide location (A=Alanine, C=Cysteine, D=,	Aspartic Acid, E=
location location Glutamic Acid, F=Phenylalar H=Histiding I=Icological	nine, G=Glycine,
	K=Lysine,
to first amino acid P=Proline October 19	=Asparagine,
amino acid residue of scraine, Q=Glutamine, R=1	1 ann à m à
social and the second of the s	lima
w=lTyptophan, Y=Tyrosine	C=Unknown, *=Ston
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TTOLTEPPLEVENERGING	VSLRALSSELPVVISL
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LPLALQSTFSCDSEGASSFFSNASDADG	YVAAELLAKDVPDDAM
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EERLLEEGVLRQI PVVGSVLNWFSPVQALQ	KGIQEAQVELQKAS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
•	corresponding	to first	L=Leucine, M=Metnionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	<u> </u>		TEPIYVYKAQGAGVTLPPTPSGSRTKQRLPGQKPFKRSLRGSDA
Į			LSETSSVSHIEDLEKVERLSSGPEQITLEASSTEGHPGAPSPQH
1		İ	TDQTEAFQKGVPHPEDDHSQVEGPESLR
5813	2936	699	HRDGVSGSLERPLTDRSRTGAFAQQRGKMATAGGGSGADPGSRG
			LLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQI
1		1	GCQSSISGDTGVIHVVEKEEDLQWVLTDGPNPPYMVLLESKHFT
1		ł	RDLMEKLKGRTSRIAGLAVSLTKPSPASGFSPSVQCPNDGFGVY
Į		1	SNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLEDENETKVI
1	į	1	KQCYQDHNLSQNGSAPTFPLCAMQLFSHMAWLSFSTAT\CMRRS
1			SIQSTFSINPKIVCDPLSDYNVWSMLKPINTTGTLKPDDRVVVA
1			ATRLDSRSFFWNV\APGAESAVASFVTQLAAAEALQKAPDVTTL
1]	1	PRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVEL
1		1	GQVALRTSLELWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVP
1			AVILRRPNQSQPLPPSSLQRFLRARNISGVVLADHSGAFHNKYY
į			QSIYDTAENINVSYPEWLEPLKE/ETWNFG*QDTAKALADVATV
ļ.		•	LGRALYELAGGTNFSDTVQADPQTVTRLLYG\FLIKANNSWFQS
l l			ILQGRDLRSYLG*RGLFQH\YIAV\SSPTNTIYV/VLQYALANL
}			TGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHSNETDRLP
į		ļ	RCVRSTARLARALSPAPELSQWSSTEYSTWTESRWKDIRARIFL
1	}	ł	IASKELELITLTVGFGILIFSLIVTYCINAKADVLFIAPREPGA
1	1		VSY
5814	8500	432	ALKCRPRRVLAILVGPVQPDRMAEEGAVAVCVRVRPLNSREESL
1			GETAQVYWKTHNNVIYPVDGSKSFNFDRVLHGNETPKNVYEA\I
ı		}	AAPIIDSAIQGYNGTIFA\YGQT\ASGKTYTMMGSEDHLGVIPQ
1	Ì		GQFHGHFSQKI+EVFLDREFLLRVSYMEIYNBTITDLLCGTQKM
1		1	KPLIIREDVNRNVYVADLTBEVVYTSEMALKWITKGEKSRHYGE
1			TKMNQRSSRSHTIFRMILESREKGEPSNCEGSVKVSHLNLVDLA GSERAAQTGAAGVRLKEGCNINRSLFILGQVIKKLSDGQVGGFI
1			GSERAAQIGAAGVKLKEGCNINKSLFILGQVIKKLISLAQVGSFI NYRDSKLTRILQNSLGGNPKTRIICTITPVSFDETLTALQFAST
1	1.		NYKOSKITKILONSLIGHTKITCIII PUTBULANIA AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLETRAQ
1	\	į	AKYMKNIPI VNEVSIDEALIDKKIKKE IMDIKKQDDEL
ļ	•		KAKRKRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL
			LREIDESVCSESDVFSNTLDTLSEIEWNPATKLLNQENIESELN
1			SLRADYDNLVLDYEQLRTEKEEMELKLKEKNDLDEFEALERKTK
}			KDQEMQLIHEISNLKNLVKHREVYNQDLENELSSKVELLREKED
İ			QIKKLQEYIDSQKLENIKMDLSYSLESIEDPKQMKQTLFDAETV
1			ALDAKRESAFLRSENLELKEKMKELATTYKOMENDIQLYQSQLE
1		}	AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLELEGK
1	(ITDLQKELNKEVEENEALRBEVILLSELKSLPSEVERLRKEIQD
1		į.	KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ
		Ì	SNYKSTDOEFONFKTLHMDFEQKYKMVLEENERMNQEIVNLSKE
1			AOKEDSSI.GALKTELSYKTOELOEKTREVQERLNEMEQLKEQLE
		1	NRDSPLOTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL
-	j	1	OTERDOLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS
		1	KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL
	Ī	1	TADVKDNEIIEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL
1	Į.	1	KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR
	1		TCDRLAEVEEKLKEKSQQLQEKQQQLLNVQEEMSEMQKKINEIE
		1	NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL
		\	KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE
1	1		TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP
-			NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF
}	}		QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE
		1	SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG
			LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV
}			AKHLETEEELKVAHCCLKEQEETINELRVNLSEKETEISTIQKQ
1			LEAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNELKQFKEFR
1			KAKDSALQSIESKMLELTNRLQESQEEIQIMIKEKEEMKRVQEA
			LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE
1		1	LQIERDQLKENTKEIVARMKESQEKEIQFIRMTANDIQLKEND IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD
			DLRSVEETLKVERDQLKENLRETITRDLEKQEELKIVHMHLKEH
ì	1	1	DDK2AFET DYACKTWOVET T T KDORUGER TY THE MANAGEMENT AND MANAGEMENT

SEC	Predicted	Predicted end	
ID		nucleotide	
NO:		location	I WALLEY CHUVSEDING DENOMERAL NESS -
	location	corresponding	Turality ACIG, Fephenylalaning C.C.
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine V-V-line
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine Y-Unknown + G
1	amino acid sequence	sequence	Codon, /=possible nucleofide deletion
	pedgette		\=Possible nucleotide insertion\
i			QETIDKLRGIVSEKTNEISNMOKDLEHSNDALVAODI VIOLEVA
1		İ	I TATHUMAEQUETIDELEGIVSEKTOKI.CNMOKOT ENGNAKT COM
1			TOPUNAMENDULTUKKOVNETOKKVSEMPOLVVOTVDOG OF
}		i	DETENDING ACKURENDEEMKSVMKEDDNI DDUFFFT VI FDDOT IS
ſ	1		ESLQETKARDLEIQQELKTARMLSKEHKETVDKLREKISEKTIQ
		İ	ISDIQKDLDKSKDELQKKIQELQKKELQLLRVKEDVNMSHKKIN
1			EMEQLKKQFEPNYLCKCEMDNFQLTKKLHESLEEIRIVAKERDE LRRIKESLKMERDQFIATLREMIARDRQNHQVKPEKRLLSDGQQ
1			HLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFH
· ·			RIMKKLKYVLSYVTKIKEEOHECINKFEMDEIDEVERKOVELLIV
İ		1	1QHLQQDCDVPSRELRDLKLNONMDLHIREILVDECERROLV
ı			1 PP OOM TO THE PROPERTY OF TH
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- [AN IQIDATSDASGAQVNPTTODNKNPHVTSPATOLTTPPVTDFF
			INSUREARESAMHKESKIIKMOKELEVTNDTTAKT.OBKUURCHKO
1	Í		LEKTKETIQVLQDKVALGAKPYKEBIEDLKMKLGKIDLEKMKNA
I	}		KEFEKEISATKATVEYQKEVIRLLRENLRRSQQAQDTSVISEHT DPQPSNKPLTCGGGSGIVQNTKALILKSEHIRLEKEISKLKQQN
1	[EQLIKQKNELLSNNQHLSNEVKTWKERTLKREAHKQVTCENSPK
1			SPROTGTASKKKQITPSOCKERNLODPVPKESPKSCPPDCPCVC
l			DESTREVATEDNSSLGLCPEVONAGAESVDSOD\CDWADIEOOV
5815	23	1450	DVP \ECKTQ
		1460	SELVMWTVQNRESLGLLSFPVMITMVCCAHSTNEPSNMSYVKET
1			VDRUUKGIDIRURPDFGGPPVDVGMRIDVAGIDMUGEVAMDVER
1			TMYFQQSWKDKRLSYSGIPLNLTLDNRVADQLWVPDTYFLNDKK
İ		[SFVHGVTVKNRMIRLHPDGTVLYGLRITTTAACMMDLRRYPLDE CNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIELPOFSIVDY
1		1	KMVSKKVEFTTGAYPRLSLSFRLKRNIGYFILQTYMPSTLITIL
1		 	SWVSFWINYDASAARVALGITTVI,TMTTTSTHI,DETI,DVIDVIV
1			AIDIILMGCFVFVFLALLEYAFVNYTFFGKGDOKYGAGYODOGA
1			NEANALEMNKYQVDAHGNILLSTLETRNETSGSEVIJTSVSDDVA
1			IMISIDSASIQYRKPLSSRE\A*GRAPDRHGVPSKGPIDDDAG\
5816	861	191	OLKVKIPDLTDVNSIDKWSRMFFPITFSLFNVVYWLYYVH
ł			TSSRSRAAAQEGDAETPGSVERRGRRAGAEDGMSQAPGAQPSPP
1 .	1		TVYHERORLELCAVHALNNVLQQQLFSQEAADEICKRLAPDSRL NPHRSLLGTGNYDVNVIMAALQGLGLAAVWWDRRRPLSQLALPQ
	1		VLGLILNLPSPVSLGLLSLPLRRRHLRNPCARL/VTVSYYNLDS
1			K\LRAPEGPGGLRTE*GPFLAAALAQGLCEVLLVVTKEVEEKG
5817	851		SWERTE
1	"	118	RLFRGPGANRGRSCRGCSGGREPSGGALPKRHCPC*PPSPPAAD
ļ			VMSNTTVPNAPQANSDSMVGYVLGPFFI.ITI.VGVVVAVAMVVOV
1			ARRYDRIANHULPMYSYDPAEELHEAEOELLSDMGDDKXXX OAG
1			RVATSTSGCHCWMSRRDLTPLPHPSEPGVLDCLGPCHLLPLLSP
L			GSPCWVLGLHFSLHPPSAASASHALTITSLPPGLLPFVGVELTA HPQALMGRGFPSGMAAAGRHLCFL
5818	3	3918	QALRDKLWIFLVQSFYAVRHTESWKLMSTDDQQKIQAAAFDKGD
ł			DRRIGKEPIFSSSQORKOVSDSGDIKTESWDGNNEEGWEVEGE
	ļ		NROWESDGLGASGHSSSTNRNSINKTLKODDUKEKDGTVTAGVT
			TRELKTGGKNVSGKPKTVTKSKTENGDKARTENMSPROMÆRER
		ļ	TAAAAATGQKNLLNGKGVRNOEGOISGARPKVT.TGNI.MVOAKAK
			PLKKATGKDSPCLSIAGPSSRSTDSSMEFSISTECT.DEDKENGS
		ļ	TEEERPSGHKLSPCDSPGOMMKNSVDSVKNSTVATKSRDVSDVT
		i	NGTSNKKSIHEQDTNVNNSVLKKVSGKGCSEPVPQAILKKRGTS
		1	NGCTAAQQRTKSTPSNLTKTQGSQGESPNSVKSSVSSRQSDENV AKLDHNTTTEKQAPKRKMVKQVHTALPKVNAKIVAMPKNLNQSK
]	KGETLNNKDSKQKMPPGQVISKTQPSSQRPLKHETSTVQKSMFH
		Ì	DVRDNNNKDSVSEQKPHKPLINLASEISDAEALQSSCRP\DPQK
1	.		PLNDQEKEKLALECQNISKLDKSLKHELESKOICLDKSETKERN
1			HKETDDCDAANICCHSVGSDNVNSKFYSTTAIKYMVSNPNENSI.
j			NSNPVCDLDSTSAGQIHLISDRENOVGRKDTNKOSSIKCVZDVS
			LCNPERTNGTLNSAQEDKKSKVPVEGLTIPSKLSDESAMDEDKH

beginning corresponding to first control of the corresponding to first amin acid amin acid fresidue of amin acid amin acid fresidue of amin acid sequence se	~===	5 . 37 . 6 . 3	Predicted end	Amino acid segment containing signal peptide
NO: location corresponding to first amino acid residue of amino acid residue of amino acid sequence corresponding to first amino acid residue of amino acid sequence corresponding to first amino acid sequence corresponding to first amino acid sequence company to first control of amino acid sequence corresponding to first control of amino acid sequence corresponding to first corresponding	SEQ	Predicted		(A-Alamine C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid nce sequence s				Glutamic Acid F=Phenylalanine, G=Glycine.
to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence Peproline, Q=Glutamine, R=Arginine, w=Trytopien, Y=Pyrosine, Y=Dyrosine, Y=Str amino acid sequence Peproline, Q=Glutamine, V=Vallne, amino acid sequence ATADSDVSSKCPSOQUSKNSPKNMETSESPESJETPETPY MLSTCVLHGRSSESPESTGSATTSSIDL FRRSEPLYDAGGGG GSNDRGISKGTMLCHDFLGRSSSDTSTFEELKTYDSHLAH MKXQSSNDLEPONTSDDETPERRESTRASSATVHSRFSINNARGGG GSNDRGISKGTMLCHDFLGRSSSDTSTFEELKTYDSHLAH MKXQSSNDLEPONTSDDETPERRESTRASSATVHSRFSINNARGG GINLAFEDATERNECERSPSNMKFRYSTRSSEPSEED VHYPPOASVDSSSSDDETDETSERSERVLSVDECESSED VHYPPOASVDSSSSDDVFDGISHENBERTVLSVDECESSED VHYPPOASVDSSSSSDVFDGISHENBERTVLSVDECESSED VHYPPOASVDSSSSSDVFDGISHENBERTVLSVDECESSED VHYPPOASVDSSSSSDVFDGISHENBERTVLSVDECESSED VHYPPOASVDSSSSSDVFDGISHENBERTVLSVDECESSED VHYPPOASVDSSSSSDVFDGISHENBERTVLSVDECESSED VHYPPOASVDSSSSSSVDVFDGISHENBERTVLSVDECESSED VHYPPOASVDSSSSSSVDVFDGISHENBERTVLSVDECESSED VHYPPOASVDSSSSSSVDVFDGISHENBERTVLSVDECESSED VHYPPOASVDSSSSSSVDVFDGISHENBERTVLSVDECESSED VHYPPOASVDSSSSSSVDVFDGISHENBERTVLSVDECESSED VHYPPOASVDSSSSSSVDVFDGISHENBERTVLSVDECESSED VHYPPOASVDSSSSSSSVDVFDGISHENBERTVLSVDECESSED VHYPPOASVDSSSSSSSVDVFDGISHENBERTVLSVDECESSED VHYPPOASVDSSSSSSSVDVFDGISHENBERTVLSVDECESSINT ANTALSAGDLDCTTLAQTRNTDHRSVRTLSGDISHDVSSSSSSSSVTBORD VHYPPOASVDSSSSSSSVTBAGGGRTTLLBCTGATLSGDISHDVSSSSSSSSTSSSTSSTSSSTSSSTSSSTSSSTSSSTSS	NO:			W-Wichidine T-Teoleucine K=Twaine.
maino acid maino acid				
amino acid residue of amino acid sequence shryptophan, Y=Tyxosine, X=Unknown, *=Stc Codon, /=possible nuclectide insertion)				
residue of amino acid sequence	i			paproline, Qadiutamine, Ranginine,
amino acid sequence codon, /=possible nuclectide insertion				S=Serine, T=Threonine, V=Valine,
### SEQUENCE APADSDVSSKCFSGLEKNISFKMETGESPEHETETT WILLSTOVLHORESPESITISATTSSDD IK PRSEDVAGGSQ GNORG IS KCOTHICHOPLGASSSDTTPEELK IVENILAI MKXGSSINDLFOVASTSDDB IPEKRPEIWSRSALVHSREREN MKXGSSINDLFOVASTSDDB IPEKRPEIWSRSALVHSREREN GSVGFAGEIDOVSSADETEDERSEADENVARSISISINDAO GI INLAFEDATEMBCREFSANKKKRSVLLSVDCCEBLIGSD VIPTPOLAVUNSFSDDVFDGI SHEHHGARTCYSFSRSEEN CKONKGNSVCINESVILLISSI DESKRINGSVSATEKKNTI SARROLLREDKKWINGSNVENDIOPORSFYLDIOVSSGERF DANGEPRIS DIPWINSTRISLISFRSOVLOGSEPVESISITI DANGEPRIS DIPWINSTRISLISFRSOVLOGSEPVESISITI DANGEPRIS DIPWINSTRISLISFRSOVLOGSEPVESISITI DANGEPRIS DIPWINSTRISLISFRSOVLOGSEPVESISITI DANGERS DIPWINSTRISLISFRSOVLOGSEPVESISITI DANGERS DIPWINSTRISLISFRSOVLOGSEPVESISITI DANGERS DIPWINSTRISLISFRSOVLOGSENLOPT KVESSTHVINDEP*DOCHRAKODITLIKULISFOSINLOPT REPEDISIAO YLINGTVILLARDS KOPG THINDIAMSSLTS SARSI ITMAS PS SEDCES POGENTILLEETOR SISSI ITMAS PS SEDCES POGENTILLEETOR SISSI ITMAS PS SEDCES POGENTILLEETOR SISSI ITMAS PS SEDCES POGENTILLEETOR SISSI ITMAS PS SEDCES POGENTILLEETOR SISSI ITMAS PS SEDCES POGENTILLEETOR SISSI ITMAS PS SEDCES POGENTILLEETOR KREWYLLIN PS SEP 'ITTIAS I RATTISHIPAS PRONKILLEE SEDVEN / VERREVUNGVERNITLE ITTIAS PONKILLEE SEDVEN / VERREVUNGVERNITLE ITTIAS PONKILLEE SEDVEN / VERREVUNGVERNITLE ITTIAS PONKILLEE SEDVEN / VERREVUNGVERNITLE ITTIAS PONKILLEE SEDVEN / VERREVUNGVERNITLE ITTIAS PORTUNINGS SERADBITAR I INABBITE I ILDUEVERVITARGI Y SETTEMBOPPOTING PURPA I ILDUARDON SERADBITE I ILDUEVERVITARGI Y SETTEMBOPPOTING PURPA I ILDUEVER PURPA I IL		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
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GINLAFEDATENECRFSANKKFKRSVLLSVDECESLISD VHTPFOASVUSPSPSDVFDGISHBHINGTYSRFSRESEN CKOMKGNSVCKNESTVLDLSSIDSSRNNKGSVSATEKKNTI SSRSDGLLEDKKNNNGSVSATEKNTI SSRSDGLLEDKKNNNGSVSATEKNTI SSRSDGLLEDKKNNGSVSATEKNTI SSRSDGLLEDKKNNGSVSATEKNTI SSRSDGLLEDKKNNGSVSATEKNTI SSRSDGLEDKKNTLEDSSTRSLDSFRSQUIPOEGPVEESIST ANIALSAGDIDDCDTLAQUFMVDHEPSKIPTYEMOVIBA KVESSITIVTDMDF*DDQHFAKQDWTLLKGLLSSGDSNLDVT FEDLSLAQVLINQTILLIARDSSKPQGITHIDTLNRWSELTS SSASITMASSSSCDSPGGWTILLETTGN INTERCOMMENT FEDLSLAQVLINQTILLIARDSSKPQGITHIDTLNRWSELTS SSASITMASSSSCDSPGGWTILLETGN INTERCOMPT INT			1	GSVOFAGEIDOVSSSADETEDERSEAENVAENFSISNPAPQQFQ
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CKONKKINSVUKNESTVLDLSSIDSSRINKGSVSATEKRINIT SSRRGULLEDKKNINKSVENDIOQRELDDVANGERP DLHQRENSDIPKNISTKSLDSFRSQVLPQEGPVKESHSTT ANIALSADIDPCDTLAQTEMYDHEPSELTYTEMOVIEA KVESSTHVTDMDF*DDDHFAKQDWTLLKQLLSEQDSNLDVT PEDLSLAQVLINQTILLARDSSKPGGITHLDTLNWSELTS SSASITMASFSSECSSPGGWTILLELTQH SSASITMASFSSECSSPGGWTILLELTQH 1 5557 AAAGLIGALHLUWITUVAAARAEKSAFVGGSSIIEVURPDD LQTSTTGLISSYQKSISLYKRONCP, IRFSPPMLDFHSPV KMEKVYLHMPSSE*TITUVSIFATTSHFHASFFQNKRLLGG SDVS/VPLARVVENVENTLFINTSNRAGVSTY\QVGVGVP REPPLARVTNNSSFSDIINHINPHSEPLQVVEWYNSGGD RLPPTQQGGTRKLMSIPPYTKGVWRASAFSSREANNHTAF TINASDSTEFIILPVEVEVTTAPGIVSSTEMLDFGTLRTQDL IMHILINSGTRDVPTTSVRPTPQ\NDAITVHYPITLLARS\ TINASDSTEFIILPVEVEVTTAPGIVSSTEMLDFGTLRTQDL IMHILINSGTRDVPTTSVRPTPQ\NDAITVHYPITLTRAFSILLH LGPEAKTMFKVINFSKVLTLLENSGSTYLLTHEFTSTALLH LGPEAKTMFKVINFSKVLTLLENSGSTYLLTHEFTSTALLH LGPEAKTMFKVINFSKVLTLLENSGSTYLLTHEFTSTALLH LGPEAKTMFKVINFSKVLTLLENSGSTYLLTHEFTSTALLH LGPEAKTMFKVINFSKVLTLLENSGSTYLLTHEFTLGVUL EASNILPAILINSDPIELAIKSHIIGGSLSLAVVATRAKI NGAGGITTUTVELITTPVK_AVIAVAGSLTCSPKHVVLPPSF VIGSINITMSFSGKVKTQGTRSLSBVVFYYKRLRKNKDL KKSILANITYPDPOLCGGHCYVCLPPLSEPKYVQFVAK NGAMDLHQSLPKGWTGIKENGKPLXVAKFVLTKKKLK NGAGGITTYPDPOLCGGHCYVCLPPLSEPKYVQFVAK NGAMDLHQSLPKGWTGIKENGKNEDLYKSKRILITSPROTUCKYNIT TABLSWPSILSSPRILKPPLTNITNGS\EETILENP/SQI TYGTPILLISSPSTVDLXSRFNLKTRAKKLNGKDLOKKI SCHWALFLLVGTSLLVANVQCGGTERVAKCKLOGGG SHADVGFPLKSTRFVAKTAGCHSAGK SCHWALFTTSGSBFYFILNRSLPYKNGKLOGGHS GSHQV GFSGHPHSSTRSNKNSADVDDVSRGGTSSMTS SCHMKTRFLVUDDNTGAGGHSAGKKSKGARQSGGSGH VREPPLERTVGISSEGNEFNTSADSGTSMTS SCHMKTRFLVUDDNTGAGGHSAGRKSKGARQSGGSGH PLEGHPGPPLPPFVPQPGBPDRSLSPRANGRTSSMTS SCHMKTRFLVUDDNTGAGGHSAGRKSKGARQSGGSGH PLEGHPGPPLPFVPQPGBPLBFRANGGTSSMTS SCHMKTRFLVUDDNTGAGGHSAGRKSKGARNESHERSPRANGRTSSMTS SCHMKTGTSLLVANDRPALAKFLINSGETSSMTS SCHMTTSLLKAMBTGGTSLVANDRFRANGGTSSMTS SCHMTTSLLKAMBTGGRKGAMPERESPMSQVKKKKK KKEITTUKPSSCHUNGTSSEGEL TSNBOTTEFLIKEPTPALAFFTSPSSLTMSSRGTSSMTS SCHMTTATSVLLGNTSSLEEBMSQVKKKKKR KKEITTUKPSSCHUNGTSSGGEN SCHMTTATSVLLGNTSGLWANTSPSSPAPONSPN VFSKLGLISTSCAGAGGGGGGARVSSNTTGFSSS SCHUTTATSVLLGNTSSRGENEFNSGVY		,		WITHFOASVDSFSPSDVFDGISHEHHGRTCYSRFSRESEDNILE
SSRRQLLRENKUNNGSWIENDIQORSKPLDSDVKSGERP DLHQGENSDIPKNSGTKSLDSFRSQUT/DEGEFVKESHSTY ANIALSAGDIDDCTLAQTEM/DBRPSKTLSPIYGWIEN KVESETHVTDMDP+DDDH-PAKOMPTLKGLLSSGDSNLDMY FEDLSLAQVLINQTLLIARDSKYPGITHIDTINRWSELTS SSASITWASFSSEDCSPQGEWTILELETQH SANALLGALHLWMTLVVAARAREKEAFVGSESIIEVLRFDD LQTETTIGISSYQOKSISLYRCNCR?IRFESPMLDFHQV KMELVYLHMPSSE*TITLVSIFATTSHHASFFQNKKLLGS SPDVS/VFLARVVGNVENTLFINTSHGVFTY\QVFGVGVF RLRPFLGARAVTVNSSFSIIINIHRHEHASFFQNKKLLGS SPDVS/VFLARVVGNVENTLFINTSHGVFTY\QVFGVGVF RLRPFLGARAVTVNSSFSIIINIHRHEHASFFQNKKLLGS SPDVS/VFLARVVGNVENTLFINTSHGVFTY\QVFGVGVF RLRPFLGARAVTVNSSFSIIINIHRHEHASFFQNKKLLGS SPDVS/VFLARVVGNVENTLFINTSHGVFTY\QVFGVGVF RLRPFLGARAVTVNSSFSIIINIHRHENGFTLRFUGL LDFLAKKTMSFTILPVVENTTAGRIYSSFSMLDFGTLRFUGL LLMILLINGSTKDVPTTSVRFTPQ\NDATTVHFFFITLKAS\ YTKVASISPDASKAKVSPSFSKLITAGRIYAFT LDGPLAKTMFKVHNPSKPVLLLRMEGGYIFTLLFMPSTSSM NILLITTAGSKFFILPVRVYTGFLDYFVLTNFFSFALLH LDFLAKTMFKVHNPSKPVLLLRMEGGYIFTLLFMPSTSALH LDFLAKTMFKVHNPSKPVLLLRMEGGYIFTLLFMPSTSALH LDFLAKTMFKVHNPSKPVLLLRMEGGYIFTLLFMPSTSALH RLLITTAGSKFFILPVRVYTGFLDYFVLLPMSTSTLLFNCTURPST NILLITTAGSKFFILPVRVYTGFLDYFVLLPMSTSTLLFNCTURPST NILLITTAGSKFFILPVRVYTGFLDYFVLLPMSTSTLLFNCTURPST NILLITTAGSKFFILPVRVYTGFLDYFVLLPMSTTSTLLFNCTURPST NILLITTAGSKFFILPVRVYTGFLDYFVLLPMSTTSTLLFNCTURPST NILLITTAGSKFFILPVRVTTGCSSEETTLERHPSOL VRQSINITMSFSQKVLGOTISSLSDESHYYKKLRANKLD LSSLSVENSTLSSFFILKKPFILTNTCSS\EESTILLBR/SQL VRQSINITMSFSQKVLGURLSSFFILSKSLFTYRMLDR/SQL NAMAWDADDLAGSLFGSTTGTKSTNSTSSEETTLERHPSOL VRQSINITMSFSQKVLGTHASTAFTVARTDLLQKNIT RTUSSLI ILVSNNSTVSUNDATSRSTTSSTNSS SASPANTATRIVLUDSNTGARTSTLSCARGAVGAGGGGGH FKITTALLKCTDSLKLEENPTILKTFKVENTGOLGHHI ISGYSCEGYGFKVNNCOGPTISANASRII ILTPTPPTTASI ELKFITTTSGEFVFILNGSRAFAKVSNKTGFSSTSS SGPANKTRIPLVLDSNTGAGGGGGGGGKKKSAGKAGGGGGGH VRGFPDLRFTVATVAGGTBARDFTASSADADHURARSKSVLGARGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		1	1	CVONVENCYCKNESTYLDLSSIDSSRKNKOSVSATEKKNTIDVL
DLHOREPHSDIPRNSTISJUSTRSQULPGRGPVESHSTT. ANIALSAGDIDDCTILAQTRNYDHRPSKTLSPIYEMDVIEA RVESITHVTMMP*DDQHFAKQDWTLLKQLLSEDSHLDVT PEDLSLAQVINQTILLAQDSKPGOTHIDTINRWSELTS SSASITWASFSSEDCSPQGEWTILLETQH 5839 1 5557 ARAGLIGAHHLWMTLVVAARAREKEAFVQSESITEVLRFDD LOTETTIGLSSYQQKSISLYRGNGR-1 RYEPPMLDFHEQPV KMEKVYLHNPSSE*TITLVSIFATTSHFHASFFQNKKLLEG SPDW_VYLARVVGMVENTLFINTSHGYPTYQVFYNGVGFY RRPFLGARTVTWSSFSPINHHPHSEPLQVFWYSSGGI ELPFGQGGTRKLMEIPPPETKGWMRASFSREADNHTAFI TRASDSTEFIILPVEVEUTTAGIYSSTEMLDFGIRTQDI LNHHLMSGTRDVPITSVPPPQ-NDAITVHFKPITLKAS YTKVASISFDASKAKKPSQFSKITVKAKEKSYSKLEIPYQ LDGYLGGDHAATLFHIRDSPADDVERPIYLTKAMS YTKVASISFDASKAKKPSQFSKITVKAKEKSYSKLEIPYQ LDGYLGFDHAATLFHIRDSPADDVERPIYLTKAMS HILLITANSKFHLPVRVTTGFLDYFVLPFKLERFIDGFVL EASHILFAINSMPILAIKSWHILGGG\LSIELAVAVDRGN HISSIPECEKSSSDQSSVTLASGYF\AVPRVLTAKKLYPSF VHQSINIMMSFSQKVKIQQIRSLSEDVRFYYKLTAKKLYPSF VHQSINIMMSFSQKVKIQQIRSLSEDVRFYYKLTAKKLYPSF VHQSINIMMSFSQKVKIQQIRSLSEDVRFYYKLTAKKLYPSF VHQSINIMMSFSQKVKIQQIRSLSEDVRFYKHLAKKLYPSF VHQSINIMMSFSQKVKIQQIRSLSEDVRFYKHLRANKEDI KKSKIANIYTPDGLQCOBLCYVGLPFLSKSBPKVQRGVAM WDADDDLHQSLFKGWTGIKENSGRRLSAIFEWNTDLQNII TABLSWPSILSSPRHLKYPLTMTNCS-JEERITLEMPJON YQPIPLALISMBSVFVDKLVSRFNLSKVAKLIDLRTLEFQ SAHPLQSSTGFMEX\LSPHLINDILLFCGKKVXVK\FTI RTVSSLI VYNNITYWDDWMVQCGTTENLRVAGKLAPGGG FKITEALLKCCTDSLKLRSPHFTLKRTFKVENTGQLQIHII ISGYSCEGYGFKVNOCQETTSLANAVANNGCTTSMTSS SANGAMKTRPLVLDSHTGAQGRSAGKSKGKQQGGGGGG FKKG*GGYGFGFCGGGSGSSSI GSGKG*GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		1	\	CONCORD T DEDVERBUCENTEND TOOR SKELDSDVKSOERPCHI.
ANIALSAGDIDDCTTLAGTRNYDHRSKTLSTYRMOVIEA RYBSSITVTNDMP*DODIPHACMOWILKGLLSEGDSNLDVT PEDLSLAQVILINGTILLARDSSKPOGITHIDTLIRWSELTS SSASITWASFSSEDCSPOGEWTILELETQU ARAGLLGAHHLWMTLVVAAARAEKEAFVOGESITEVLRFDD LQTETTIGLSSYQQKSISLYKGNCR:1RFPDFMDFHEGEV WREKVYLHNDSSE*TITUSTSTATSTHASFFQNKKLLGG SFDVS/VFLARVVGNVENTLSITSNIGGVFT/VOFGGVFV MREKVYLHNDSSE*TITUSTSTATSTHASFFQNKKLLGG SFDVS/VFLARVVGNVENTLSITSNIGGVFT/VOFGGVFV REPPICAGAGTRKLWEIPPYETKGWMRASFSSRADNITAFT TNASDSTEFIILPVEVEVTTAGGITSTHLDFGTLRTQDL LDGYLGFDHAATLFHIRDSPADVERERILDFGTLRTQDL LDGYLGFDHAATLFHIRDSPADVERERIVINTSFSFALLE LDEGAKTMFKVHNFSKPVLILIPNSSGYIFTLLMPSTSSWR NILLITASKFHLPVEVYTTGFLDYVLPPKIERFIIDEGVL EASNILFRIINSKFSLVATGVTGFLDYVLPPKIERFIIDEGVL RASNILFRIINSKFSLGVKTGGIRSLSEDVFYKRLKARKLL DGAIGITTDVSILTIPVXLAVIAVGSLTCSPKKVVLPSFF WROSINIMNSFSQKVKIQQIRSLSEDVFYYKRLKGNKEDL KKSKIANIYPDPGLQCGDGCVGLPFLSKSEPKVQDGVAM WDADWDLHQSLFKGWTGIKENGGIRLSA IFEVNYDLQVAM WDADWDLHQSLFKGWTGIKENGGIRLSA IFEVNYDLQVAM WDADWDLHQSLFKGWTGIKENGGIRLSA IFEVNYDLQVAM WDADWDLHQSLFKGWTGIKENGGIRLSA IFEVNYDLQVAM WDADWDLHQSLFKGWTGIKENGGIRLSA IFEVNYDLQVAM WDADWDLHQSLFKGWTGIKENGGIRLSA IFEVNYDLQVAM WDADWDLHQSLFKGWTGIKENGGIRLSA IFEVNYDLQVAM WDADWDLHQSLFKGWTGIKENGGIRLSA IFEVNYDLQVAM WDADWDLHQSLFKGWTGIKENGGIRLSA IFEVNYDLQVAM WDADWDLHQSLFKGWTGIKERPHTLAKERFKKVENKVKLFT TREISBYSLISSTRHKFFFLVINTISCDGRKSVKVKVKLFT RIVSSLIIVRNNITVONDAWNOGGGTTENLRAGKLPGGG FXITEALLKOCTOSLKIR PNWTLKFFKKVENTGQLQHHI ISGYSCGYGFKVNNCQEFTLSANASRDIILTTPPOFTASI SKENGTANKTPLVLDSNTGAQGRSAGKSKGGAGGGGAG GGRGFGGGGGGGGGGGGGGGGGGGGGGGG		1	ł	
NVESTHYTMMP*DDOHFAKONTLIKGLISEDGSHIDTY PEDISLAQVIINGTLIARDSSKPOGITHIDTINWSELTS SSASITMASFSSEDCSPQGEWTILELETQN PEDISLAQVIINGTLIARDSSKPOGITHIDTINWSELTS SSASITMASFSSEDCSPQGEWTILELETQN ARAGLIGAHHIVWTLVVAARAREKEAFVQSESITEVLRFDD LOTETTLISSYQQKSISLYRGNCG 1RFEPPMLDFHEQEV KMEKVYLHNPSSS*TITLVSIFATTSIFHASFFQNKKLLEG SPDWS/VPLARVVGRWYENTLFINTSAUFTYTQVGVGFVY REPPELGARVTVMSSFSPITMIHNPHSEPLOVYMYSGGG ELPTGQQGTRKLMEITPPYETKGWARAFSSRRANNHTAFT TRASDSTEFIILPVEVEVTTAPGIYSSTEMLDFGTLRTQDL INHHLMSGTKDVFITSVEPTQVNDAITVHFREFTLKASK VTKVASISFDASKAKPSOFSGKITVKAKEKSYSKLEIPYQ LDGYLGFDHAATLFHIRDSPADPVERFILVTHFFFALLH LDERAKTMFKWHNFSKPVLILPNSGYIFTLHFMPSTSALLH LDERAKTMFKWHNFSKPVLILPNSGYIFTLHFMPSTALLH LDERAKTMFKWHNFSKPVLILPNSGYIFTLHFMPSTALLH LDERAKTMFKWHNFSKPVLILPNSGYIFTLHFMPSTALLH LSENGRENSSSDQSSVTLASGYF\AVFRVLITAKKL\A DOAIQITTDVEILTIPVK\AVTAGUSITCSPHVVLIPPKIERFIDGGVL RASNILPAIINNSFSQKVKQQIRSLEEDVRFYYKRLKRNEDL KKSKIANIYFDPGLQCOBCVYGLPFLSKSEPKVQFQVAW WADAWDLAGSLFKKWTQQIRSLEEDVRFYYKRLKRNEDL KKSKIANIYSPDGLQCOBCVYGLPFLSKSEPKVQFQVAW WADAWDLAGSLFKKWTQQIRSLEEDVRFYYKRLKRNEDL KKSKIANIYSPDGLQCOBCVYGLPFLSKSEPKVQFQVAW WADAWDLAGSLFKKWTQQIRSLEEDVRFYYKRLKRNEDL KKSKIANIYSPDGLQCOBCVYGLPFLSKSEPKVQFQVAW WADAWDLAGSLFKKWTQQIRSLEEDVRFYYKRLKRNEDL KKSLILVRNNLTVHDAVMVQGQGTTENLRVAGLLOPGO VQPPPLLXSPPGLLKRFFKVENTGQLQHHI ISGYSCBGYGFKVNCQEFTLSANASRDIILTLEPDFTASI SHAPLIKACTOSLAKLRSPHFTLKRFFKVENTGQLQHHI ISGYSCBGYGFKVNCQEFTLSANASRDIILTLEPDFTASI ELKFITTSGSFFVILNSLDYHMATAGARLPRPWELAI LSGIMSALFLLVIGTAYYLGAGIMBP\FRRES\FRRMSTSSISSSGE GSHKG*GFSGFANSSHSHNNSADVDDVRAYNSGRTSSMTSI SSQFANKTRPLVUDSNTGAQGHSAGRKSKGARGGGGCH PLEGHPOPLPPPVPQCQFGPOPERLSRAPLAHSHEERAS SSEDSDITSLIRAMDKDFDHHDSPALKFFEDSPSLIKSNTSS SSPANKTRPLVUDSNTGAQGHSAGRKSKGARGGGGCH KKRIPTDVKPGSLEPYTPPLSKGRCHSSEDGDSKKKKK KKEIPTDVKPGSLEPYTPPLSKGRCHSSEGGE PPEMDSVVHKPGSTDSLYKLSLOTUNDIFLKQRGTFF PSPAAPCPYARGSYSLINNSSSDFLKISSALPFT SRRAKKTRGTSKLVDNRFPHSN VFKLGLSRSCNQASQRSWNEFNSGPSLWSSHSADSAPT TLASIGLMGTNRSPADHASTSSPADDLGGTYNPWINDS SGDPWSNSHPPHSN VFKLGLGMTSNSPAPHAPSTSSPADDLGGTYNPWINDS			}	
PEDLSLAQVILINOTILLARDSSKPGGITHILDTINWSELTS SASITMAS FSSEDCE POGENT ILLELTON AAGLIGALHLVMTLVVAAARAEKEAPVGESI IEVLEPDO LQTETTIGISSYQGKSISLYRGNCR) IEPSPMLDPHEQPV KMEKVYLHNSSSE TILVSITATTSSFFARSTFORKKILEG SPDVS/VPLARVVGKVENTLFINTSNIGVETT/QVFGGVPV KMEKVYLHNSSSE TILVSITATTSSFFARSTFORKKILEG SPDVS/VPLARVVGKVENTLFINTSNIGVETT/QVFGGVPV RUPPICLAGRAVTVMSSFSSI INIHMHSEPLQVVENYSSGGD ELPTGQGGTRKLMEIPPYETKGVMRASFSSREADNITAST TRASDSFFILIPEVEUVTTAPGIYSTEMLDFGTLRTQDL LNIHLLNSGTKDUPITSVEPTPQ NDDAITUHFKPITLKAS/ TYKVASISFDASKAKKPSOPSGKITVKAKRKSYSKLEIPYQ LDGYLGFDHAATLFHIRDSPADVERPIYLTNTFSFAILH LLEERAKTMFKVHNFSKPULLIPENSGYIFLLTWFSFSAILH LLEERAKTMFKVHNFSKPULLIPENSGYIFLLTWFSFSAILH LLEERAKTMFKVHNFSKPULLIPENSGYIFLLTWFSTSAILH LSLPSECKSSSSDGSSYTLASGYTAVFRVKLTAKKL\K DGAIGITTDVRILITIPVK\AVIAVSLTCSPHKVULPPSF VYGSLINIMSFSGKKVIQQIRSLEBUPFYYRLRKGNKED KKSKIANIYPDPGLQCGDHCYVGLPFLSKSEPKVQPGVAM WDADWDLHQSLFKKWTGIKENGGRRLGAIFFVNTULDKNII TRABISWESILSSFRHKFFFLYNTINCS\EERITLENF/SQI VYQFIPLALYSNBSVFVDKLVSRKNLSKVAKKINKED KKSKIANIYPDPGLQCGDHCYVGLPFLSKSEPKVQPGVAM WDADWDLHQSLFKKWTGIKENGGRRLGAIFFVNTULDKNII TRABISWESILSSFRHKFFFLVNTURSS\EERITLENF/SQI VYQFIPLALYSNBSVFVDKLVSRKNLSKVAKKINKED KKSKIANIYPDPGLQCGDHCYVGLPFLSKGRKSVKVK\FT RYUSSLIIVRNNLTVVDDAVMVGGGTTENLRWGKLPGGGGGF FKITEALLKCDTDSLKARPHFTLKRFFKVENNGGLQIHHI ISGYSCBGYGFKVVNCOEFTLSANASRDIIILTPDFTASI ELKFITTSGSEFVFILNASLPYHMLATCAEALPRPWMELAI UVRFFDLRRTVGISSENNINSADVDVRANNSGRTSSMTSS SSGANKTRPLVLDSNTGAGGGAGAGSKSKGGKGGAGGGFA VGRGFGGFGFGFSSENNINSADVDVRANNSGRTSSMTS SSGSDITSLIRAMDKOFDHHDSPALBVFTEQPSPLKPGISMTS SSGSDITSLIRAMDKOFDHHDSPALBVFTEQPSPLKPGISMTS SSGDSDITSLIRAMDKOFDHHDSPALBVFTEQPSPLKSKSKKKKKKKLPSSSE SSGSDITSLIRAMDKOFDHHDSPALBVFTEQPSPLKRIL SLPGKKGRYFFRAAYTAGYKKSPGGGGFAKVSKKKTGFSSS EPPEMDSVPVHKPGSSTDSLYKLSLOTINADIFLKGRGTSPL SRRAKKTRGTSKLVDMRPPALAKFLPRNGGELGNTSSSBES PPEMDSVPVHKPGSSTDSLYKLSLOTINADIFLKGRGTSPL SRRAKKTRGTSKLVDMRPPALAKFLPRNGGELGNTSSSBES HAPVDSDGSDSSGLMSPVSNPSSDPLNSFSSPLNSSBADSADFTT TLASIGLGMTSNRSPAPHAPSTSSPADLINGSLYSLSALPTF TLASIGLGMTSNRSPAPHAPSTSSPADLINGSLYSLSALPTF TLASIGLGMTSNRSPAPHAPSTSSPADLINGSTLYSAP		1	1	ANIALSAGDIDDCDTLAQIRMIDHRPSAILSFII LEDVILAFEQ
SSASITMASFSSEDCSPOGENTILELETQH AMGLICALHLWMIVVAAARAEKEAPVOSESITEVLRFDD LQTETTIGLSSYQQKSISLYRGNCR: IRVERPDD LQTETTIGLSSYQQKSISLYRGNCR: IRVERPDMLDFHEDPY KMEKVYLHNPSSE* TITLVSITATTSHFHASFFQNRKILPG SPDWS/VPLARVVUNGVNETHISTNISHGYFTY\COVFGVGVF RLRPFLGARVTVNSSFSPIINIHNPHSEPLOVVEMYSSGGD LEPTGQCGTRKLMEIPPTETKARAFSSSREADHNITAFI TMASDSTEFIILPVEWEVTTAPGIYSSTEMLDFGTLRTQDL LMLHLNSGTKDVPITSVRPTDQD NDAITWHRWFITLKAS\ YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYQ LDGYLGFDHAATLFHIRDSFADDVERFIYLTNTFSFAILLH LEERKIMFKVHNENSKEVLLLTHSGSY'LAVFVKLTAKKLL, LSERLKTMFKVHNSKEVLLTHSGSY'LAVFVKLTAKKLL, LSENLFAINSNFIELAIKSHHIIGDG\LSISLUAVDRGM IISSLPECEKSSSDQSSVTLASGY'LAVFVKLTAKKLL, DGAIQITTDYEILTIPVK\AVIANGSLTCSPHKVVLUPSFF WORDMDLHQSJFKCKTGIKENSGAYFAVFVKLTAKKLL, DGAIQITTDYEILTIPVK\AVIANGSLTCSPHKVVLUPSFF WORDMDLHQSJFKCKTGIKENSGRENSATFEVNTDLQKNII TABLSWPSILSSPRHLKFPLTNTNCSS\CEETILENP/SQI VQPTPLALIYSNPSFYDKLVSRFNLSKVAKIDLETLENP/SQI VQPTPLALIYSNPSFYDKLVSRFNLSKVAKIDLETLEPP/SGI SAHPLQSSTGMEG\LSPHILLULLLLKPGEKKSVXVK\FT RIVSSLIIVRNNLTVMDAVMQCQCTTENLRVAGKLPGGG FKITEALLKDCTDSLKLRENPFTILKTFKVESTGLQIHI ISGYSCEGYGFKVVNCCEPTLSANASRDIILIFTPDFTASI ELKFITTTSGSFEVFLINASLPYHMLATCAEALPFRWMELA ISGIMSALFLLUGTAY\LECQGIMBF\FRRIS\FEASI SGCHTTTSGSFEVFLINASLPYHMLATCAEALPFRWMELA ISGIMSALFLLUGTAY\LECQGIMBF\FRRIS\FEASI SGCHKQ*GPSGHPHSSHNRNSADVDDVAAVNSGRTSSMTS SGCHKQ*GPSGHPHSSHNRNSADVDDVAAVNSGRTSSMTS SSGSANKTREDVLDNNTAGGGHSAGRKKGAKQSQGSGGH PLECCHPOPLPPFVPQCQEDQPERLSBADLAHPSHPERAS SSEDSDITSLIBAMDKDFDHDSPALEVFTCOPPSDLRKSI KPLCRKVKPFYKKGRKYAFPERSCEDELKDSLADDBSS' TSMPDTEPLLKBDTEKQKKGAMPEKHESBMSQVKGKSKK KKEIPTDVKPSSLELPYTPPLESKGRNLPSKIPLEDTMTT SRNACKTKGTSKLVNNRPFALAKFLPNSQELGNTSSSEGE PPEMDSVPVHKPGSSTDGLYKLSIOTINANDIFLKORGTIS SRPSNTTATSVLGNTSGLWSTSSSSDPKIKQPNGSMKKTGFSSS BLAVVDSGAGSGSSSGMTFARSVSSNKTGFSSS PPEMDSVPVHKPGSSTDGLYKLSIOTINADIFLKORGTIS PSPEMDSVPVHKPGSSTDGLYKLSIOTINADIFLKORGTIS SGSPTHTATSVLGNTSGLWSTSSSSPADDLGGTYNPMKIMS SGSPTHTATSVLGNTSGLWSTSTRAGKRCAKQSNLESDALPSPT SGSPTHTATSVLGNTSGLWSTSTRAGKRCAKQSNLESDALPSPT SGSPTHTATSVLGNTSGLWSTSTRAGKSTRUSSNLSSALPFT SSDDWSNSHPPHEN RSSDPWSNSHPPH				KAEZELHALDMDL*DDÖHLAVÖDMLTPKÖTPREÖDRUPDALUZA
AAAGLIGALHUWMILVVAAARAEKEAPVQSESIITEVREPDU LQTETTLGLSSYQQKSIISLYRGNEI PREPPMDEPHEDEV KMEKVYLHNESSE*TITLVSIFATTSHFHASFFONRKILPG SEDVS/VPLARVVGNVENTLFINTSHGYFTY\QVFGVGVP REPPELGARVTVNSSFSPIININGSEPLQVVENYSSGGD ELPTGQQGGTKKLMEIPPTETKGVMRASFSSREADNHTAFI TNASDSTEFIILPUEVEVTTAGISTEMDLOFTLRTQDL LMIHLLNSGTKDVPITSVRPTPQ\NDAITVHKPITLKAS\ YTKVASISFDASKAKKESGPSGKITVKAKEKSYSKLEIPYQ LIGYLGFDHAATLHHIDSPADPVERPIYLITHYSFFAILH LDEEAKIMFKVHNESKPULIPNESGYIFTLLFMESTSHH NILLITNASKFHLEVRYTTGFLYVLPKIERSFIIDFGVL EASNILFAIINSNPIELAIKSHHIIGGGLSIELVAVDRGK IISSLPECEKSSSDQSVXLAGGYPAVFVKLTAKKL\ DGAIQITTDYBILTTPVK\AVIAVGSLTCSPHAVVLPPSFF VHQSLNIMNSFSQKVKLQOTRSLSEDVRFYYRLLGGNEEDI KKSKIANIYFDPGLCGCHCYVCLIPLISKSPKVQGVAM WADAWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLQNIII TABLSWPSILSSPRHLKFPLINTNS\EXERTLENP\SQS YQPIPLALYSNPSVFDDKLVSRFNLSKVEKVDGVAM WADAWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLQNII TABLSWPSILSSPRHLKFPLINTNS\EXERTLENP\SQS YQPIPLALYSNPSVFDDKLVSRFNLSKVEKVDGVAM WADAWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLQNII TABLSWPSILSSPRHLKFPLINTNS\EXERTLENP\SQC SAHPLQSSTGFMEG\LSPHLIKAILIKPGEKKSVKVK\FT RIVSSILTVRNILTNMAVWQCGTENLKVAKIDLRTLEFO\ SAHPLQSSTGFMEG\LSPHLIKAILIKPGEKKSVKVK\FT RIVSSILTVRNILTNMAVWYGGTTENLRVAGKLPGPGS FKITEALLKDCTDSLKLREPNFTLKTFKVENTGQLQIHII ISGYSCGGYGFKVWCOEPTLSARGHIIISTEPDFTASI EKFITTSGSEFVFILNASLPYHMLATCABALPRDWBLAI ISGINSALFILVIGTA\YLEGGAGKSKIILTLSCDEGHSRGFCGAGGSSSI GSHG\G*GSGFHSSSHNTSHNSADVDDVRAYNGGTTSSMTSS\ SSCBDSITSLITSLLBAMMKDDDDVRAYNGGTTSSMTSS\ SSCBDSITSLITSLLBAMMKDDDDVRAYNGGTTSSMTSS\ SSCBDSITSLITSLLBAMMKDDDDVRAYNGGTTSSMTSS\ SSCBDSITSLITSLLBAMMKDDDDVRAYNGGTTSSMTSS\ SSCBDSITSLITSLLBAMMKDDDDVRAYNGGTTSSMTSS\ SSCBDSITSLLBAMMKDDDDVRAYNGGTTSSMTSS\ SSCBDSITSLLBAMMKDDDDVRAYNGGTTSSMTSS\ SSCBDSITSLLBAMMKDDDDVRAYNGGTSPHPERNS\ SSCBDSTITSLLBAMMKDDDDVRAYNGGTTSSMTSS\ SSCBDSTITSLLBAMMKDGTHDDDSALAFFLYFTEQPESPLPKSI KPCKRVEPPKGSTDSLYKLSLOTLANDIFLEFTAMT SRNQKTKGTSKLVDNRPPALAKFLDROBERSFRGGVKQKGKG KKSIPPDVAPSSLEBPTYPPLESGRAFGNSNN VFSKLGLSRSCNDASGSSSDPKKGRGFPTLNSSCBLATTPSSSIWSSNLSSALPTT SRNQKTKGTSKLVDNRPSSTBOLGGTTMPMKINSP RSSDPWANSHPPHEN SSGPWHANSHPFALAKSTRGKRDRVAYMNTIAM				
LOTETTIGLSSYQOKSISLYRCATTSHPASFORMILDER KMKVYLHNPSSEFTITUSISLENHASFORMIKLES SPDVS/VPLARVVGNVENTLFINTSHGYFTY\QVFGVGVY RLRPFLGARVTVNSSTSPIINIHPHSSEPLQVVEMYSSGD ELPTGQOGTRKLMEIPPYETKGVMRASFSSREADNHTAFI THASDSTEFIILPVEURUTTAPGIYSSTEMLDFGTLRTQDL LIMHLUSGTKDUFITSVPFTPG\ LIMHLUSGTGUFITSVPFTVLLUSGYFLAVFVKLTAKKLL\ LIMHLUFALSVPSILSPRILKFPLTNINGSY\EETILENP/SQI KKSKLANIYFDGGLQCGDHCYVGLPFISKSEPKVQPGVAM WADDDDLOGSIFKCWTGIKENSGRLSAFFEVNTDLQNII TAELSWPSILSSPRHLKFPLTNINGS\EETILENP/SQI VQFIPLALIYSNPSYFVDKLVSKRNISKVAKIDLETLENP/SQI VQFIPLALIYSNPSYFVDKLVSKRNISKVAKIDLETLENP/SQI SAHPLQSSTGFMEG\LSPRILKFPLTNINGS\EETILENP/SQI SAHPLQSSTGFMEG\LSPRILKFRVAKIDLETLEPFTASI ELKFITTTGGSEFVFTLANSAFBIILILITEPFFTASI ELKFITTTGGSEFVFTLANSAFBIILITFTPFFTASI ELKFITTTGGSEFVFTLANSAFBIILITFTPFFTASI SGIMSALFILVIGTA\LLEQGIMBEF\FRRIS\FEASI VGRPFDLRIVGISSEGNINFYSLOOPGRSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				SSASITMASFSSEDCSPQGEWTILELETQH
LOTETTIGLSSYQOKSISLYROCKPIEPPBMLDFHEDPWLDFHEDPY MREKVYLHNPSSE TITLUSIRATTSHHASFORNKILEG SPDUS/VPLARVVGNVENTLFINTSNHGUFTY\QVFGUGVP RLRPFLGARVTVNSSFSPIININHPKSPLQVUSYSSGG LEPTGQQGGTKKLMEIPPTETKGVMRASFSSREADNHTAFI TNASDSTEFIILPVEURVTTARGIYSSTEMLDFGTLRTQDL LIMHLUNGTKDUPITSVPTPG\NDATTVHKPKITLKAS\ YTKVASISPDASKAKKPSOPSGKITVKAKEKSYSKLEIPYY LOGYLGFDHAATLHHIRDSPADVEPIVLTHTFSFALLH LPEEAKTMFKVHNPSKPVLILPNESGYIFTLLFMPSTSSM NILLITNASKFHLPVRVYTOFLDYFVLPKHEERFIDFGVL ESNILFAIINSNHILLAIKSHHIIGDG\LSIELVAVURGN TISSLPECEKSSSDQSSVTLASGYF\AVFYKLTAKKL\\$ DGAIGITTDYRILTIFVK\AVIAGSIT\SHYWKLTAKKL\\$ DGAIGITTDYRILTIFVK\AVIAGSIT\SHYWKLTAKKL\\$ WOGININNBFSQKVKIQOTRSLSGDVFFYKRLKGNEDD KKSKIANIYFDGGLQCGHCYVGLPPLSKSPEKVQDGVAM WDADDCHQSLFKGWTGIKENSGHRLSAIFEVNTDLQKNII TABLSWPSILSSPRHLKFPLTNINGS\\SEETILENF/SQI YQFIPLALYSNBFSVFDKLVSFRNLSKVAKIDLETLENF/SQI YQFIPLALYSNBFSVFDKLVSFRNLSKVAKIDLETLENF/SQI SAHPLQSSTGFMEG\LSPHILKFPLTNINGS\\SEETILENF/SQI SKILTVRNILTIVMAVAVVOGSTERLIKAVGKLPGGG FKITEALLKDCTDSLKLREPNFTLKRTFKVENFGQLQHNI ISSYSCEGYGFKVVNCOFFILSNASRDIILIFTPDFTASI ELKFITTGSSEFVFILNSLDFYHLKATCAEALPRINNBLAI ISGIMSALFLUJGTA\TLEGGGBFSFFRRLS\FEASH VGRPFDLRIVGISSEGNINFTSCDGGHRGFGCAGGSSSI GSHKO*GPSGHPHSSHSNRNSADVDDVARAYNGGTTSSMTSI SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAKGAGGGGSH PLEGHPOPPLPPPVQCGEOPERLSPAPLAPSPPERLSS SSDDSITSLIBAMDKDFDHDBSPALEVFTEOPPSPLRKSI KPLCRKVKPPKKGGRKSKKGKGAMPEKKESERMSQVKGKSKK KKEIPTDVKPSSLBELPYTPPLESGRELDDBSS' TSNPDTEPLLKBDTEKKGKKGAMPEKKESGRSCDYKGKSKK KKEIPTDVKPSSLBLPYTPPLESGRELDFTANSSSEGE PPEMDSVEVHKRGSSTDSLYKLSQTILNADIFLKGURTSSFEGE PPEMDSVEVHKRGSSTDSLYKLSQTILNADIFLKGURTSSFEGE PPEMDSVEVHKRGSSTDSLYKLSQTILNADIFLKGURTSSFEGE PPEMDSVEVHKRGSSTDSLYKLSQTILNADIFLKGURTSSFEGE PPEMDSVEVHKRGSSTDSLYKLSQTILNADIFLKGURTSSFEGE PPEMDSVEVHKRGSSTDSLYKLSQTILNADIFLKGURTSSFEGE PPEMDSVEVHKRGSSTDSLYKLSQTILNADIFLKGURTSSFEGE PPEMDSVEVHKRGSSTDSLYKLSQTILNADIFLKGURTSP SLEGKNGUPTFFAAVTAGGTUSKSLSSLSSALPTDFFS SGSPHTHATAVTAGTUKGSTTFMSSSSSADDLGGTYNPMKIMSP RSSDPMSNSHPPHEN PVSIGNGWSTGULGCRSSTMGKRDAVAMNTIAMARSR	5819	1	5557	AAAGLLGALHLVMTLVVAAARAEKEAFVQSESIIEVLRFDDGGL
SPDYS/VPILARVVGNVENTLFINTSINHGUFTY\QUFGUGUP RLRPFLGARVTVNSSFSIINHHPHSEPLGVVENYSSGSE LPPTGQGGTRKLWEIPPYETKGVMRASFSSREADNHTAFI THASDSTEFILIPVEVEVTTAPGIYSSTEMLDFGTLATQDL LIMHLINGSTKDVPITSVRPTQ\NDAITVHFKPITLKAPJ LIMHLINGSTKDVPITSVRPTQ\NDAITVHFKPITLKAPJ YTKVASISFDASKAKKPSOFSGKITVKAKEKSYSKLEIPYG LDGYLGFDHAATLFHIRDSPADPVERPIYLITHFSFALIH LDEEAKTMFKVMNFSKPVLILIPNESGYIFTLLFMPSTSME NILLITNASKFHLPVVYTGFLDYYVLPPKIEERFIDFGVL ESNILFAIINNFDELAIKSHIIGGC\LSIELVAVDRGG LISSLPECEKSSSDOSSTLASGYF\AVFRVLTAKKL\R DGAIGITTDYELLTIPVK\AVIAVGSLTCSPKHVVLPPSFE VHOSLINIMMSFSQKVKLQQIRSLSEDVRFYYKRLGNKEDI KKSKIANIYFDPGLQCGDHCYVGLPFLSKSPKVQFQVAM WADADDLHGSLFKGMFGIKENGGHRLSAIFFUNTDLQNII TABLSWPSILSSPRHLKFPLTNTNCGS\SEETLENP/SQI YVQFIPLALYSNPSYFVKLVSRFNLSKVAKIDLRTLEFQ\ SHPLQSSTGFMEGG\LSPHLILINLIKFGEKKSVKVK\T\FT RTVSSLIIVRNNLTVMDAMVQGQGTTENLRVAGKLDGGG FKITEALLKDCTDSLKLRPNFTLKTFKVENTGQLOIHI ISGYSCEGYGFKVVNCQEFTLSANASRDIIILFTDFTASI ELKFITTSGSEVFILINASLPYHMLATCABALDRINMLAI JSGIMSALFILLVIGTA\YLLBAPHMLATCABALDRINMLAI SGIMSALFILLVIGTA\YLLBAPHMLATCABALDRINMLAI SGIMSALFILLVIGTA\YLLBAPHMLATCABALDRINMLAI SGYSCEGYGFKVNNCQEFTLSANASRDIIILFTDFTASI GHKQ'GPBGHPSSHSNNLNSLOVDURNAYNGRTSSMTS SSCPANKTRPLVLIDSNTGAGGHSAGKKKGAKQSQHSQH PLEQHBOPPLPPPVPQGBPQFERISPAPLAHPSHPERAS SSCPANKTRPLVLIDSNTGAGGHSAGKKKGAKQSQHSQH PLEQHBOPPLLPPPVPCPQBPQFERISPAPLAHPSHPERAS SSCPANKTRPLVLIDSNTGAGHSAGKKKGKKGNALGANGKKKG KKSIPTDVKPSSLELPYTPPLESKGRRILPSKIPLPTAMT' SRNAGKTKGTSKLVDNRPPALAKFLOTNADIFIKORGTSF PPEMDSVPVHKRGSSTDGISKLOTNADIFIKORGTSF PSPDAAPCPFVARGSYSSIVNSSSSDPKIKGPSSSE PPEMDSVPVHKRGSSTDGISKLSOLNENTISSSEE PPEMDSVPVHKRGSSTDGISKLSOLNENTISSSEE PPEMDSVPUKRGSSTDGISKLSOLNENTISSSEE PPEMDSVPOKRGSSTDFTLNNSSAGRMFKYSSKTGFSSSI SGSPPHTATSVLGNTSGPSTUMESSPATDHSSS SGSPHKATSVLGNTSGPSTUMESSPATDHSSS SGSPHTATSVLGNTSGPSTUMESSPATDHSSS SGSPHKSSHFPHEN VFSKLGLSRSCNQASQRSWNENSGSPSTUMESSPATDHSSS SGSPHTATSVLGNTSGPSTUMESSPATDHSSS SGSPHTATSVLGNTSGPSTUMESSPATDHSSSSSEE PSSDPSSSHFPHEN VFSKLGLSRSCNQASGRSWNENSGSPSTUMESSPATDHSSPS SGSPPHSNSHFPHEN PSSIGGPSSLGVLLCARSSTMGKRDNRVYMMFIAMASSR		1	1	LQTETTLGLSSYQQKSISLYRGNCRPIRFEPPMLDFHEQPVGMP
RIRPPICARVITVISSES I INIHHPHSEPLOVVEMYSSGED ELPTGQQGGTRKLMEIPPYETKGWMRAS FSSREADNITAFI TINASDSTEF I LIPVEVEVTTAPGIYSSTEMLDFGTLRTQDL LINIHILINGTKDVPITSVRPTPQ\NDAITVHFKPITLKAS\ YYKVASISPDASKAKKPSQFSKITVKAKEKSYSKLEIPYQ TICKASISPDASKAKKPSQFSKITVKAKEKSYSKLEIPYQ TYKVASISPDASKAKKPSQFSKITVKAKEKSYSKLEIPYQ LDGYLGFDHAATLFHIRDSPADPVERPIYLTNTFSFAILH LEEEAKTMFKVHINFSKPVLILPNESGYIFTLLFMPSTSSME NILLITNASKFHLPVRVTGFLDYFVLPPKLEERFIDFGVL EASNILFAIINDNPIELAIKSWHIIGDG\LSIELVAVDRGN IISSLPCEKSSSOQSSVTLASGYF\AVFRKVLTAKKL\ DGAIGITTDYELITTPVK\AVIAVGSLTCSPKHVVLPPSFF VMOSLNINMSFSGKVKLQQIRSLERDWFYYKRLGKNEDL KKSKTANIYPPDELQCGDECTVGLPFLSKESPKVQPGVAM WDADWDLHQSLPKGMFGIKENSGRBLSAIFEVNTDLQNII TAELSWPSILSSPRHLKPPLININCSS\EEEITLENP/SQI VQCPIPLALIYSMPSVFVDKLVSRFRLSKVAKLDLRTLEFGO SAHPLQSSTGFMEG\LSPHLINALIKFGEKKSVKVK\FTI RIVSSLIIVRNNLTVADAWWQCGTTENLRVACKLPGPGS FKITEALLKCCTDSLKLREPNFTLKRTFKVENTGQLQIHII ISGYSCEGGGFKVVNCQGFTELSANASRDIILFTPDFTASI ELKFITTSGSEFVFILNASLDYHMLATCAEALPRINBELA ISGIMSALFLLVIGTA\YLEAGGIMEP\FRRIS\FFRASNI VGRPFDLRRIVGISSEGNINTLSCDPGHSGFGCGAGGSSSI GSHKG\G*GFGFFFILNASLDYHMLATCAEALPRINBELA ISGIMSALFLLVIGTA\YLEAGGIMEP\FRRIS\FFRASNI VGRPFDLRRIVGISSEGNINTSCDPGHSGFGFCGAGGSSSI GSHKG\G*GFGFAFSSHSNISADVDUVRAYNGGRTSSMTSS SSCPANKTRPLVLDSNTGAGGGRAGRKSGRANGSGHGGH PLEQHPQPPLPPPVPQPQPDPBERLSPAPLAHPSHPERSS SSCDSDITSLIRMMKDFHHIDSPALEVFTEQPPSPLPKSI KPLGRKVKPPKKGEEKEKKGKCKPGEDLKOSLADDDSSS TSMPDTEPLLKERDTEKOKGKAMPEKHESEMSVAVKKKK KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPSTAMT SRNAGKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGE PERMOSVPVHKRGSSTDSLYKLSLOTLNADIFLKGRQTSSP PSPRAPCPPVARGSSTDSLYKLSLOTLNADIFLKGRQTSSP PSPRAPCPPVARGSSTDSLYKLSLOTLNADIFLKGRQTSSP PSPRAPCPPVARGSSTDSLYKLSLOTLNADIFLKGRQTSSP PSPRAPCPPVARGSSTDSLYKLSLOTLNADIFLKGRGNISH VFSKLGLSRSCNQASGRSNNERNSGPSYLWESPATDPSPSI SGEPTHATATVALVLANTSGLMSTPSSSP SPDFTLINSSAFGNSN VFSKLGLSRSCNQASGRSNNERNSGPSYLWESPATDPSPSI SGEPTHATATVALVLANTSGLMSTPSSSP SPDFTLINSSAFGNSN VFSKLGLSRSCNQASGRSNNERNSGPSYLWESPATDPSPSI SGEPTHATATVALVLANTSGLMSTLSSLPFT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP RSSDPWSNSHFPHEN		1		KMEKVYLHNPSSE*TITLVSIFATTSHFHASFFQNRKILPGGNT
ELPTGQCGGTRKLMELPPYETKGVMRASFSSREADNITAFI TNASDSTEFILLPVEVEVTACITYSTEMLDFGTLRTQDL LINHHLINGGTKDVPITSVRPTPQ\NDAITVHFKPITLKAS\ YYKVASISFDASKAKKRSOPSGKITVKAKEKSYSKKEIPYQ LIGGYLGFDHAATLFHIRDSFADPVERPIYLTNTFSFAILH LPEEAKTMFKVINFSKPVLILPNESGYIFTLLFMPSTSSMI NILLITNASKFHLPVRVTTGFIDFYVLPPKIERFIDFGVL EASNILFAIINSMPIBLAIKSWHIIGDG\LSIBLVAVDRGN TISSLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\ DGAIGITTDYELITIPVK\AVAUAGSLTCSFKHVVLDPSF VHQSLNIMNSFSQKVKIQQIRSLSBDVFFYYKRLRGKKEDL KKSKIANIYFDDGLQCDHCYVCLPFLSKSPKVQDVAMW WDADDLHGSFKGWTGIKENSCHRLSAIFEVNTDLQKNII TRALSWPSILSSPRHLKPPITNINGS\EBEITLENP/SQU YVQPIPLALYSNPSVFDVALVSRRNLSKVAKIDLRTLEFQV SAHPLQSSTGFMEG\LSPHLLINLILKFGEKKSVKVK\FTI RTVSSLIIVRNNLTVWDAVWVQCGTTENREVACKLGGDGS FKITEALLKOCTDSIKLREPNFTLKFFFKVENTGQLQTHI LSGYSCGGYGFKVVNCQEFFLSANASRDIIILFPDFTASI ELKFITTSGSEFVFILNASLBYHMLATCAEALPRPNWELAI ISGIMSALETLLVIGTA\YLEAQGIWBF\FRRRLS\FEASNI VGRPFDLRRTVGISSENINTLSCDFGHSRGFCGAGGSSSI GSIKQ\GPSGHPHSHSHNSDVDDVRAYNSGTTSSMTSI SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAGGGHGSGH PLEGHPOPPLPPPVQPQPGPOPBELBPALAHPBHPERAS SSCDSITSLIBAMDKDFDHDDSPALEVFTTQPPSPLPKSI KPLQRKVKPPKKQBEKEKKKKGKPQEBELKOSLADDDSSS' SSCPSITISLIBAMDKDFHHDSPALEVFTTQPPSPLPKSI KPLQRKVKPPKKQBEKEKKKKGKPQEBELKOSLADDDSSS' TSMPDTEPLLKEDTEKQKKGKJMPEKHESEMSQVKKSKK KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMT: SRRAQKTKGTSKLJVDNRPPALAKFLPNSQELGNTSSSSGE PEPEMDSVPVIKRGSSTSSILKSLGTCHADTFSSSSGE PEPEMDSVPVIKRGSSTSSILKSLGTCHADTFSSSGEN PSPPAAPCPFVARGSYSIVMSSSSDPKIKOPNGSKHKL' SLPGKKGNPTFAAVTAGYDKSPGSSUFMSKNSCHSPSSI PSPPAAPCPFVARGSYSIVMSSSSDPKIKOPNGSKHKL' SLPGKKGNPTFAAVTAGYDKSPGSSUFMSSNSSDPKIKPGSSTSSALPFT TLASIGLMGTHSRSPNAPSTSSPADDLGQTYNPWRIMSP SGSPPHATSVLGNTSGLWSTTFPSSSI WSSNLSSALPFT TLASIGLMGTHSRSPNAPSTSSPADDLGQTYNPWRIMSP SGSPPHATSVLGNTSGLWSTTFFSSST SSSSLPSSALPFT TLASIGLMGTHNSPSAPHAPSTSSPADDLGQTYNPWRIMSP RSSDPMSNSHPHEN				SFDVS/VFLARVVGNVENTLFINTSNHGVFTY\QVFGVGVPNPY
INASDSTEFILIPVEVEVTTAPGITYSTEMLDRGTLETQDU LINLILLINGTKDVPITSVRPTPQ\NDAITVHFRPITLKAS\ YTKVASISFDASKAKRSGFSGKITVKAKEKSYSKLEIPYQ LDGYLGFDHAATLFHIRDSPADPVERPIYLTNTTSFAILH LDEBAKTMFKVNMPSKPVLILPNESGYIFTLLFMPSTSSMM NILLITNASKFHLPVRVYTGFLDYFVLPPKIERFIDFGVL EASNILFAIINSMPIBLAIKSWHIJGDG\LSIELVAVDRGM IISSLPECEKSSSDGSVTLASGYF\AVFRVLTAKKL\E DGAIQITTDYEILTIPVK\AVIAVGSLTCSPKHVVLPPSFF VHQSLNIMMSFSQKVKIQQIRSLSEDVRFYYKRLRGNKEDD KKSKIANIYFDPGLQCGDHCYVGLPFLSKSEPKQPGVAMM WADMDLHQSLPKGWTGIKENSGHRLSAIFFVNTDLQKNII TABLSWPSILSFRHLKFPLTNTNCSS\EEFITLENP/SQI YQPIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQ\ SAHPLQSSTGFMEG\LSPHLILMLILKFIEKKVKVK\FTI RTVSSLIIVMNNITVEMDAVQGGTTENLRVAGKLPGGG FKITEALLKDCTDSLKLRENPTLKRFFKVENTGGLQHHI ISGYSCEGGYGFKVVNCQEFTLSANASRDIILFFDFTASI ELKFITTSGSEFVFILNASLPYHMLATCAEALPPRNMELAI SGIMSALFLLVIGTAYLEAQGIWEP\FRRLS\FFASNI SGSHK\GPSGHPHSSHNRNSADVDDVRAYNSGRTSSMTSI SSGPANKTRFLVLDSNTGAQGHSAGRKSKGAKGSGHGSGH PLEQGHOPPLPPPPPQPGEPOPELISPAPLAHPSHPERAS SSGPANKTRFLVLDSNTGAQGHSAGRKSKGAKGSCHGSGH PLEQGHOPPLPPPPPPPQEPOPELISPAPLAHPSHPERAS SSGPANKTRFLVLLDSNTGAQGHSAGRKSKGAKGSCHGSGH PLEQGHOPPLPPPPPPPPPPPPGEPQEPLKDSLADDBSSS' SSCDSDITSLIEAMDKDFDHHDSPALEVFTEQPPPPLKSI KPLCRKVKPPKKGBEKEKKGKGKPGDELKDSLADDBSSS' SSCDSNTKGTSLKLEDTTERGKRQAMPEKLESEMSQVKQKKK KKEIPTDVKBSSLELPYTPPLESKQRRNLPSKSEEDE PPEWDSVPVKKPGSSTDSLYKLSJQTLUNDIFLKRGRTSP PSPPAAPCPPVARGSYSSIVMSSSSDPKIKPNGSKHKLS SLPGKNGNPTFAAVTAGYDKSPGSMGPAFKSSNTGNSSSEGS HAPVDSDGSDSSGLWSPVSPSSPDFPPLNSFSAFGNSFN VFSKLGLSRSCNQAQRSWMEFNSGSPYLWSSPATDPSPSI SGSPHTATTSVLGNTGSWFTFPFSSIV KSSLSSALPFT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP RSSDPWSNSHFPHEN VFSKLGLSRSCNQAQRSWMEFNSGSPYLWSSPATDPSPSI SGSPHTATTSVLGNTGSWFTFPFSSIV KSSLSSALPFT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP RSSDPWSNSHFPHEN VFSKLGLSRSCNQAQRSWMEFNSGSPYLWSSPATDPSPSI SGSPHTATTSVLGNTGKARSTTFPFSSIV KSSNLSSALPFT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP RSSDPWSNSHFPHEN		1	ļ	RLRPFLGARVTVNSSFSPIINIHNPHSEPLQVVEMYSSGGDLHL
IMHILINSGTKDVPITSVRPTPO\UNDAITVHFKPITIKAS\ YTKVASISPDASKAKKPSOFSGKITVKAKEKSYSKLEIPYQ LDGYLGFDHAATLFHITGSPADFVERPIYLINTFSFAILIH LDEEAKTMFKVHNFSKYVLILPNESGYIFTLLFMPSTSSME NILLITNASKFHLPVRVYVLILPNESGYIFTLLFMPSTSSME NILLITNASKFHLPVRVYVLILPNESGYIFTLLFMPSTSSME NILLITNASKFHLPVRVYVLILPNESGYIFTLLFMPSTSSME NILLITNASKFHLPVRVYVLILPNESGYIFTLLFMPSTSSME NILLITNASKFHLPVRVYVLILTPEVKLISKFIDFGVI EASNILFAIINSMPIELAIKSWHIIGDG\LSIELVAVDRGN IISSLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\ DGAIOITTDYELITIPVK\AVIAUGSLITCSFKHVVLDPSFI VROSLNIMMSFSQKVKIQQIRSLSEDVRFYYKRLRGNKEDL KKSKIANIYFDDGLQCDHCYVCLPFLSKESFKVQDGVAMW MDADDHLGGLFKGWTGIKRNSGHRLSAIFEVNTDLQKNII TABLSWPSILSSPHLKFPLTNINGS\EERITLENP/SQL YQPIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQY YQPIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQY YQPIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQY SHPLQSSTGHFME\LSPHJLINLILLFGEKKSVKVK\FTI RTVSSLIIVRNNLTVMDAVMVQCGGTTENLRVAKKLPGPGS FKITEALLKDCTDSLKLREPNFTLKRTFKVENTGQLQHHI ISGYSCEGYGFKVVNCQEFTLSANASRDIIILFTPDTFASI ELKPITTSGSFFVILMASLDYHMLATCAEALPRNWELAI ISGIMSALFILVIGTA\YLEAQGIWBP\FRRLS\FEASNI VGRFFDLRRIVGISSEGNIANSSDIIILFTPDTFASI ELKPITTSGSFFVILNASLDYHMLATCAEALPRNWELAI ISGIMSALFILVIGTA\YLEAQGIWBP\FRRLS\FEASNI VGRFFDLRRIVGISSEGNIANSSDDVAYNSGRTSSMTSS SQSANKTRPLVLDSNTGAQGHASARKS KEAQGGGGSGGH PLEQHOPPLPPPVPQCBPOPERLSPAPLAHPSHPERAS SSEDSDITSLIBAMDKDFDHHDSPALBYFTGOPPSPLPKSI SSEDSDITSLIBAMDKDFDHHDSPALBYFTGOPPSPLPKSI SPLORHVKYPKKQBEKEKKGKGKPQEDELKDSLANDDSSS TSNPDTEPLLKEDTEKÇKGKQAMPEKHESEMSQVKQKSKU KKSIPTDVKPSSLELPYTPPLESKQRRNLPSKILDPTAMTI SRNAQKTKGTSKLLDNRPALKFLPNSGELGNTSSSSES FPPEMDSVPVHKPGSSTDSLYKLSLOTLNADIFLKGRGFSSS PSPRAAPCPFVARGSYSTUNGSSSSDPKIRQPMSKHKLY SLPRGKGNGTFAVGLAGRTFTPSSSI WSSSSSDPKIRGSSSS HAPVDSDGSDSGLWSPVSNPSSPDFTPLNSFSAFGNFN VFSKLGLSRSCNQASQRSWMEFNSGGSVLWESPATDPSPS SGSPTHTATSVLGNTSGWTFTSPSSI WSSNLSSALPFT TLASIGLMGTENSPAPHAPSTSPADDLGGTYNPWRIWSP RSSDPNSNSHPHEN SSDPSDNSNSHPHEN		1	1	ELPTGQQGGTRKLWEIPPYETKGVMRASFSSREADNHTAFIRIK
IMHILINSGTKDVPITSVRPTPO\UNDAITVHFKPITIKAS\ YTKVASISPDASKAKKPSOFSGKITVKAKEKSYSKLEIPYQ LDGYLGFDHAATLFHITGSPADFVERPIYLINTFSFAILIH LDEEAKTMFKVHNFSKYVLILPNESGYIFTLLFMPSTSSME NILLITNASKFHLPVRVYVLILPNESGYIFTLLFMPSTSSME NILLITNASKFHLPVRVYVLILPNESGYIFTLLFMPSTSSME NILLITNASKFHLPVRVYVLILPNESGYIFTLLFMPSTSSME NILLITNASKFHLPVRVYVLILPNESGYIFTLLFMPSTSSME NILLITNASKFHLPVRVYVLILTPEVKLITSFKHVVLPSFI LESSIPECEKSSSSDQSSVTLASGYFAVFRVKLTAKKL\ DGAIOITTDYELITIPVK\AVIAVGSLTCSFKHVVLPSFI VROSLNIMMSFSQKVKIQQIRSLSEDVRFYYKRLRGNKEDL KKSKIANIYFDDGLQCDHCYVCLPFLSKESFKVQFCVAMW MDADDLHQSFKGWTGIKRNSGHRLSAIFEVNTDLQKNII TABLSWPSILSSPHLKFPLTNINGSS\EERITLENP/SQL YQPIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQY YQPIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQY YQPIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQY SAHPLQSSTGFMES\LSPHILINLILLFGEKKSVKVK\FTI RTVSSLIIVRNNLTVMDAVMVQCGGTTENLRVAKKLPGPGS FKITEALLKDCTDSLKLREPNFTLKRTFKVENTGQLQHHI ISGYSCEGYGFKVVNCQEFTLSANASRDIIILFTPDTFASI ELKPITTSGSFFVILMASLDYHMLATCAEALPRNWELAI ISGIMSALFILVIGTAS\YLEAQGIWBP\FRRLS\FEASNI VGRFFDLRRIVGISSEGNIANTLSCDPGHSRGFCGAGGSSSI GSHKO*GFBGHPHSSHSNRNSADVDUVRAYNSGRTSSMTSS SSQSANKTRPLVLDSNTGAQGHSARKSK KRAKQSGHGSGH PLEQHPOPPLPPPVPQCBPOPERLSPAPLAHPSHPERAS SSCDSDITSLIBAMDKDFDHHDSPALBYFTGQPSPLPKSI SSCDSDITSLIBAMDKDFDHHDSPALBYFTGQPSPLPKSI SSCDSDITSLIBAMDKDFDHHDSPALBYFTGQPSPLPKSI SKDSDITSLIBAMDKDFDHHDSPALBYFTGQPSPLPKSI SKDSDITSLIBAMDKDFDHHDSPALBYFTTQPSPSPLAKSI SKDSDITSLIBAMDKDFDHHDSPALBYFTTQPSPLPKSI SKDSDYVKKPBKKKGKGKPQEDELKDSLADDBSS' TSNPTPEPLLKEDTEKÇKGKQAMPEKHESEMSQVKQKSKK KKSIPTDVKPSSLELPYTPPLESKQRRNLPSKILDPTAMTA SRAQKTKGTSKLLDNRPALKFLPNSGELGNTSSSSES PPEWDSVPVHKPGSSTDSLYKLSLOTLNADIFLKGRGFSSS PSPARAPCPFVARGSYSSTUNSSSSDPKIRQPMSKHKL' SLPRCKGMPTFAAVTAGVDKSPGSSUMSFTNSGSSVLMEDPATDPSPS HAPVDSDGSDSGLWSPVSNPSSPDFTPLNSFSAFGNSFN VFSKLGLSRSCNQASQRSWMEFNSGSSVLMEDPATDPSPS SGSPTHTATSVLGNTSGWTFTPSSSI WSSNLSSALPFT TLASIGLMGTENSPAPHAPSTSPADDLGQTYNPWRIWSP RSSDPMSNSHPHEN SSDPSDNSNSHPHEND 310 320 320 320 320 320 320 320		j	i.	TNASDSTEFIILPVEVEVTTAPGIYSSTEMLDFGTLRTQDLPKV
YTKVASISPDASKAKKPSOPSGKITVKAKEKSYSKLEIPYO LDGYLGFDHAATLFHIRDS PADPVERPI YLINTYFSFAILH LPEEAKTMFKVHNFSKPVLILPNESGYIFTLLFMPSTSSME NILLITNASKPHLPVRYTTGFLOFYVLPPKIERFIDFGVI EASNILFAI INSNPIELAIKSWHI IGGO ILSIELVAUDGGN IISSLPECEKSSSDQSSVTLASGYF\AVFRVKLTAKKL\N DGAIGITTTVEILITIPVK\AVIAVGSLTCSPKHVVLPPSFI VHOSLNIMMSFSQKVKIQQIRSLSBUPKFYYKKLRGKKEDL KKSKIANIYFDPGLQCGDHCYVGLPFLSKSBPKVQFGVAMM WDADWDLHQSLFKGWTGIKENSGHRLSA IFFVNTDLQKNI TARLSWPSILSSPRHLKFPLTNTNCSS\EEITLENP/SQI YVQFIPLALYSNPSVFVVKLVSRFNLSKVAKIDLRTLEFGY SAHPLQSSTGFMEG\LSPHLILNLILKPGEKKSVKVK\FTI RTVSSLI IVRNNLTVMDAWNVGQGTTENLRVAGKLPGPGS FKITEALLKDCTDSLKLREPNFTLKTFKVUNTGQLGIHI ISGYSCEGYGFKVVNCOFTLSANASRDI IILFPDFTASI ELKFITTSGSEFVFILNASLPYHMLATCAEALPRPNWELAI ISGIMSALFLLVIGTA\YLEAGGIWBP\FRRRLS\FEASNI VGRPFDLRRIVGISSEGFTLSANASRDI IILFPDFTASI GSHQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSS GSHKQ*GPSGHPLSPPVPCBPQBERGFCGAGGSSGI GSHKQ*GPSGHPLPPVPCPGPQEPGERLSPAPLAHPSHPERASI SSCPANKTRELVLDSNTGAGGHSAGRKSKGAKQSGHGSQH PLECHPOPPLPPPVPCPGPQPEPCERLSPAPLAHPSHPERASI SSEDSDITSLIEAMBKDFDHHDSPALBVFTEQPSPPLPKSI KPLCRKVKPPKKGEEKEKKKGKKPQEDELKDSLADDDSSS' TSMPDTEPLLKEDTEKQKKGAMPEKHESEMSQVKQKSKK KKSIPTDVKPSKGEKKKKKGKKPQEDELKDSLADDDSSS' TSMPDTEPLLKEDTEKQKKCAMPEKHESEMSQVKQKSKK KKSIPTDVKPSSTDSIYKLSLOTINADIFLKORGTSP PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPMGSKHKIL SLPGKNGNPTFAAVTAGYDKSPGGLGNTSSSEGE PPEMDSVPVHKPGSSTDSIYKLSLOTINADIFLKORGTSP PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPMGSKHKIL SLPGKNGNPTFAAVTAGYDKSPGGRGAKVSSNTGFSSS HAPVDEDGSDSSGLWSPNPSSPDPTPLNSFSAFGNSFN VFSKLGLSRSCNQAGGRSWEFNSGPSYLWESPATDPSPSI SGSTHTATSVLGNTSGNTSTPFSSSIWSSNLSSALPFT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP RSSDPWSNSHFPHEN PSSILSGPVLGLLLCARSSTMGKRDNRVAYMNPIAMASSR		ì		LNLHLLNSGTKDVPITSVRPTPQ\NDAITVHFKPITLKAS\ESK
LDGYLGFDHAATLFHIRDSPADPVERPIYLTNTFSFAILH LPEEAKTMFKVHNFSKPVLILPNESGYIFTLLFMPSTSSMH NILLITNASKFHLPVRYTGFLDYFVLPFKLERFIDFGVI EASHILFAIINSHPIELAIKSWHIIGDG\ISIELVAVDROK IISSLPECEKSSSDQSSVTLASGYF\AVPRVLITAKL\F DGAIGITTDVEILTIPVK\AVIAVGSLTCSPKHVVLPPSFF VHOSLMIMMSFSGKVKIQQIRSLSBDVRFYYKRLRGKKEDL KKSKIANIYFDPGLQCGVYGLPPLSKSPFKVQPGVAM WDADWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLQKNII TABLSWPSILSSPRHLKFPLTNTNCSS\EEEITLENF\SQI YVQPIPLALYSNPSVFVKLVSRFNISKVAKILDKTLEFOV SAHPLQSSTGFMEG\LSPHLILNLILKPGEKKSVKVK\FTI RIVSSLIIVRNNLTVMDAVMVQGGTTENLRVAGKLBGPGS FKITEALLKOCTDSLKLKEPNFTLKRFFKWPNTGLQUHHI ISGYSCEGYGFKVVNCQEFTLSANASRDIIILFTPDFTASI ELKFITTSGSEFVFILNASLPYHMLATCABALBPRPNELAI ISGIMSALFLLVIGTA\LLAQGIWBF\FRRIS\FFASNI VGRFFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSS GSHKQ*GFSGHPHSSHSNRNSADVDDVRAYNSGKTSSMTS SSQPANKTRPLVLDSNTGAGGHSAGRKSKGAKGSGHGSQH PLEGHPQPPLPPPVPQPQEPPERLSPAPLAHPSHPERASI SSEDSITSLIEAMMKDEPHHDSPALEVFTEQPSPLYKSI KPLCRKVMPPKKGEEKEKKGKCPGELKDSLADDDSSS* KPLCRKVMPPKKGEEKEKKGKCPGELKDSLADDDSSS* KPLCRKVMPPKKGEEKKKGKCPGELKDSLADDDSSS* KPLCRKVMPPKKGEEKKGKGKQEDELKDSLADDDSSS* KPLCRKVMPPKKGEEKKGKGKPQEDELKDSLADDDSSS* SPPHDSVPVHKPPSSTDSLYKLSLOTLNADIFLKORGTSPS PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKGPGSSSSE PPEWDSVPVHKPGSSTDSLYKLSLOTLNADIFLKORGTSPS SRAQKTKGTSKLIVNRPPALAKFLENSQELGNTSSSSEG PPEWDSVPVHKPGSSTDSLYKLSLOTLNADIFLKORGTSPS SPARACKTRGTSKLIVNRPPALAKFLENSQELGNTSSSSEG PPEWDSVPVHKPGSSTDSLYKLSLOTLNADIFLKORGTSPS SGSGHTHTATVLGNTSGLMSTTFFSSSIWSSNLSSALPFT TLASIGLMGTENSPAPHAPSTSPADDLGQTYNPWRIWSP GSSPTHTATSVLGNTSGLMSTTFFSSSIWSSNLSSALPFT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP RSSDPWSNSHPPHEN RSSDPWSNSHPPHEN		ì	4	YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYQAEV
LPEEAKTMFKVUNDFSKPULILPRESGYIFTLLFMPSTSSME NILLITNASKPHLPVRVYTGFLDYFVLPPKIEERFIDFGVL EASNILFAI INSNPIELAIKSWHIIGDG\LSIELVAVDRGM IISSLPECEKSSSDQSSVTLASGYF\AVFVKLTAKKL\F DGAIQITTDYELITIPVK\AVIAVGSLTCSPKHVVLPPSFF VHGSLNIMNSFSGKVKIQQIRSLSEDVRFYYKRLRGNKEDL KKSKIANIYFDPGLQCGDHCYVGLPFLSKSEPKVQPGVAMM WDADWDLHQSLFKGWTGIKENGSHRLSAIFEVNTDLQKNII TABLSWPSILSSPRHLKFPLTNINCSS\EETILENP\SQC YVQFIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQV SAHPLQSSTGFMEG\LSPHLIKNILKFGEKSVKVK\FTI RTVSSLIVANNLITVNDAVMVQGGTTENLRVAGKLPGPGS FKITEALLKDCTDSLKLREPNFTLKRTFKVENTGQLQHHII ISGYSCEGYGFKVVNCQEFTLSANASRDIILJETPDFTASI ELKFITTGSSEFVFILNASLDYHMLATCAEALPRPNMELAI ISGIMSALFLLVIGTA\YLEAQGIWBP\FRRRLS\FEASNI VGRPFDLRRIVGISSEGNLITLSCDPGHSRGFCGAGGSSSI GSHQX*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSS SQFANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHGSQH PLEQHPQPPLPPFVQQPGEPOPERLSPAPLAHPSHPERASI SSEDSDITSLIBAMDKDFDHDLSPALWFTEQPPSPLPKSI KPLCRKVKPPKKQEKKEKKKGKPQEDELKDSLADDDSSST TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKK KKEIPTDVKPSSLELPYTPPLESKGRRNLFSKTLPTPAMTI SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEI PPEMDSVPVHKPGSSTDSLYKLSLOTLNADIFLKQRGTSP PSPPAAPCPFVARGSYSSIVNSSSSDPKIKQPNGSKKKL SLPCKNGMPTFAAVTAGYDKSPGGMGFAKVSSKKTGFSSSI HAPVDSDGSDSSGLWSPVSNPSSDPTPLNSFSAFGNSFN VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATSVLCANTSGLWSTTPFSSSIWSSNLSSALPFT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP RSSDPWSNSHFPHEN PSVSSSPWSNSHFPHEN PSVSSSPWSNSHFPHEN		1	ł	LDGYLGFDHAATLFHIRDSPADPVERPIYLTNTFSFAILIHDVL
NILLITNASKPHLPVRVYTGFLDYFVLPPKIERFIDFGVL EASNILFAIINSNPIELAIKSWHIIGDG\LSIELVAVDRGN IISSLPECKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\B DGAIQITTDYBILTIPVK\AVIAVGSLTCSPKHVVLPPSFF VHQSLNIMNSFSQKVKIQQIRSLSEDVRFYYKRLRGNKEDI KKSKIANIYFDPGLQCGHCYVGLPFLSKSEPKVQEVANW WDADWDLHQSLPKGWTGIKENSGHRLSAIFEVNTDLQKNII TARLSWPSILSSPRHLKFPLTNINCSS\EEFITLENP/SQI YVQFIPLALYSMPSVPVDKLVSRFNLSKVAKIDLRTLEFQV SAHPLQSSTGFMEG\LSPHLILNLILKPGEKKSVKVK\FTI RTVSSLIIVRNNLTVMDAVMVQQGTTENLRVAGKLPGPGS FKITEALLKDCTDSLKIREPNFTLKRTFKVENTGQLQIHII ISGSCEGYGFKVVNCQEFTLSANASRDIIILFTPDFTASI ELKPITTSGSEFVFILNASLPYHMLATCAEALPRPNWELAI ISGIMSALFLLVIGTA\YLEAQGIMEP\FRRRLS\FEANNI VGRPFDLRRIVGISSEGNIMTLSCDPGHSRGFCGAGGSSI GSHKQ*GPSGHPHSSHNRNSADVDDVRAYNSGRTSSMTSI SSCPANKTRPLVLIDSNTGAQGHSAGRKSKGAKQSQHGSQHI PLEQHPQPPLPPPVQCPEQDERLSPAPLAHPSHPERASI SSEDSDITSLIBAMDKDFDHHDSPALEVFTEQPPSPLPKSI KPLCRKVMPPKKQESKEKKKGKGKPQEDELKDSLADDDSSS* TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKK KKETTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMT: SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGE PPEWDSVPVHKPGSSTDSLYKLSLOTLNADIFLKORGTSP' PSSPAAPCFPVARGSYSSIVNSSSSDPKIKQPNGSKHKL SLPCKNGGNFFFAAVTAGYDKSPGGMGFARVSSNKTGFSSS' HAPVDSDGSDSSGLWSPVSNPSSDPDFTPLNSFSAFGNSFN VFSKLGLSRSCNQASQRSWREFNSGPSYLWESPATDPSPSI SGSPTHATTSVLGNTSGLWSTTPFSSSIWSSNLSSALPFT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP- RSSDPWSNSHFPHEN PVSSIGMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP- RSSDPWSNSHFPHEN		1	•	LPEEAKTMFKVHNFSKPVLILPNESGYIFTLLFMPSTSSMHIDN
EASNILFAI INSNPIELAIKSWHI IGGG\LSIELVAUDRON IISSLPECEKSSSSDQSVTLASGYF\AVFRYKLTAKKL\B DGAIQITTDYEILTIPVW\AVIAVGSLTCSPKHVVLPPSFI VHQSLNIMNSFSQKVKIQQIRSLSEDVFYYYRLRGNKEDL KKSKIANIYFDPGLQCGDHCYVGLPFLSKSEPKVQPQAM, WDADWDLMQSLFKGWTGIKENSGHRLSAIFEVNTDLQKNII TABLSWPSILSSPRHLKFPLTNTNCSS\EEEITLENP/SQI YVQFIPLAIJSNPSVFVUKLVSRFNLSKVAKIDLRTLEFOJ SAHPLQSSTGFMEG\LSPHILINILIKYPGEKKSVKVK\FVI RIVSSLIIVRNNLTVMDAVMVQCQGTTENLRVAGKLPGPGS FKITEALLKDCTDSLKLREPNFTLKRTFKVENTGQLQIHTI ISGYSCEGYGFKVVNCQEFTLSANASRDIIILTPTPPTASI ELKFITTSGSEFVFILNASLPYHMLATCAEALPRPNWELAI ISGIMSALFLLVIGTA\LLEAQGIWBF\FRARIS\FEASNI VGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSI GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSI SQPANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHSQHH PLECHPOPPLPPPVPQQEPPQPERDPERLSPAPLAHPSHPERASI SSEDSITSLIBAMDKDFDHHDSPALBVFTEQPPSPLPKSI KPLCRKVKPPKKQEEKEKKGKGKPQEDELKDSLADDSSS: TSNPDTEPLLKEDTEKÇKKQAMPEKHESEMSQVKKKKK KKETPTDVKPSSLELPYTPPLESKQRRNLPSKTPLPTAMT SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEI PPENDSVPVHKPGSSTDSLYKLSLOTLNADIFLKQRGTSP' SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSSGEI PPENDSVPVHKPGSSTDSLYKLSLOTLNADIFLKQRGTSP' PSPPAAPCPFVARGSYSSIVNSSSSDPKIKDPNSSHKLFL SLPGKKGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSI HAPVDSDGSDSGGLWSPVSNPSSPDFTFINSFSAFGNFNI VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATSVLGATSGLWSTTFFSSSIWSSNLSSALPFT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP' RSSDPWSNSHFPHEN PSUSGPVSIGVLLCARSSTMGKRDNRVAYMNPIAMARSR		· ·	1	NILLITNASKFHLPVRVYTGFLDYFVLPPKIEERFIDFGVLSAT
IISSLPECEKSSSDQSSVTLASGYF\AVFRVLTAKKL\E DGAIQITTDYEILTIPVK\AVIAVGSLTCSPKHVVLPPSFE VHGSLNINMSFSGVKIQQIRSLSBDVRFYYRRLGGNKEDL KKSKIANIYFDPGLQCGDHCYVGLPPLSKSEPKVQPGVAMQ WDADWDLHQSLFKGWTGIKENSGHRLSAIFFUNTDLQKNII TABLSWPSILSSPHLKFPLTNINCSS\EEETTLENP/SQI SAHPLQSSTGFMEG\LSPHLILNIILKPGEKKSVKVK\FTI RIVSSLIIVRNNLTVMDAVMVQGQGTTENLRVAGKLPGPGS FKITEALLKDCTTDSLKLREPNFTLKRTFKVENTGQLQIHII ISGYSCEGYGFKVVNCQEFTLSANASRDIIILFTPDFTASI ELKFITTSGSEFVFILNASLPYHMLATCAEALPRPHWELAI ISGIMSALFLLVIGTA\VLEAQGIMEP\FRRILS\FFASNI VGREFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSI GSHKQ*GPSGHPSSHSNRNSADVDDVRAYNGGRTSSMTSI SSQFANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHGSQHI PLECHPQPPLPPPVQPQEPQDEPQERLSPAPLAHPSHPERASI SSEDSDITSLIRAMDKDFDHHDSPALEVFTEQPPSPLPKSI KPLCRKVKPPKKQEEKEKKGKGKPQEDELKDGLADDBSS: TSNPDTEPLLKEDTEKQKKCKQHAPEKESEMSQVKQKSKKI KKEIPTDVRPSSLELPYTPPLESKQRRNLPSKIPLPTAMTI SRNAQKTKGTSKLUDNRPPALAKFLPNSQELGNTSSSEGE PPEMDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSP' PSPPAPACPFVARGSYSSTDNLYKLSLQTLNADIFLKQRQTSP' PSPPAPACPFVARGSYSSTUNSSSSDPKIKQPNGSSHKL' SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSI HAPVDSDGSDSGLWSPVSNPSSDPDFTLNSFSAFRNSFN VFSKLGLSRSCNQASQRSWNEFNSGPSVLWESPATDSPSI SGSPTHTATSVLGATSGLWSTTPFSSSIWSNLSSALPFT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP RSSDPWSNSHFPHEN PVSKGPGVSGVLLLCARSSTMGKRDNRVAYMNPIAMARSR			1	EASNILFAIINSNPIELAIKSWHIIGDG\LSIELVAVDRGNRTT
DGAIQITTDYEILTIPVK\AVIAVGSLTCSPKHVVLPPSFF VHOSLNIMNSFSQKVKIQQIRSLSEDVRFYYKRLRGNKEDI KKSKIANIYEPDGLQCGDHCYVGLPFLSKSEPKVQPGVAMG WDADWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLQKNII TABLSWPSILSSPRHLKFPLTNINCSS\SEEITLENP/SQI YVQFIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFOV SAHPLQSSTGFMEG\LSPHLILNLILKPGEKKSVKVK\FTI RTVSSLIIVENNLTVMDAVNVQGQGTTENLRVAGKLPGPOG FKITEALLKDCTDSLKLREPNFTLKRTFKVENTGQLQIHII ISGYSCEGYGFKVVNCQEFFLSANASRDIIILFTPDFTASI ELKFITTSGSEFVFLINASLPYHMLATCAEALPRPNMELAI ISGIMSALFLLVIGTA\YLEAQGIWBP\FRRRLS\FEASNI VGRPFDLRRIVGISSEGNLNTLSCDFGHSRGFCGAGGSSSI GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSI SQPANKTRPLVLDSNTGAGGHSAGKKSKGAKQSQHGSQHH PLEQHPQPPLPPPVPQPQEPPOPERLSPAPLAHPSHPFRASI SSEDSDITSLIBAMMKDFDHHDSPALEVFTEQPPSPLPKSI KPLCRKVKPPKKQEEKEKKGKGVPDELKDSLADDDSSS' TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKG KKEIPTDVKPESLELPYTPFLESKQRRNLPSKIPLPTAMTI SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGE PPEMDSVPVHKPGSSTDSLYKLSLOTLNADIFLKORQTSP' SRNAQKTKGTSKLVDNRSSSSDPKIKGPNSPSSP PSPPAAPCPPVVHRGSSTDSLYKLSLOTLNADIFLKORQTSP' PSPPAAPCPPVVHRGSSTSDLYKLSLOTLNADIFLKORQTSP' PSPPAAPCPPVVHRGSSTSDLYKLSLOTLNADIFLKORQTSP' PSPPAAPCPPVVHRGSSTSDLYKLSLOTLNADIFLKORQTSP' PSPPAAPCPPVVHRGSSTSDLYKLSLOTLNADIFLKORQTSP' PSPPAAPCPPVVHRGSSTSDLYKLSSSDPKIKGPNSSSSHLSSALPSTS HAPVDSDGSDSGLWSPVSNSSSDPKIKGPNSSSSHKKTGPSSSI HAPVDSDGSDSGLWSPVSNSSPPFPLNSFSAFGNSFNI VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATSVLGNTSGLWSTTPFSSSIWSRLSSALPFT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP RSSDPWSNSHPPHEN PKSGPVSLGGLLCARSSTMGKRDNRVAYMNPIAMARSR		1	1	TISSI, PECEKSSSSDOSSVTLASGYF\AVFRVKLTAKKL\EGIH
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ELKFITTSGSEFVFILNASLPYHMLATCAEALPRPNWELAI ISGIMSALFLLVIGTA\YLEAQGIWBP\FRRIS\FEASNI VGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSI GSHKQ*GPSGHPHSSHNRNSADVDDVRAYNSGRTSSMTSI SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHGSQHI PLEQHPQPPPLPPPVPQPQEPQPERLSPAPLAHPSHPERASS SSEDSDITSLIBAMDKDFDHHDSPALEVFTEQPPSPLPKSI KPLQRKVKPPKKQEEKEKKGKGKQPQEDELKDSLADDDSSS' TSNPDTEPLLKEDTEKQKGKQAMPEKFESEMSQVKQKSKKI KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMTI SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEI PPEWDSVPVHKPGSSTDSLYKLSLOTLNADIFLKQRQTSP' PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKL' SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSI HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNI VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP' RSSDPWSNSHFPHEN				TOO YOUR CONTROL OF THE TAXABLE PROPERTY CONTROL OF TAXABLE PROPERTY CONTROL OF TAXABLE PROPERTY CONTROL OF TAXABLE PROPERTY CONTROL OF TAXABBLE PROPERTY CONTROL OF TAXABBLE PROPERTY CONTROL OF TAXABBLE PROPERTY CONTROL OF
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GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTS/ SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHGSQHI PLEQHPQPPLPPPVPQPQEPQPERLSPAPLAHPSHPERAS! SSEDSDITSLIEAMDKDFDHHDSPALBYTEQPPSPLPKSI KPLQRKVKPPKKQEEKEKKGKGKQEDELKDSLADDDSSS' TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKKI KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMT' SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEI PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSP' PSPPAAPCPPVARGSYSSIVNSSSSSDPKIKQPNGSKHKL' SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSI HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNI VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFT' TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP' RSSDPWSNSHFPHEN			1	ISGIMSALFLLVIGTA\YLEAQGIWEP\FKKKLS\FEASNPPFD
SSQPANKTRPLVLDSNTGAQGHSAGRKS KGAKQSQHGSQHI PLEQHPQPPLPPPVPQPQEPQPERLSPAPLAHPSHPERASI SSEDSDITSLIRAMDKDFDHHDSPALEVFTEQPPSPLPKSI KPLQRKVKPPKKQEEKEKKGKGKQEDELKDSLADDDSSS' TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKKI KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMT' SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEI PPEWDSVPVHKPGSSTDSLYKLSLOTLNADIFLKQRQTSP' PSPPAAPCPPVARGSYSSIVNSSSSSDPKIKQPNGSKHKL' SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSI HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNI VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFT' TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP' RSSDPWSNSHFPHEN				VGRPFDLRRIVGISSEGNLNTLSCDPGHSKGFCGAGGSSSKPSA
PLEQHPQPPLPPPVQPQEPQPERLSPAPLAHPSHPERASS SSEDSDITSLIBAMDKDFDHHDSPALBVFTEQPPSPLPKSI KPLCRKVKPPKKQEEKEKKGKGKPQEDELKDSLADDDSSS' TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKKI KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMTS SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEI PPEWDSVPVHKPGSSTDSLYKLSLOTLNADIFLKQRQTSP' PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKL' SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSI HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNI VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFT' TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP' RSSDPWSNSHFPHEN				GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSAQAA
SSEDSDITSLIEAMDKDFDHHDSPALEVFTEQPPSPLPKSI KPLCRKVKPPKKQEEKEKKGKGKPQEDELKDSLADDDSSS: TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKKN KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMT: SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEI PPEWDSVPVHKPGSSTDSLYKLSLOTLNADIFLKQRQTSP: PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKL: SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSI HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFN: VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP' RSSDPWSNSHFPHEN		j	1	SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHGSQHHAHS
KPLÇRKVKPPKKQEEKEKKGKGPQEDELKDSLADDDSSS' TSNPDTEPLLKEDTEKQKGKQAMPEKESEMSQVKQKSKKI KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMTI SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEI PPEWDSVPVHKPGSSTDSLYKLSLOTLNADIFLKQRQTSP' PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKL' SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSI HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNI VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTT TLASIGLMGTENSPAHAPSTSSPADDLGQTYNPWRIWSP' RSSDPWSNSHFPHEN				PLEQHPQPPLPPPVPQPQEPQPERLSPAPLAHPSHPERASSARH
TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKKI KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMT: SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEI PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSP' PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKL' SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSI HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNI VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFT' TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP' RSSDPWSNSHFPHEN PSVLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSR				SSEDSDITSLIBAMDKDFDHHDSPALEVFTEQPPSPLPKSKGKG
TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKKI KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMT: SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEI PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSP' PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKL' SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSI HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNI VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFT' TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP' RSSDPWSNSHFPHEN PSVLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSR			1	KPLCRKVKPPKKQEEKEKKGKGKPQEDELKDSLADDDSSSTTTE
KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMTS SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEI PPEWDSVPVHKPGSSTDSLYKLSLOTLNADIFLKQRQTSP: PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKL: SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSI HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNI VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATTSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPITLASIGLWSTTPFHEN RSSDPWSNSHFPHEN PSYLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSR		İ	1	TSNPDTEPLLKEDTEKOKGKQAMPEKHESEMSQVKQKSKKLLNI
SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEI PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSP' PSPPAAPCPFVARGSYSSIVNSSSSSDFKIKQPNGSKHKL' SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSI HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNSV VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATTSVLGNTSGLWSTTPFSSSIWSSNLSSALPFT' TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP' RSSDPWSNSHFPHEN RSSDPWSNSHFPHEN	1	1	1	KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMTSGSK
PPEWDSVPVHKPGSSTDSLYKLSLOTLNADIFLKQRQTSP' PSPPAAPCPFVARGSYSSIVNSSSSSDPKI KQPNGSKHKL' SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSI HAPVDSDGSDGSGLWSPVSNPSSPDFTPLNSFSAFGNSFNS VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFT' TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP' RSSDPWSNSHFPHEN PSYLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSR	1	İ	1	SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEKDSP
PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKL/ SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSI HAPVDSDGSDSSGLWSPVSNPSSPDFTFLNSFSAFGNSFNI VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP- RSSDPWSNSHFPHEN PSYLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSR	j	1	1	PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSPTPAS
SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSI HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNI VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTT TLASIGLMGTENSPPAPHAPSTSSPADDLGQTYNPWRIWSPTRSSDPWSNSHFPHEN RSSDPWSNSHFPHEN PSYLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSR	1	1	1	PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKLTKAA
HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFN. VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPT RSSDPWSNSHFPHEN RSSDPWSNSHFPHEN PVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSR		1	1	SEPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSLGIS
VFSKLGLSRSCNQASQRSWNEFNSGPSYLWESPATDPSPSI SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP RSSDPWSNSHFPHEN PVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSR	ļ	1	[HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNLTGE
SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFT TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP RSSDPWSNSHFPHEN RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSR			1	VESKLCT.SPSCNOASORSWNEFNSGPSYLWESPATDPSPSWPAS
TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSP RSSDPWSNSHFPHEN RSSDPWSNSHFPHEN RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSR		1	1	CCCDTUTATOUT CNTCCT WCTTDFSSSTWSSNI.SSAI.PFTTPAN
RSSDPWSNSHFPHEN RSSDPWSNSHFPHEN RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSR	ł	1	1	MAY SELOT WOMENODY BRY DEAGEDY DUT COULAND MA LAGOLLUS
ES30 310 1370 RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSR	1	1	1	
5820 310 1270 RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMAKSR	<u> </u>			RSSDPWSNSHFPHEN
	5820	310	1270	RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSRGPIQ
SSGPTIQ\VI*IDQGLPGKK*KSN*KRKRK/DSKALAEFE	1			SSGPTIQ\VI*IDQGLPGKK*KSN*KRKRK/DSKALAEFEEKMN
ENWKKELEKHREKLLSGSESSKKRQRKKKEKKKSW*\DS	1			ENWKKELEKHREKLLSGSESSSKKRORKKKEKKKSW*\DSSSS\
SSSSDSSSSSSEDEDKKQGKRRKKKNRSHKSSESSMS	ł		1	SSSSDSSSSSSSDSEDEDKKQGKRRKKKNRSHKSSESSMSETES

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	I M-MIGHTIE, CELVSTRING National and a second
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, E=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L-Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- 1	amino acid	residue of	S=Serine, T=Threonine, V-Valine
	residue of	amino acid	W=Tryptophan, Y=Tyrosine Y-Unknown + Ch-
i	amino acid	sequence	Couon, /=possible nucleotide deleti-
	sequence		\=possible nucleotide insertion)
			DSKDSLKKKKKSKDGTEKEKDIKGLSKKBYMYSEDVDLGGEG
		1	ESELIBEVRAKKKKSSEEREKATEKTKKKKKHYVUCVVVVVV
1			335PD5P"H"EKSGFPYKESAMSEETSTVKTTTVI.I.KCMNET UE
5821	179		GIIPGHESSHSDATV
	1 ***	915	KWRNQSWRWPKPGTNWMLSCSVCWRRVTWTGSVWMRKLGKHPQT
1			PI/IKUCSIAATGKRPSARFPHORRKKRPRMDDGLAFCCBORGN
			I I V I A LE DES VOLA OFSENT PLYPICE AUMPNE DE VIDE DE CEDE
i	1		SPLPPLPEDEEG\SEVTNSKSR+CVOACPDTHTDGGODVNACD\
j			SKIPSPLAALRNQGTP*RWSPFEPFPSPSTT.TVPNMOPWPTPO
5822	464	4379	RWKEASHRNQLRYSESMKILREMYERQ
Ì	İ	13/3	QTLKEMPIVMARDLEETASSSEDBEVISQEDHPCIMWTGGCRRI
			PVLVFHADAILTKDNNIRVIGERYHLSYKIVRTDSRLVRSILTA
-	ļ		HGPHEVHPSSTDYNLMWTGSHLKPFLLRTLSEAQKVNHFPRSYE
	1		LTRKDRLYKNIIRMOHTHGFKAFHILPOTFLLPAEYAEFCNSYS
	1		KDRGPWIVKPVASSRGRG\VYLINNPNQISLEENILVSRYINNP LLIDDFKFDVRLYVLVTSYDPLVIYLYEEGLARFATVRYDQGAK
	<u> </u>		NIRNQFMHLTNYSVNKKSGDYVSCDDPEVEDYGNKWSMSAMLRY
1	í I		LKQBGRDTTALMAHVEDLIIKTIISAELAIATACKTFVPHRSSC
1			FEDIGEDVLIDSTLKPWLLEVNI.SPSI.ACDADI.DI.VIVACNICO
	1 1		FIFTVVGFVCQDPAORASTRPTVPTFEGGPPNDFQVDQDQDDT 0.
1			SDABUKNLVGSAREKGPGKLGGSVI.CI.CMPFTVV// DDIVVERVDD
1	1		RGGFIRIFPISETWEIYGSYLEHKTSMNVMI.ATDI.FOODWTADG
	ł i		APELKI*SLNSKAKLHAALYERKLISI.EVPREPPPEGET DAMPE
	1		A LPVITQPAEMNVKTETBSEEEEVALDNEDEROEDSOSSOSSOS
1	1		DRENQARI IPSLIALVENTPKENSMKVPEWNNVCCHCCVI ETCO
1	1		LEPKINLMQILQDNGNLSKMOARIAFSAVLOHVOI\ PLMVDSCC
1			QIPSASWAAKEDEQMELVVRFLKRASNNI,OHSI,DMUI,DCDD7 37
1			LERIKILAHQLGDFIIVYNKETEOMARKKSKKVFFFFFFFFFF
1			ENFORTINGASEAELEEVLTFYTOKNKSASVFI.GTHCKTCKARDY
1			NISUSGARGURPETIMEEVKIKPPKOOOTTETUSDYLSDEMMON
1 1	1		EKEAKLVYSNSSSGPTATLQKIPNTHLSSVTTSDLSPGPCHHSS
1	ľ		LSQIPSAIPSMPHQPTILLNTVSASASPCLHPGAQNIPSPTGLP
	1		RCRSGSHTIGPFSSFQSAAHIYSQKLSRPSSAKAGSCYLNKHHS
1	1		GIAKTOKEGEDASLYSKRYNOSMVTAELORLAEKQAAROYSPSS
1	1		HINLLTQQVTNLNLATGIINRSSASAPPTLRPIISPSGPTWSTQ SDPQAPENHSSSPGSRSLQTGGFAWEGEVENNVYSQATGVVPQH
			KYHPTAGSYQLQFALQQLEQQKLQSRQLLDQSRARHQAIFGSQT
1 1	ł		LPNSNLWTMNNGAGCRISSATASGQKPTTLPQKVVPPPSSCASL
1 1			VPKPPPNHEQVLRRATSQKASKGSSAEGQLNGLQSSLNPAAPVP
5823			11SSIDPAHIKIMNHKHTEKOPVHHSWAID
3023	42	2293	LLTALSMEGGGGRDEPSACRAGDVNMDDDKKEDILLLADEVEDE
]			DISCUSSION OF THE PROPERTY OF
	i		TSESPEAWSPLAGEKEVEVYKEAHLI.ALHTEGGGDNOAAAAAVD
	1	1	BDPRSQGVERFIQESKF\KINLFEKEKEMKKCDTCI.VDDTVVI O
1		j	DSPLEGPPVGEPRLLASSPALPSSGAOAPI.TDADGDDUGATATA
]	1		RESCIAHAASQAATORKPGTKLLLPRAASVPGPGTPGAAPPPVC
		ſ	ELPASPSKTKIPAEKESHRDVLPDKPAPGAIARIDAAGGULGOGU
1			RAIPVF\NKLGLKKTLLKAPGSYSN\I.ORKSSSGA\\TUGGASGA
l	ļ		CIPUPVAKAKSSEFASIPAN*I.PGI.CPNTSKS\GDMGDAMIDDA
			L\PAGPVG\ASSWQAKRVDVSELAAFQI.TAPP\SASPTQPQTPE
1			GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN
1			OFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
j			RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS
ſ	1	ļ	PL\CVPARRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR
	İ		GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS
		1	EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE
		ļ	SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK ENVDSPLLKF
5824	42		
[LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLLADEKFDF DLSLSSSSANEDDEVPFGPFGHKERCIAASLELNNPVPEQPPLP
			TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP
			- TANAMIDIALITIESSSKNUAAQAAKP

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	1
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	• • • • • • • • • • • • • • • • • • • •
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYYLS
1		{	DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP
1			RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK
Į	[EIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGQGK
1	[ļ	RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA
i	Į.	1	CTPQPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA
1	Į.	į	L\PAGFVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE
			GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMFTPTN
1	ľ	l .	OFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
1	1	ļ	RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS
}	į	1	PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR
1			GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS
1	1	}	EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE
1		1	SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK
1		}	ENVDSPLLKF
L		4555	FLQIESASPAPFSSGFLAAHPHSPGGSLATKGRSRLSAPGMLHL
5825	2	4210	SAAPPAPPPEVTATARPCLCSVGRRGLGGKMAAAGALERSFVEL
1	ļ		SAAPPAPPPEVTATARPCLCSVGRRGLGGRAAAGADERSTVED
}			KLFSVTRNRFIHWKTSGDTLELMEESLDINLLNNAIRLKFQNCS
1		ļ	VLPGGVYVSETQNRVI:LMLTNQTVHRLLLPHPSRMYRSELVVD
l			
	1.	i	SQMQSIFTDIGKVDFTDPCNYQLIPAVPGISPNSTASTAWLSSD
ı		Į.	GEALFALPCASGGIFVLKLPPYDIPGMVSVVELKQSSVMQRLLT
	1	1	GWMPTAIRGDQSPSDRPLSLAVHCVEHDAFIFALCQDHKLRMWS
İ			YKEQMCLMVADMLEYVPVKKDLRLTAGTGHKLRLAYSPTMGLYL
1		}	GIF\MHAPKRGQFCIFQLVSTESNRYSLDHISSLFTSQETLIDF
1	Ì		ALTSTDIWALWHDAENQTVVKYINFEHNVAGQWNPVFMQPLPEE
1			EIVIRDDQDPREMYLQSLFTPGQFTNEALCKALQIFCRGTERNL
i	1	}	DLSWSELKKEVTLAVENELQGSVTEYEFSQEEFRNLQQEFWCKF
1	1	l	YACCLQYQEALSHPLALHLNPHTNMVCLLKKGYLSFLIPSSLVD
1	1	1	HLYLLPYENLLTEDETTISDDVDIARDVICLIKCLRLIEESVTV
-	i e	•	DMSVIMEMSCYNLQSPEKAAEQILEDMITIDVENVMEDICSKLQ
}	1	1	EIRNPIHAIGLLIREMDYETEVEMEKGFNPAQPLNIRMNLTQLY
I	1	l	GSNTAGYIVCRGVHKIASTRFLICRDLLILQQLLMRLGDAVIWG
İ	1	i	TGQLFQAQQDLLHRTAPLLLSYYLIKWGSECLATDVPLDTLESN
	ŀ	}	LQHLSVLELTDSGALMANRFVSSPQTIVELFFQEVARKHIISHL
}			FSQPKAPLSQTGLNWPEMITAITSYLLQLLWPSNPGCLFLECLM
1	.1		GNCOYVOLODYIOLLHPWCQVNVGSCRFMLGRCYLVTGEGQKAL
1			ECFCOAASEVGKEEFLDRLIRSEDGEIVSTPRLQYYDKVLRLLD
1			VIGLPELVIQLATSAITEASDDW\KSQATL\RTCIFKHHL\DLG
1	ł		\HNSOAYGSL*PQIPDSSRQLDCLRQLVVVLCERSQLQDLVEFS
}			YVNLHNEVVGIIESRARAVDLMTHNYYELLYAFHIYRHNYRKAG
			TVMFEYGMRLGREVRTLRGLEKQGNCYLAALNCLRLIRPEYAWI
			VOPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE
Į.	1		CSLARIRLTLAOHD?SAVAVAGSSSAEEMVTLLVQAGLFDTAIS
İ	1		LCQTFKLPLTPVFEGLAFKCIKLQFGGEAAQAEAWAWLAANQLS
}			SVITTKESSATDEAWRLLSTYLERYKVONNLYHHCVINKLLSHG
1			VPLPNWLINSYKKVDAAELLRLYLNYDLLDLTPYQVIRICGC
	 	073	KSQLLRDHSAPPPKPCTSVGAMGC*PRQ/SPKEQQRQLKKQKNR
5826	3	871	AAAQRSRQKHTDKADALHQQHESLEKDNLALRKEIQSLQAELAW
		ļ	WSRTLHVHERLCPMDCASCSAPGLLGCWDQAEGLLGPGPQGQHG
- L			CREQLELFQTPGSCYPAQPLSPGPQPHDSPSLLQCPLPSLSLGP
1		1	CKEATERIA TEACHECES OCCCENT SYLVES INVOIN
l l		i	AVVAEPPVQLSPSPLLFASHTGSSLQGSSSKLSALQPSLTAQTA
		1	PPQPLELEHPTRGKLGSSPDNPSSALGLARLQSREHKPALSAAT
L	<u> </u>	<u></u>	WQGLVVDPSPHPLLAFPLLSSAQVHF
5827	194	2287	GMGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYK
1			RENEDKVNKAAKVP**HLKTLRHPCLLRFLSCTVEADGIHLVTE
	}		RVQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHLTHNNVCL
]	SSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP
		1	EEMSPEFTTLPECHGHARDAFSFGTLVESLLTILNEQVSADVLS
1		1	SFOOTLHSTLLNPIPKWRPALCTLLSHDFFRNDFLEVVNFLKSL
1	1]	TLKSEEEKTEFFKFLLDRVSCLSEELLASRLVPLLLNQLVFAEP
	. t	_1	

SEO	Predicted		
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	A=Alanine, C=Cysteine, D=Aspartic acid E
ł	location	corresponding	Glucamic Acid, F=Phenylalanine c-classic-
ļ	corresponding	to first	
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
j	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
!	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	_	\=possible nucleotide insertion)
1			VAV\KSFLPYLLGPKKDHAOGETPCLLSPALEOSPYTDVITOTE
	1		EVHEEHVRMVLLSHIEAYVGALSLREOLKKW II. DOWN ICLAN
			DATSUSIVAITLHSLAVLVSLLGDEVVVCGEDTVIEVDTADA
1			TK\NTDLSLEGDPFSOPIKFPINGISDVKNTSEDSENEDSSKY
1			SEEWPDWSGPE\EPENOTVNI\OIWP\REP\CDDVKSOCTTU DV
- 1		1	BESSWODCEPSSLOTKVNPGGGITATKPVTSGEOKDIDATISIE
İ	1		EESMPWKSSLPQKISLVORGDDADOIEPPKVSSORPDIKUDSEI
ı	i		GLGEEFTIQVKKKPVKDPEMDWFADMIPETKPSAAFITI.DELDE
- 1		ł	EMVPKKDDVSPVMQFSSKFAAAEITEGEAEGWEEEGELNWEDNN
5828	2	257	W
	- ·	257	AREGGSLGAVAACGELSYSCDFCPARPHTSWLTRFVKMEFQAVV
	1	ļ	MAVGGGSRMTDLTSSIPKPLLPVGNKPLIWY?LNLLERVGFEEV
	İ		IVVTTRDVQKALCAEFKMKMKPDIVCIPDDADMGTADSLRYIYP
1	ł		KLKTDVLVLSCDLITDVALHEVVDLFRAYDASLAMLMRKGQDSI
İ			EPVPGQKGKKKAVEQRDFIGVDSTGKRLLFMANEADLDEELVIK GSILQKHPRIRFHTGLVDAHLYCLKKYIVDFLMENG\SITSIRS
ı	1	1	EL\IPYLV/RGKQFSSASSQQGTRKEKEGGSKGKRGLKSFRISY
			SFY*KEANYTGTGAPY\D\ACWI
5829	260	1259	PDGRLIVSCSEDKTIKIWDTTNKQCVNNFSDSVGFANFVDFNPS
İ	1		GTCIASAGSDQTVKVWDVRVNKLLQHYQVHSGGVNCISFHPSGN
1			YLITASSDGTLKILDLLKGRLIYTLOGHTGPVFTVSFSVGGET E
i i		İ	ASGGADTQVLLWRTNFDELHCKGLTKRNLKRLHFDSDDHLLDIV
I			PRTPHPHEEKVETVEDFFLHLLRLIOSIR*SICESIT.DITMICE
1	1		LLILPQQQKPVVGLCOTRVKRPVDIS*TIP*CHOMYCOODBYDY
	1	•	QXT*VTSPVKVK/VSIPLAVTDALEHIMEOLMULTOTUCTI FOR
5830	4496	3139	LTLTEDKLKDCLENOOKLFSAVOOKS
		3139	GGKMAAPEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQHNW
			NIEAAVQDRLNEQEGVPSVFNPPPSRPLQVNTADHRIYSYVVSR
1	1 1		PQPRGLLGWGYYLIMLPFRFTYYTILDIFRFALRFIRPDPRSRV TDPVGDIVSFMHSFBEKYGRAHPVFYQGTYSQALNDAKRELRFL
	i i	•	LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNKPE
1			GYRVSQALRENTYPFLAMIMLKDRRE*PV\VGRLEGLI\QPDDL
1			INQLTFIMDANQTYLVSERLERBERNQTQVLRQQQDEAYLASLR
1	1		ADQEKERKKREERERKRRKKEEVOOOKI AEEDDONI OEDVOOR
	1		LECLPPEPSPDDPESVKIIFKLPNDSRVERPEPBEDECT TUTTURE
ł	1	ı	LFSLKESP\EKFQIEA\NFPRR\VLPCIPSEE\WPNPPTLOF\A
5831	71		GLSHTEVLFVQDLTDE
1 3031	'-	2897	FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQVKD
j	1		TDDIESPKRSIRDSGYIDCWDSERSDSLSPDPHGPDDGEDGIDG
	1 1		FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKT.PDVKKDDMC
•	j		ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREEYR
į		ĺ	KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRCSE
	[EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS
i	1		QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKERRE
ł	1		RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPKILE
1	1	•	RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS
	1		VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVARVH
	į į	1	GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQEDKND
	í l	1	GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQLKND
}		i i	VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFPFLD
		f	KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEERRR
			QEKWQQEQERLLQERYQ\KEODK\LKEE\WEKAOKEVEEEEDDV
			YEEEP*II\EDPVVPFTVSSSSADOLSTSSSMTEGSGTMNKTDI
			GNCQDEKQDRRWKKSFQGDDSDLLLKTRESDRLEEKGGLTEGAL
		i	AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN
			PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL
			PLGKGAAMIIETLNLYFHIQCFRCG\ICKGOLGDAVSGTDVRIP
5832	2454		NGLLNCNDCYMRSRSAGQPTTL
	4734	829	PGRRFRHGSCAFQKQCIMLHICQYFLQGECKFGTSCKRSHDFSN
			SENLEKLEKLGMSSDLVSRLPTIYRNAHDIKNKSSAPSRVPPLF

SEQ		Predicted end	Amino acid segment containing signal peptide
02 ₈	Predicted		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	Glutamic Acid, Faphenylalanine, Gaglycine,
j	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ		residue of	S=Serine, T=Threonine, V=Valine,
ŀ	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ.	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	aedneuce	Codon, /=possible indefedence delection/
i	sequence	ļ	\=possible nucleotide insertion)
			VPQGTSERKDSSGSVSPNTLSQEEGDQICLYHIRKSCSFQDKCH
. 1		ļ	RVHFHLPYRWOFLDRGKWEDLDNMELIEEAYCNPKIERILCSES
		ŧ	ASTFHSHCLNFNAMTYGATQARRLSTASSVTKPPHFILTTDWIW
			YWSDEFGSWQEYGRQGTVHPVTTVSSSDVEKAYLAY/WYTGV*R
		1	WSDEEGSWOELGROOT VAFVII TOOS POEKDOLWUM+VOLDOTOLD\ AD
Į		[PGSHLEVPGRKAQLRVRFQSLRSEKPGLWHN*KGLPQTQIR\AP
- 1		1	QDVTTMQTCNTKFPGPKSIPDYWDSSALPDPGFQKITLSSSSEE
i		Ì	YQKVWNLFNRTLPFYFVQKIERVQNLALWEVYQWQKGQMQKQNG
i		i	GKAVDERQLFHGTSAIFVDAICQQNFDWRVCGVHGTSYGKGSYF
		1	ARDAAYSHHYSKSDTQTHTMFLARVLVGEFVRGNASFVRPPAKE
		1	ARDAAISHHISASDIQITTIHE MAKADAGSE TAGAKADI TAGAKADI
		t	GWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVIQYTTSSKPSV
		1	TPSILLALGSLFSSRQ
5833	170	3289	SILCLLSPCVVQFGKPVVSILSSRSRHSPCTKKGWEGMRKHLHT
2833	1 1,0	1	RQGHK*VHVEISKALWVYRDDYFIRHSISVSAVIVRAWITHKYR
	1		GRDWNVKWEENLLHAVAKNYTLLQTIPPFERPFKDHQVCLEWNM
		ļ	GYIWNLRANRIPQCPLENDVVALLGFPYASSGENTGIVKKFPRF
	1	į.	GATAMPENENTA CALLES AND AND THE LEAD OF TH
	1	Į.	RNRELEATRRORMDYPVFTVSLWLYLLHYCKANLCGILYFVDSN
	1	ľ	EMYGTPSVFLTEEGYLHIQMHLVKGEDLAVKTKFIIPLKEWFRL
l	1	1	DISFNGGOIVVTTSIGQDLKSYHNQTISFREDFHYNDTAGYFII
	1]	GGSRYVAGIEGFFGPLKYYRLRSLHPAQIFNPLLEKQLAEQIKL
į.	į.	1	YYERCAEVQEIVSVYASAAKHGGERQEACHLHNSYLDLQRRYGR
l	1	1	PSMCRAFPWEKELKDKHPSLFQALLEMDLLTVPRNQNESVSEIG
	1	1	PSMCRAPPWEREDRORMPS DE CAMBRIDADO LE PROPERTIE DE CACCOLLINA CAMBRIDADO DE LA CONTRACTOR DE CACCOLLINA CAMBRIDADO DE LA CONTRACTOR DE CACCOLLINA CAMBRIDADO DE LA CONTRACTOR DE CACCOLLINA CAMBRIDADO DE LA CONTRACTOR DE CACCOLLINA CAMBRIDADO DE LA CONTRACTOR DE CACCOLLINA CAMBRIDADO DE LA CONTRACTOR DE CACCOLLINA CAMBRIDADO DE LA CONTRACTOR DE CACCOLLINA CAMBRIDADO DE LA CONTRACTOR DE CACCOLLINA CAMBRIDADO DE LA CONTRACTOR DEL CON
ĺ	1	1	GKIFEKAVKRLSSIDGLHQISSIVPFLTDSSCCGYHKASYYLAV
l .		1	FYETGLNVPRDQLQGMLYSLVGGQGSERLSSMNLGYKHYQGIDN
1	1	1	YPLDWELSYAYYSNIATKTPLDQHTLQGDQAYVETIRI.KDDEIL
1	1	[KVOTKERGRUFMWLKHEATRGNAAAQQRLAQMLFWGQQGVAKNP
1	1	1	EAAIEWYAKGALETEDPALIYDYAIVLFKGQGVKKNRRLALELM
1	1		KKAASKGLEQAVNGLGWYYHKFKKNYA\KAAKYWLKA\EE\MGN
ļ	1	1	PDASYNLGVLHLDGIFPGVPGRNQTLAGEYFHKAAQGGHMEGTL
Į	1]	PDASYNLGVLHADGIFPGVPGRNQIMAGEIFRAMQOCIMAGEA
i	4		WCSLYYITGNLETFPRDPEKAVVWAKHVAEKNGYLGHVIRKGLN
İ		i	AYLEGSWHEALLYYVLAAETGIEVSQTNLAHICEERPDLARRYL
l	1		GVNCVWRYYNFSVFQIDAPSFAYLKMGDLYYYGHQNQSQDLELS
ļ	1		VQMYAQAALDGDSQGFFNLALLIEEGTIIPHHILDFLEIDSTLH
J	j	Į	SNNISILQELYERCWSHSNEESFSPCSLAWLYLHLRLLWGAILH
i	1	1	SALIYFIGTFLLSILIAWTVQYFQSVSASDPPPRPSQASPDTAT
Į.	1	1	
			STASPAVTPAADASDODOPTVTNNPEPRG
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG REFRGGGRVPPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG SAAPGPIPGOSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG SAAPGPIPGOSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGGRVPPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TIRDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGGRVPPGAFPASPSDSLGQGNSQGPFRTPKPPRT/QECG SAAPGPIPGQSSS+VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEOATVHSSMNEMLEEGGEYAVMLYTWRSCSRAI
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGGRVFPGAFPASPSDSLGQGNSQGPFRTPKPPRT/QECG SAAPGPIFGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI POVKCNEOPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRRLCHAERKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAOFLRKMADPQSIQESQNLSMFLANHNKITQSLQ
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ OOLRVISGYBELLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ OOLRVISGYBELLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLBVISGYEBLLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF GLYIMDGSVGNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGGRVPPGAFPASPSDSLGQGNSQGPFRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGGEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLBVISGYEBLLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELABVIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGRVPPGAFPASPSDSLGQGNSQGPFRTPKPPRT/QECG SAAPGPIFGQSSS*VPLRLEQIQQKACDPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGGEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLBVISGYEBLLADIVNLCVDYYENRMYLTFSEKHMLKVMGF GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGRVFPGAFPASPSDSLGQGNSQGPFRTPKPPRT/QECG SAAPGPIFGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQOPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLBVISGYEBLLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM FISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL SOMSAHVMEVVSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQOPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGGEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLEVISGYEBLLADIVNLCVDYYENRMYLTPSEKHMLLKVMGF GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL SWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNTTS EPRKBLJEVIAMIKGLOVLMGRMESVFNHAIRHTVYAALQDFSQ
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLEVISGYEELLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEYKKLFDLALQGLQLLL SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ UTIMEPLROAIKKKKNVIOSVLQAIRKTVCDWETGHEPFNDPAL
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLEVISGYEELLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEYKKLFDLALQGLQLLL SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ UTIMEPLROAIKKKKNVIOSVLQAIRKTVCDWETGHEPFNDPAL
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGRVPPGAFFASPSDSLGQGNSQGPFRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGGEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQBSQNLSMFLANHNKITQSLQ QQLEVISGYEELLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL SQWSAHVMEVYSWKLVHPTDKYSNKDCFDSAEEYERATRYNYTS EEKPALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ VTIMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGGRVPPGAFFASPSDSLGQGNSQGPFRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGGEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLBVISGYEBLLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ VTIMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGGRVPPGAFPASPSDSLGQGNSQGPFRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGGEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLBVISGYEBLLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ VTIMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK KTLRSSLEGPTILDIEKFHRESFFYTHLINFSETLQQCCDLSQL WFDRPFIELTMGRRIOFPIEMSMPWILTDHILETKEASMMEYVL
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGRVPPGAFPASPSDSLGQGNSQGPFRTPKPPRT/QECG SAAPGPIFGQSSS*VPLRLEQIQQKACDPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGGEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLBVISGYEBLLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF GLYIMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL SQWSAHVMEYYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK KTLRSSLEGPTILDIEKFHRESFFYTHLINFSETLQQCCDLSQL WFREFFLELTMGRRIQFPIEMSMPWILTDHILETKEASMMEYVL VS.DLYNDSAHVALTRFNKOFLYDEIEAEWNLCFDQFVYKLADQ
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGRVFPGAFPASPSDSLGQGNSQGPFRTPKPPRT/QECG SAAPGPIFGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQOPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLBVISGYEBLLADIVNLCVDYYENRMYLTFSEKHMLLKYMGF GLYIMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEYKKLFDLALQGLQLL SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK KTLRSSLEGPTILDIEKFHRESFFYTHLINFSETLQQCCDLSQL WFREFFLELTMGRRIQFPIEMSMPWILTDHLLETKEASMMEYVL YSLDLYNDSAHYALTRFNKQFLYDEIEAEVNLCFDQFVYKLADQ
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGRVFPGAFPASPSDSLGQGNSQGPFRTPKPPRT/QECG SAAPGPIFGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQOPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLBVISGYEBLLADIVNLCVDYYENRMYLTFSEKHMLLKYMGF GLYIMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEYKKLFDLALQGLQLL SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK KTLRSSLEGPTILDIEKFHRESFFYTHLINFSETLQQCCDLSQL WFREFFLELTMGRRIQFPIEMSMPWILTDHLLETKEASMMEYVL YSLDLYNDSAHYALTRFNKQFLYDEIEAEVNLCFDQFVYKLADQ
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGRVPPGAFFASPSDSLGQGNSQGPFRTPKPPRT/QECG SAAPGPIPGQSSS+VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTMFEDR NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNNKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLEVISGYEELLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEVRKLFDLALQGLQLL SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK KTLRSSLEGPTILDIEKFHRESFFYTHLINFSETLQQCCDLSQL WFREFFLELTMGRRIQFPIEMSMPWILTDHLLETKEASMMEYVL YSLDLYNDSAHYALTRFNKQFLYDEIEAEVNLCFDQFVYKLADQ IFAYYKVMAGSLLLLDKRLRSECKNQGATIHLPPSNRYETLLKQR
5834	17	4020	STASPAVTPAADASDQDQPTVTNNPEPRG RFRRGGGRVPPGAFFASPSDSLGQGNSQGPFRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTMFEDR NAFVTGIARYIEQATVHSSMNEMLEEGGEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQBSQNLSMFLANHNKITQSLQ QQLEVISGYEELLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAESYERATRYNTTS EEKPALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK KTLRSSLEGFTILDIEKFHRESFFYTHLINFSETLQQCCDLSQL WFREFFLELTMGRRIQFPIEMSMPWILTDHILETKEASMMEYVL YSLDLYNDSAHYALTRFNKQFLYDEIEAEWNLCFDQFVYKLADQ IFAYYKVMAGSLLLDKRLRSECKNQGATIHLPPSNRYETLLKQR HVQLLGRSIDLNRLITQRVSAAMYKSLELAIGRFESEDLTSIVE LDGLLPINDMTHKILSRYLTLDGFDAMFREANHNVSAPYGRITL
5834	17	4020	RFRRGGRVPPGAFFASPSDSLGQGRSQFPRTPKPPRT/QECG SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTMFEDR NAFVTGIARYIEQATVHSSMNEMLEEGGEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLBVISGYEBLLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ VTIMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK KILRSSLEGPTILDIEKFHRESFFYTHLINFSETLQQCCDLSQL WFREFFLELTMGRRIQFPIEMSMPWILTDHILETKEASMMEYVL YSLDLYNDSAHYALTRFNKQFLYDEIEAEVNLCFDQFVYKLADQ IFAYYKVMAGSLLLDKRLRSECKNQGATIHLPPSNRYETLLKQR HVQLLGRSIDLNRLITORVSAAMYKSLELAIGRFESEDLTSIVE LUCLLEINRMTHKLLSRYLTLDGFDAMFREANHNVSAPYGRITL
5834	17	4020	RFRRGGRVPPGAFPASPSDSLGQGNSQFPRTPKPPRT/QECG SAAPGPIPGQSSS+VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGGEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLBVISGYEBLLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ VTIMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK KTLRSSLEGPTILDIEKFHRESFFYTHLINFSETLQQCCDLSQL WFREFFLELTMGRRIQFPIEMSMPWILTDHILETKEASMMEYVL YSLDLYNDSAHYALTRFNKQFLYDEIEAEVNLCFDQFVYKLADQ IFAYYKVMAGSLLLDKRLRSECKNQGATIHLPPSNRYETLLKQR HVQLLGRSIDLNRLITORVSAAMYKSLELATGRFESEDLTSIVE LDGLLEINRMTHKLLSRYLTLDGFDAMFREANHNVSAPYGRITL HVFWELNYDFLPNYCYNGSTNRFVRTVLPFSQEFQRDKQPNAQP OVLUGENALNIAYSSIGSSYRNFVGPPHFQVICRLLGYQGIAVV
5834	17	4020	RFRRGGRVPPGAFPASPSDSLGQGRSQGPFRTPKPPRT/QECG SAAPGPIFGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGGEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QLBVISGYEBLLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL SQWSAHVMEYYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK KTLRSSLEGPTILDIEKFHRESFFYTHLINFSETLQQCCDLSQL WFREFFLELTMGRRIQFPIEMSMPWILTDHILETKEASMMEYVL YSLDLYNDSAHYALTRFNKQFLYDEIEAEVNLCFDQFVYKLADQ HVQLLGRSIDLNRLITQRVSAAMYKSLELATGRFESEDLTSIVE LDGLLEINRMTHKLLSRYLTLDGFDAMFREANHNVSAPYGRITL HVFWELNYDFLPNYCYNGSTNRFVRFVBPPFQVICRLLGYQGIAVW MPETLKWUNSLLGTILGYVKTLMEVMPKICRLLGYPGIGIAV
5834	17	4020	RFRRGGRVFPGAFPASPSDSLGQGRSQGPFRTPKPPRT/QECG SAAPGPIFGQSSS*VPLRLEQIQQKAQCPLSLELALKPRMAAQV TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR NAFVTGIARYIEQATVHSSMNEMLEEGGPYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC GEVRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ QQLBVISGYEBLLADIVNLCVDYYENRMYLTFSEKHMLLKVMGF GLYIMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS EEKPALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ VTIMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK KTIRSSLEGPTILDIEKFHRESFFYTHLINFSTLQQCCCDLSQL WFREFFLELTMGRRIQFPIEMSMPWILTDHILETKEASMMEYVL YSLDLYNDSAHYALTRFNKQFLYDEIEAEWNLCFDQFVYKLADQ IFAYYKVMAGSLLLDKRLRSECKNQGATIHLPPSNRYETLLKQR HVQLLGRSIDLNRLITQRVSAAMYKSLELAIGRFESEDLTSIVE LDGLLEINRMTHKLLSRYLTLDGFDAMFREANHNVSAPYGRITL HVFWELNYDFLPNYCYNGSTNRFVRTVLPFSQEFQRKQPNAQP QYLHGSKALNLAYSSIYGSYRNFVGPPHFQVICRLLGYQGIAVV MEELLKVVKSLLQGTILQYVKTLMEVMPKICRLPRHEYGSPGIL
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	SEQ	Predicted	Predicted end	Amino acid comest
	ID	beginning	nucleotide	
	NO:	nucleotide		In-Aldning, C=CVSteine D-Appartic Acid n
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	1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	ł .	corresponding	to first	L-Louis M. Martine, K-Lysine,
	į	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	1	amino acid		P=Proline, Q=Glutamine, R=Arginine
	1		residue of	S=Serine, T=Threonine, V=V=line
	i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	1	amino acid	sequence	Codon /=noco:bl
	ı	sequence		Codon, /=possible nucleotide deletion,
				\=possible nucleotide insertion)
	l .		1	LIERLGTPQQIAIAREGDLLTKERLCCGLSMREVILTPIDGETS
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	1	1	i	EQCFGDGLHWAGCMIIVLLGQQRRFAVLDFCYHLLKVQKHDGKD
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	Glutamic Acid, Fernenylatanine, George
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
1	corresponding	to first	LaLeucine, Mamethionine, Namasparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į.	amino acid	residue of	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, A=Omkhown,
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
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	ļ	Į.	HOSPATPAFKSLEAFFLYGRLYEFWWSLSRPCPNSSVWVRAGHR
	1	Ļ	TLSVEPSQQLDTASTEETDPETSQPEPNRPSELDLRLTEEGERM
į	1		LSTFKELFSEKHASLQNSQRTVAEVQETLAEMIRQHQKSQLCKS
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1	l	i	ANQRMAKFPESIKAWPFPDVLECCLVLLLIRSHFPGCLAQEMQQ
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			PRGEPGPRGPPGPPGLPGHGIPGLRGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGOKGEIGPMCIDEDGRAPGMPGM
		·	PRGEPGPRGPPGPPGLPGHGIPGLRGKPGPCGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP+PQGPPGPHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPOGLPGARGAY
			PRGEPGPRGPPGPPGLPGHGIPGLRGKPGPCGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP+PQGPPGPHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPOGLPGARGAY
			PRGEPGPRGPPGPPGLPGHGLEGVKEKEIPLASLRGEQG PRGEPGPRGPPGPPGLPGHGLPGLKGKPGPQGYPGVGKPGMPGM PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGJJGCEPGAPGV
		·	PRGEPGPRGPPGPPGLPGHGIPGIKKEKPIKKGKEIPLASLRGEQG PRGEPGPRGPPGPPGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PGGPGLPGQPGPKGDRGPKGLPGPQGLRCPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEP GPQGPIGVPGVOGPPGIPGIGKPGODG\PGAPGEP
		E CONTRACTOR DE KGEIGPMGIP*PQGPPGPHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEP GPQGPIGVPGVQGPPGIJGKPGQDG\IPGQPGFPGGKGEQGL PGLPGPPGLPGIGKPGFPGPKGDPGMGCAPGALGDPGH	
		j	PRGEPGPRGPPGP PGLPGPMGPMGKEAVPKKGKEIPLASLRGEQG PRGEPGPRGPPGP PGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP*PQGPPGHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGGP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGEQGL PGLPGPPGLPGIGKPGPPKGDRGMGGVPGALGPRGEKGPIGA PGIGGPPGEPGLPGIPGPPMGPPGALGRAGNCOCOLUMN
		j	PRGEPGPRGPPGP PGLPGPMGPMGKEAVPKKGKEIPLASLRGEQG PRGEPGPRGPPGP PGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP*PQGPPGHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGGP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGEQGL PGLPGPPGLPGIGKPGPPKGDRGMGGVPGALGPRGEKGPIGA PGIGGPPGEPGLPGIPGPPMGPPGALGRAGNCOCOLUMN
			PRGEPGLYGET PLASLRGEQG PRGEPGLYGET PLASLRGEQG PRGEPGPRGPPGP PGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP*PQGPPGHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFFGGKGEQGL PGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGA PGLGGPPGEPGLPGIPGPPGALGPPGPKGEGGIVGPQGPPG PKGEPGLQGFPGKPGFLGEVGPPCMPGFPGLIGNVGVF
			PRGEPGLAGFPGLEGEPGLICGPBGLEGEPGGLGCPGCCGCGCGCGCGCGCGCGCCGCCCCCCCCCC
			PRGEPGLPGPPGFPGTCK POLYACIL HORDONGOLD PGPKGEPGLPGPFPGTCK POLYACIL HORDONGOLD PGPKGEPGLPGPFPGTCK POLYACIL HORDONGOLD PGPKGEPGLPGPFPGTCK PGPKGEPGPFPGFPGFFFFFFFFFFFFFFFFFFFFFFFFF
			PRGEPGPRGPPGPPGLPGHGLEVAPRMGKEAVPKKGKEIPLASLRGEQG PRGEPGPRGPPGPPGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP+PQGPPGPHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFF0F\QGPLGK\PGAPGEP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGKGEQGL PGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGA PGLGGPPGEPGLPGIPGPPGPPGARGFPGPKGEGGIVGPQGPPG PKGEPGLQGFPCKPGFLGEVGPPGMRGFPGPIGPKGEHGQKGVP GLPGVPGLLGPKGEPGIPGPGGKPGALGPPGIPGI PGPPGPPGPPGPPGPPAVMPPTPDPOGFVLDDMGLGFPGALGPQGQPGL
			PRGEPGPRGPPGPPGLPGHGLEVAPRMGKEAVPKKGKEIPLASLRGEQG PRGEPGPRGPPGPPGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP+PQGPPGPHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFF0F\QGPLGK\PGAPGEP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGKGEQGL PGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGA PGLGGPPGEPGLPGIPGPPGPPGARGFPGPKGEGGIVGPQGPPG PKGEPGLQGFPCKPGFLGEVGPPGMRGFPGPIGPKGEHGQKGVP GLPGVPGLLGPKGEPGIPGPGGKPGALGPPGIPGI PGPPGPPGPPGPPGPPAVMPPTPDPOGFVLDDMGLGFPGALGPQGQPGL
			PRGEPGPRGPPGPPAWMPKEAVPKKGKEIPLASLRGEQG PRGEPGGPRGPPGLPGHGIPGIKGKPGPQQYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP+PQGPPGPHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFF0P\QGPLGK\PGAPGEP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGOPGFFGGKGEQGL PGLPGPPGLPGIGKPGFPGPKGDRGMCGVPGALGPRGEKGPIGA PGLGGPPGEPGLPGIPGPPGPPGAIGFPGPKGEGGIVGPQGPPG PKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPIGPKGEHGQKGVP GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI PGPFGEPGLPGPPGFPGIGKPGVAGLHGPPGKPGALGPQGQPGL PGPPGPPGPPGPPGPPAVMPPTFPPQGEYLPDMGLGIDGVKPPHAYG AKKGKNGGPAYEMPAFTAELTAPETBARGARGKGRPGNGYPRUFNELL
			PRGEPGPRGPPGP PGLPGHGRPGKEAVPKKGKEIPLASLRGEQG PRGEPGPRGPPGP PGLPGHGIPGIKGKPGPQGYPGVKKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP * PQGPPGPHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGGP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGEQGL PGLPGPPGLPGIPGIPGPKGDRGMGGVPGALGPRGEKGPIGA PGIGGPPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVGPQGPPG PKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPLGPKGEHGQKGVP GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI PGPRGEPGLPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHAYG AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRONY
			PRGEPGPRGPPGP PGLPGHGRPGKEAVPKKGKEIPLASLRGEQG PRGEPGPRGPPGP PGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP * PQGPPGHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGEQGL PGLPGPPGLPGIPGIPGFPGFKGDRGMGGVPGALGPRGEKGPIGA PGIGGPPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVGPQGPPG PKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPLGPKGEHGQKGVP GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI PGPPGPBGPPGPPGPPANMPPTPPPQGEYLPDMGLGIDGVKPPHAYG AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRQNY NPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNMEPVMYTYD EYKKGFLDQASGSAVILLRFGDRVFIOMPSFONACIV
845	. 215		PRGEPGPRGPPGP PGLPGHPGHPGHPGHPGHPGHPGHPGHPGHPGHPGHPGHPGHP
845	215		PRGEPGPRGPPGP PGLPGHPGHPGHPGHPGHPGHPGHPGHPGHPGHPGHPGHPGHP
845	215	2061 I	PRGEPGPRGPPGP PGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP + PQGPPGPHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGPP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGKGEQGL PGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGA PGLGGPPGEPGLPGIPGPMGPPGALGPPGPKGEKGGIVGPQGPPG PKGEFGLQGFPCKPGFLGEVGPPGMRGFPGPIGFKGEHGQKGVP GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI PGPKGEPGLPGPPGFPGICKPGVAGLHGPPGKPGALGPQGPPGL PGPPGPPGPPGPPATAELTAPFPPVGAPVKFNKLLYNGRQNY AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRQNY PYQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYD EYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHS SFSGYLLYPM JASNKSASLQDKMANPKEKTAMCUANELAPPUNKAROUTH
845	215	2061	PRGEPGPRGPPGP PGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP+PQGPPGHPGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPOP\QGPLGK\PGAPGPP KGPPGMHGPPGPVGLPGVGKPGVTGFPOP\QGPLGK\PGAPGEP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGKGEQGL PGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGA PGLGGPPGEPGLPGIPGPPGPPGATGFPGPKGEGGIVGPQGPPG PKGEPGLQGFPGKPGFLGEVGPPGMRFPGPIGPKGEHGQKGVP GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI PGPKGEPGLPGPPGFPGLGKPGVAGLHGPPGKPGALGPQGQPGL PGPPGPPGPPGPPAVMPPTPPPQGYLPDMGLGIDGVKPPHAYG AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRQNY NPQTGIFTCEVPGVYYFAYHVHCKGGNVWALFKNNEPVMYTYD SYKKGFLDQASGSAVLLLRFGDRVFLQMPSEQAAGLYAGQYVHS BFSGYLLYPM IASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNER
845	215	2061 I	PRGEPGPRGPPGPPGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PRGEPGPRGPPGPPGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP+PQGPPGPHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFFPOP\QGPLGK\PGAPGEP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGKGEQGL PGLPGPPGLPGIGKPGFPGPKGDRGMRGFVPGALGPRGEKGPIGA PGLGPPGEPGLPGIPGPPGPPGATGFPGPKGEGGIVGPQGPPG PKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPIGPKGEHGQKGVP GLFGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI PGPKGEPGLPGPPGFPGTGKRGVAGLHGPPGKPGALGPQGQPGL PGPPGPPGPPGPPAVMPPTPPPQGYLPDMGLGIDGVKPPHAYG AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRONY NPQTGIFTCEVPGVYYFAYHVHCKGGNVWALFKNNEPVMYTYD SYKKGFLDQASGSAVLLLRFGDRVFLQMPSEQAAGLYAGQYVHS EFSGYLLYPM IASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNER SPAHSKMFSVQLSLGEQTWESEGSSIKKAQQAVGNKALTESTLP
845	215	2061 I	PRGEPGPRGPPGP PGLPGHGREAUPKRGKEIPLASLRGEQG PRGEPGPRGPPGP PGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP * PQGPPGPHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGEQGL PGLPGPPGLPGIGKPGPDRGMGGVPGALGPRGEKGPIGA PGLGGPPGLPGIPGPPGPPGAIGFPGPKGEGGIVGPQGPPG PKGEPGLQGFPCKPGFLGEVGPPGMRGFPGPIGPKGEHGQKGVP GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI PGGPKGEPGLPGPPGPFGIGKPGVAGLHGPPGKPGALGPQGPGL PGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHAYG AKKGKNGGPAYEMPAFTAELTAPFPVGAPVKFNKLLYNGRONY NPQTGIFTCEVPGVYYFAYHVHCKGGNVWALFKNNEPVMYTYD EYKKGFLDQASGSAVLLLRPGDRVFLCMPSEQAAGLYAGQYVHS SFSGYLLYPM IASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNER EPAHSKMFSVQLSLGCTWESEGSSIKKAQQAVGNKALTESTLP CPI*KPPKSNVNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK
845	215	2061 I	PRGEPGPRGPPGP PGLPGHGREAUPKRGKEIPLASLRGEQG PRGEPGPRGPPGP PGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP * PQGPPGPHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGEQGL PGLPGPPGLPGIGKPGPDRGMGGVPGALGPRGEKGPIGA PGLGGPPGLPGIPGPPGPPGAIGFPGPKGEGGIVGPQGPPG PKGEPGLQGFPCKPGFLGEVGPPGMRGFPGPIGPKGEHGQKGVP GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI PGGPKGEPGLPGPPGPFGIGKPGVAGLHGPPGKPGALGPQGPGL PGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHAYG AKKGKNGGPAYEMPAFTAELTAPFPVGAPVKFNKLLYNGRONY NPQTGIFTCEVPGVYYFAYHVHCKGGNVWALFKNNEPVMYTYD EYKKGFLDQASGSAVLLLRPGDRVFLCMPSEQAAGLYAGQYVHS SFSGYLLYPM IASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNER EPAHSKMFSVQLSLGCTWESEGSSIKKAQQAVGNKALTESTLP CPI*KPPKSNVNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK
845	215	2061 F	PRGEPGPRGPPGP PGLPGHGPGLPGHGREAVPKKGKEIPLASLRGEQG PRGEPGPRGPPGP PGLPGHGIPGIKKRPGPQGYPGVKKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP*PQGPPGHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGGP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGEQGL PGLPGPPGLPGIPGIPGPKGDRGMCGVPGALGPRGEKGPIGA PGLGGPPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVGPQGPPG PKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPLGPKGEHGQKGVP GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI PGPRGEPGLPGPPGPPGIGKPGVAGLHGPPGKPGALGPQGQPGL PGPPGPPGPPGPPANVMPPTPPPQGEYLPDMGLGIDGVKPPHAYG AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRONY NPQTGIFTCEVPGVYYFAYHVHCKGGNVWALFKNNEPVMYTYD EYKKGFLDQASGSAVLLLRFGDRVFLQMPSEQASGLYAGQYVHS SFSGYLLYPM IASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNER PSPAHSKMFSVQLSLGEQTWESEGSSIKKAQQAVGNKALTESTLP CPP+KFPKSNVNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK FPNNRANYNFQVMYNQRYHCPIPKIFYVQLTVGNNEFFGEGKT
845	215	2061 I	PRGEPGPRGPPGP PGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PRGEPGPRGPPGP PGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP*PQGPPGHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGGP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGQGL PGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGA PGLGGPPGEPGLPGIPGPMGPPGALGPPGPKGEGIVGPQGPPG PKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPIGPKGEHGQKGVP GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI PGPPGPPGPPGPPGPFTGIGKPGVAGLHGPPGKPGALGPQGQPGL PGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHAYG AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRQNY NPQTGIFTCEVPGVYYFAYHVHCKGGNVWALFKNNEPVMYTYD SYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHS SYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHS SPAHSKMFSVQLSLGEQTWESEGSSIKKAQQAVGNKALTESTLP LPI*KPPKSNVNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK PFNNRANYNFQVMYNQRYHCPIPKIFYVQLTVGNNEFFGEGKT LQAARHNAAMKALQALQNEPIPERSPQNGESGKDMDDDKDANKS LISLVFEIALKRMMPVSFEVIKESGDDIMWSETTDLUGHFF
845	215	2061 F	PRGEPGPRGPPGP PGLPGHGIPGIRGKPGPQGYPGVGKPGMPGM PRGEPGPRGPPGP PGLPGHGIPGIRGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP + PQGPPGHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGKGEQGL PGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGA PGLGGPPGEPGLPGIPGPPGPAGTGPPGPKGEGGIVGPQGPPG PKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPIGPKGEHGQKGVP PGLPGVPGLLGPKGEPGIGKPGVAGLHGPPGKPGALGPQGQPGL PGPPGPBPGPPGPPGIGKPGVAGLHGPPGKPGALGPQGQPGL PGPPGPPGPPGPPATAELTAPFPPVGAPVKFNKLLYNGRQNY NPQTGIFTCEVPGVYYFAYHVHCKGGNVWALFKNNEPVMYTYD PXKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHS PSGYLLYPM IASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNER PSPAHSKMFSVQLSLGEQTWESEGSSIKKAQQAVGNKALTESTLP PCPI*KPPSNVNNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK PFNNRANYNFQVMYNQRYHCPIPKIFYVQLTVGNNEFFGGGKT QAARHNAAMKALQALQNEPIPERSPQMGESGKDMDDDKDANKS ISLVFEIALKRNMPVSFEVIKESGPPMKSFVTRVSVGGFFSAE EGNSKKLSKRRAATTVLOFLKKI.PPL.DRURPRYN
845	215	2061 F	PRGEPGPRGPPGP PGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP+PQGPPGHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGLKGFGMPGAPGV KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGKGEQGL PGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGA PGLGGPPGEPGLPGIPGPPGPPGALGPPGPKGEGGIVGPQGPPG PKGEFGLQGFPCKPGFLGEVGPPGMRGFPGPIGPKGEHGQKGVP GLPGVPGLLGPKGEPGIPGLQGPPGIPGIGGPSGPIGPPGI PGPKGEPGLPGPPGFPGIGKPGVAGLHGPPGKPGALGPQGQPGL PGPKGEPGLPGPPGFPGIGKPGVAGLHGPPGKPGALGPQGQPGL PGPPGPPGPPGPPAMPPTPPPQGEYLPDMGLGIDGVKPPHAYG AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRQNY NPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYD EYKKGFLDQASGSAVLLLRFGDRVFLCMPSEQAAGLYAGQIVHS EYSGYLLYPM ASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNER FPAHSKMFSVQLSLGEQTWESEGSSIKKAQQAVGNKALTESTLP CPI*KPPKSNVNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK FPNNRANYNFQVMYNQRYHCPIPKIFYVQLTVGNNEFFGGGKT QAARHNAAMKALQALONEPIPERSPQNGESGKDMDDDKDANKS ISLVFEIALKRNMPVSFEVIKESGPPHMKSFVTRVSVGEFSAE EGNSKKLSKRAATTVLQELKKLPPLPVVEKPK\HFFKKRPKT VKAGPEYGQGMMPISRLAO100AWBWENDDWILLENDER
845	215	2061 I	PRGEPGPRGPPGP PGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PRGEPGPRGPPGP PGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM PGKPGAMGMPGAKGEIGQKGEIGPMGIP*PQGPPGHGLPGIGK PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV RGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEP GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGEQGL PGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGA PGLGGPPGEPGLPGIPGPMGPPGALGFPGPKGEGGIVGPQGPPG PKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPIGPKGEHGQKGVP GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI PGPPGPBGPGPGPFGIGKPGVAGLHGPPGKPGALGPQGPPGI PGPPGPBPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHAYG AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRQNY NPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYD SYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQIVHS SYGSGYLLYPM HASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNER PSPAHSKMFSVQLSLGEQTWESEGSSIKKAQQAVGNKALTESTLP CPI*KPPKSNVNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK PSPHNRANYNFQVMYNQRYHCPIPKSPQNGESGKDMDDDKDANKS ISLVFEIALKRMMPVSFEVIKESGBDUMKGETMTHUGFFF

		· · · · · · · · · · · · · · · · · · ·	l News and amount contribute gigmal montide
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence) Sequence	\=possible nucleotide insertion)
	sequence	 	RHKVISGTTLGYLSPKDMNQPSSSFFSISPTSNSSATIARELLM
	1	1	NGTSSTAEAIGLKGSSPTPPCSPVQPSKQLEYLARIQGFQVHYC
	ŀ	İ	
	ł		DRQSGKECVTCLTLAPVQMTFHAIGSSIEASHDQV*YATAILLC
	i	}	YGPARKWKAIKMEAMCAHAALLSLIHYLLAPSARLEKSKLFALG
	1		Ŋ.
5846	1126	456	FSKLIMKTFIIGISGVTNSGKTTLAKNLQKHLPNCSVISQDDFF
		4	KPESEIETDKNGFLQYDVLEALNMEKMMSAISCWMESARHSVVS
	}	ļ	TDOESAEEIPILIIEGFLLFNYKPLDTIWNRSYFLTIPYEECKR
	i	ļ	RRSTRVYQPPDSPGYFDGHVWPMYLKYRQEMQDITWEVVYLDGT
	1		KSEEDLFLQVYEDLIQELAKQKCLQVTA*RRNTTNPS/CK*IRK
	İ	j	
		J	LQGVI
5847	2769	505	APEMEDLSSPDSTLLQGGHNLLSSASFQESVTFKDVIVDFTQEE
ł	1		WKQLDPGQRDLFRDVTLENYTHLVSIGLQVSKPDVISQLEQGTE
	1	Į.	PWIMEPSIPVGTCADWETRLENSVSAPEPDISEEELSPEVIVEK
		ļ	HKRDDSWSSNLLESWEYEGSLERQQANQQTLPKEIKVTEKTIPS
	!	1	WEKGPVNNEFGKSVNVSSNLVTQEPSPEETSTKRSIKQNSNPVK
		1	KEKSCKCNECGKAFSYCSALIRHQRTHTGEKPYKCN*/CVEKAF
	}	ì	SRSENLINHQRIHTGDKPYKCDQCGKGFIEGPSLTQHQRIHTGE
	l .	ì	KPYKCDECGKAFSQRTHLVQHQRIHTGEKPYTCNECGKAFSQRG
	1	1	HFMEHQKIHTGEKPFKCDECDKTFTRSTHLTQHQKIHTGEKTYK
	1	1	
	į	1	CNECGKAFNGPSTFIRHHMIHTGEKPYECNECGKAFSQHSNLTQ
	1	i	HOKTHTGEKPYDCAECGKSFSYWSSLAQHLKIHTGEKPYKCNEC
1	1	j	GKAFSYCSSLTQHRRIHTREKPFECSECGKAFSYLSNLNQHQKT
1	1	1	HTQEKAYECKECGKAFIRSSSLAKHERIHTGEKPYQCHECGKTF
}	ł		SYGSSLIQHRKIHTGERPYKCNECGRAFNQNIHLTQHKRIHTGA
l	1		KPYECAECGKAFRHCSSLAQHQKTHTEEKPYQCNKCEKTFSQSS
	ļ	į.	HLTQHQRIHTGEKPYKCNECDKAFSRSTHLTQHQRIHTGEKPYK
ŀ	1	ł	CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN
		h	KHORLHPGI
			AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK
5848	22	2961	GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL
	1	ļ	
	1	1	DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG
	1		YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV
ł	1	1	GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL
ļ	1	1 .	VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV
	1	i	SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY
ł	i	ĺ	PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA
i		1	ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA
İ		1	SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN
i	•	j	APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD
l	i	1	TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ
[1.		APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL
1	1	1	APACHENDVKVGGIIDGEFGNDIAGDFRSSPDIQFRDDHSKFND
	1	1	CSVPTRALLLSTYIKFVNLFPEVKPTIQDVLRSDSQLRNADVEL
1	l	1	QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK
		1	GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG
		1	LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA
1	}		RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL
1	1	.1	NFTPTLICSDDLQPNLNI.QTKPVDPTVEGGAQVQQVVNIECVSD
	1		FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ
1	I	1	
			RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP
ŀ	1		NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV
4	į.		SQRLCELLSAQF
	1		KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ
5849	3545	1895	KKKEIKEIVITAHVAQAGDEDESSSAFFSBASICSIESISSISSISSISSISSISSISSISSISSISSISSISS
5849	3545	1895	P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES
5849	3545	1895	P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES
5849	3545	1895	P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW
5849	3545	1895	P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLOWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI
5849	3545	1895	P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SOLKISDRSHROKLQLKALDVVLFGPLTRPPHNWMKDFILTVSI
5849	3545	1895	P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMKDFILTVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER
5849	3545	1895	P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATMKHSHLHRBDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMKDFILTVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER LBKAOEENRNVAVEKQNL*RKMMDEINYAKEEACRLRELREGAE
5849	3545	1895	P*DPCMSLSPPCFTEEDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMKDFILTVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER

SEO	Predicted	1 8 32 3	
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	Managuine, C=CVStelne, D=Departic Acid p
l	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		(\=possible nucleotide insertion)
			AHSSSLDEVDHKILEAKKALSELTTCLRERLFRWQQIEKICGFQ
1	1		IAHNSGLPSLTSSLYSDHSWVVMPRVSTPDVDTAGGUDDI DEDM
1		<u> </u>	PPIVSQFPGTMAKPPGSLARSSSLCRSRRSTVDCCDODDDAGA
ļ	1		PHAPHPSHPRHPHHPOHTPHSLPSPDDDTT.SVSCCDALVDNUDD
}			EEALYFSAEKQWEVPDTASECDSLNSSTGRKOSDD/GVDDDTDN
5850	3	1005	IIS/DERYQEMRCP*RIPSGGIL
		1895	KAVLNFSASGSVISLTGSNPMHDASMWHLKKNGIIVYLDVPLLN
			LICKLKLMKTDRIVGONSGTSMKDLLKFRROVVKKWVDADARGE
1	1		SGASPEEVADKVLNAIKRYODVDSETFISTPHUMDEDCEOVUCA
1		i	EFFIEAVIEGLASDGGLFVPAKEFPKI.SCGEWKGIJGATVUEDA
1	1	ľ	QILLERCIHPADIPAARLGEMIETAYGENFACSKIAPVRHLSGN
			QFILELFHGPTGSFKDLSLQLMPHIFAQCIPPSCNYMILVATSG
l l		1	DTGSAVLNGFSRLNKNDKQRIAVVAFFPENGVSDFQKAQIIGSQ
			RENGWAVGVESDFDFCQTAIKRIFNDSDFTGFLTVEYGTILSSA KSINWGRLLPQVVYHASAYLDLVSQGFISFGSPVDVCIPTGNFG
		l	NILAAVYAKMMGIPIRKFICASNQNHVWTDFIKTG\HYDLRGKE
			N*AQTFFTVQ*IFLPNLSNLERHLHLMANKDGQLMTELFNRLES
1	Ì		QHHFQIEKALVEKLQQDFVADWCSEGECLAAINSTYNTSGYILD
1	1		PHTAVAKVVADRVQDKTCPVIISSTAHYSKFAPAIMQALKIKEI
1	1		NETSSSQLYLLGSYNALPPLHEALLERTKOOEKMEVOVCA A DANK
5851	3120		VLKSHVEQLVQNQFI
1 3332	3120	1802	RCYLQFLALLLTSTSARAAAIAAAEEPAGSPSVMTRAGDHNRQ
ļ			RGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHFAVSVELVELV
į	l i		UNDULLTAVYGLVVAGSVLVI.GATTGDW/DKWADI.V//AOTICITAT
1			QNVSVILCGIILMMVFLHKHELLTMYHGWVLTSCYILIITIANI
			ANLASTATAITIQRDWIVVVAGEDRSKIANMNATIDDIDGI TOLI
	i		LAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWKVYQKT
1 1			PALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIH
j i			ELEHEQEPTCASQMAEPFRTFRDGWVSYYNQPVF/LGWHGSCFP LYDCPGL*LHHHRVRLHSGTEWFHPQYFDGSISYNWNNGNCSFY
			LATSKMWFGSDRSDLRIGTAFLFDLVCDLCIHAWKPPGLVRFSF
5852	1	422	KTTFPSSLCPLRQLPEVRGYSGQPLTDPLISLCRSHKCRGKGWG
	1		SSSYPSLPALLRARSAPGHCTHRSCGPRWPTDSTSPIPMOCADD
1 1		,	SGWAQAQPTILLLVPRLRKSLPSIWG/SLMGEFTTGGDG/WPDG
1 1	}		I I I I I I I I I I I I I I I I I I I
1 1			FVSBIKKVVAGKKQSVYFRRCGGCSRAPPI,TTCGGUGGDVODWD
5853	223	33.6	ESGAWALAPGLPAIHGRSWES
	443	1346	RLLGLSRVKGLHGPAASAWISDPETRGDPGGPWGMWRGSDLRPR
	l	ĺ	PVSLTGLTLVCK*AAOGPOV\HSVKLCFGLCG\PCLL\PDTPDD
	ł	1	DULHPRRPRLHPGTRGVAVEPHALRVVHVAHGEFAGIDAAGDGU
		Į	GGVEIPQG/VGSLGARRGLRPSRPSSRHRNRVPAPDCCDDLATD
			ARREPPDPALTCPGLGODOGPREOOKOGSGRUDTTI.CDWGECE
		ſ	SRWVRGNFRTGTAATLIGFSRNPTLINGSENWGSLVSIQEEGPDT
			GWEREKRNPAEMGNPQRWASPIHTPPLGPEILRAMPEALRAMPE
		ľ	ALGLRPDPATSVPSALS/QTF/PESWPRSCLRNQGETLGMGPVP LSSLCITESPSQNWTPCLLLLTCPRGLF
5854	86	938	KGRNTAPEKKGAALNNRENASS*NGY/SRWKQDIRRIENHIIOE
	1	1	LXHLCAMIKRVLLERLENTRKLRELTEGRTLDWPQNRITEVSAK
	İ	ļ	RQIVTEYREKGKRN*EEKKRDLEGRSRRYNLCIIGIPETEDRAS
1		ļ	GAETIKDLLE/ENFPELKNELDLOMEKAHRIPLKFNEKKAASRU
	i	i	IRVTFL/KFQRRNILQASSQRKQVTYKGAKVRLTSDFSPAILNA
1			RROW/N/PISRVLRENNFEPRIIYSAKLSFLYKGNWKTFLDIQG
			LGKYINQELSLKILLKDLLOLTENIN
5855	536	2391	LRSYGCKAPSRISHLHK\FLFLLLPSLLMGVGFGPDDTTDCGTD
1			FISHIHHVUSQSQSPLSSNCWICLSTHTO+FTALDADLITUTOS
ı	1	1	NVSLHISYLAIPFLADSFLKPV/L+PGNSAKHISFKISSISMIC
}		i	GRAVALLHLIASGLTSIOTNTASSKPPIWGY\LSTOTSFICEDED
	}	F	LCLSRTYPNPAHATMVGQVPQSLCGLIFTL/RTPCRPSTLUDNV
.		1	KIISTSAWQKVLCPSGSPTIHTSLHLTTGSSFISFHDIDGEDAA
			NSALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGSN/RLTVDKDN

			La residential
SEÇ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding		P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		ozqua	\=possible nucleotide insertion)
	sequence		FFLSPKPNSLHQLPSQ\TPYQALTGAALAGSYPIWENENTLSWL
i i	1		
	1		PTFTYNFCLSTPSLFFLCDTN*YLCLPANWSGTCTLVFQAPTIN
	<u> </u>	ì	ILPPNQTILISVEASISSSPIRNKWALHLITLLTGLGITAALGT
	1	1	GIAGITTSITSYQTLFTTLSNTVEDMHTSITSLQRQLDFLVGVI
	ł		LONWRVLDLLTTEKGGTCIYLQEECCFCVNESGIVHIAVRRLHD
	1	1	RAAEL+HQVADSWWQGSSLLRWIPWVAPFLGPLIFLFLLLMIGP
		1	KAAED*HQVADSWWQGSSEDKWIPWVAFFEGFEITEDFEIDENTGF
	1	1	CIFNLVSRFISQRLNCFIQASMQKHIDNIFHLCHV*YQSLRGNH
		-	SEAPEPRP
		1137	PWLHGLGLSAVFLFYL*/YVTFHLYGGIILLLLIFISIAGILYK
5856	173	1 113/	FQDVLLYFPEQPSSSRLYVPMPTGIPHENIFIRTKDGIRLNLIL
	1	ļ	LÄNAPPILLEÄLÄSSYKPIALLIAILIAILIAILIAILIAILIAILIAILIAILIAI
	1	1	IRYTGDNSPYSPTIIYFHGNAGNIGHRLPNALLMLVNLKVNLLL
	1	1	VDYRGYGKSEGEASEEGLYLDSEAVLDYVMTSPDLDKTKIYLSG
l		I	RSLG\GAAAIHLASDNSHRISAIMVENTFLSIPHMASTLFSFFP
1	1	1	MRYLPLWCYKNKFLSYRKISQCRMPSLFISGLSDQLIPPVMMKQ
l	1		LYELSPSRTKRLAIFPDGTHNDTWQCQGYFTALEQFIKEVVKSH
i		1	
1	1	<u> </u>	SPEEMAKTSSNVTII
5857	1597	563	KLIGKVLVLSVVADAMAAFAVEPQGPALGSEPMMLGSPTSPKPG
}	j	1	VNAQFLPGFLMGDLPAPVTPQPRSISGPSVGVMEMRSPLLAGGS
į.		1	PPOPVVPAHKDKSGAPPVRSIYDDISSPGLGSTPLTSRRQPNIS
	1	ì	VMQSPLVGVTSTPGTGQSMFSPASIGQPRKTTLSPAQLDPFYTQ
Į.	1	1	GDSLTSEDH\LDDSWGDCIWGFLKASA\SYILL\QFAQYGGIS*
ļ	1	1	GDSD1SEDR (EDDSWGDC1WGPDRAGA G11DD (Q1AQ1001D
	1	l .	NMWMSNTGNWMHIRYQSKLQARKALSKDGRIFGESIMIGVKPCI
1	1	· I	DKSVMESSDRCALSSPSLAFTPPIKTLGTPTQPGSTPRISTMRP
ì		1	LATAYKASTSDYQVISDRQTPKKDESLVSKAMEYMFGW
5858	355	1419	PPHQPAAASTSXHQQQQPPPPPPQDSSKPVVAQGPGPAPGVGSAP
3030	333	1	PASSSAPPATPPTSGAPPGSGPGPTPTPPPAVTSAPPGAPPPTP
		ļ	PSSGVPTTPPQAGGPPPPPAAVPGPGPGPKQGPGPGGPKGGKMP
1	1	1	
1	i	1	GGPKPGGGPGLSTPGGHPKPPHRGGGEPRGGRQHHPPYHQQHHQ
ì	1	Į.	GPPPGGPGGRSEEKISGPRRGFKANLSLLRRPGEKTYTQRCRFC
1	ł	1	LLGIYLLISRRMNSRRLFAKIWENQEKFLSTKAKDSEFIKLESR
}	Į.	1	ALA*NCPKPELG*YTP*GGRQLPSSLFPTHACLPLSCSVIFSPF
1		1	MFPQ*NCWGRKPFRPNLGPHLKGAVCNRWDDPWEGPTGKGHCLN
	ĺ	í	
1)	·	FAS
5859	307	1503	GGSSARPRASSRRMLSRKKTKNEVSKPAEVQGKYVKKETSPLLR
1	1	\	NLMPSFIRHGPTIPRRTDICLPDSSPNAFSTSGDGVVSRNQSFL
1	1	1	RTPIQRTPHEINRRESNRLSAPSYLARSLADVPREYGSSQSFVT
1	1	l .	EVSFAVENGDSGSRYYYSDNFFDGQRKRPLGDRAHEDYRYYEYN
1	1	1	EAGLUA BURDOROK I I TODAL I PORTUE PORTUE DEL DE SEGUE
1	1	Į.	HDLFQRMPQNQGRHASGIGRVAATSLGNLTNHGSEDLPLPPGWS
ŀ	1	1	VDWTMRGRKYYIDHNTNTTHWSHPLEREGLPPGWERVESSEFGT
1	[1 ·	YYVDHTNKKAQY\RHPCAPTCTSV*STTSCHI/AS/RQQTERNQ
l	1	ļ	SLLVPANPYHTAEIPDWLQVYARAPVKYDHILKWELFQLADLDT
I	ļ	1	YQGMLKLLFMKELEQIVKMYEAYRQALLTELENRKQRQQWYAQQ
1	1	1	
l _			HGKNF
5860	2956	1270	TIRVEEFPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFP
1		1	LLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQI
1	1	1	SWEKIHGKSSOTVAVHHPQYGFSVQGEYQGRVLFKNYSLNDATI
1	1	1	TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG
{	1	1	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFP
1	1	1	PDSLIDGGNETVAALCIAATGAFVAHIDWEGDDGEMESITISFP
1	l	1	NETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDI
1	1	1	QYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDG
1		1	OWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEVTQK
1	1	1	VHPTFQDPSLPTYPPLPALQFQWASPSTA*TSRD\LATEP*KIA
1		1	PSPLSTL\ATIKGWTQLPTIIA*CSGVGALFIV\LVKCFGLGIF
1		1	PSPLSTL ATTRGWTQLPTLIA*CSGVGALFIV LUNCEGLGIF
I	I	i	CYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDPYPDSV
1		ł	KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL
1			KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
<u> </u>			EVCACVQAFNLVASSGDDSQGGDKCGCEVGSWVGSMRVVMARLL
5861	2051	1305	EACULATION OF THE COURT AND COURT AN
1		1	SEGEQGIPTACAAFAQQPAG/EPRRGLAGVGEGGPQCSWVNYRC
Į.	ł	- 1	TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI
- [l	î.	LE*RMNSGSPARDNAPSQRFCTNLSEGLRFGISPSWREALYGCH
1		i	

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	1 detail containing cianti
NO:	nucleotide		1 to-organitie, CELVSTP1ne D_Nemambic Nett n
1	location	location	Gidtamic Acid, F=Phenvlalanine C_Cl
ŀ		corresponding	n=nistidine, l=180 encine V_Train-
ı	corresponding	to first	L=Leucine, M=Methionine N-Assamatica
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ı	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W-Trantophon & manager
ł	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	- agacinet	Codon, /=possible nucleofide delation
	· · · · · · · · · · · · · · · · · · ·		\=possible nucleotide insertion)
5862	1556		A
	1 2330	483	PPFQLIMGEIKVSPDYNWFRGTVPLKKIIVDDDDSKIWSLYDAG
1	1		PRSTRUPLIFLPPVSGTADVFFROILALTGWGVPVTALOVDVVW
J	1	1	DHLEFCDGFRKLLDHLQLDKVHLFGASLGGFLAQKFAEYTHKSP
j	l	}	RVHSLILCNSFSDTSIFNQTWTANSFWLMPAFMLKKIVLGNFSS
1	ŀ		GPVDPMMADAIDFMVDRLESLGQSELASRLTLNCQNSYVEPHKI
	1		RDIPVTIMDVFDQSALSTEAKEEMYKLYPNARRAHLKTGGNFPY
	1	Į.	LCRSAEVNLYVQIHL/R/RNSMEPNTRPLTHQWSVPRSLRCRKA
]	ALASAPPECCUCI ALBURE TO THE THOUSE PRINTED THOUSE P
i	ľ	1	ALASARRSSSVSLAVNDELTRCVLV*SVASAPVSRPFPSGSSGS PVLTVSGK
5863	2714	249	
		1 223	PFPSRGSLPLAAPREDTMGPLMVLFCLLFLYPGLADSAPSCPQN
1	1	1	VNISGGTFTLSHGWAPGSLLTYSCPQGLYPSPASRLCKSSGQWQ
	1	i	TPGATRSLSKAVCKPVRCPAPVSFENGIYTPRLGSYPVGGNVSF
			ECEUGFI \LRGSPVROCRPNGMWDGETAVCDNGACUCDNDGT OF
j]	i	GP \VRIGEREGHGDKVRYRCSSNT.VI.TGSSEDECOGNOUNCOMD
ŀ	ļ		PICKQPYSYDFPEDVAPALGTSFSHMLGATNPTOKTVFSLCDVT
]	1		1 212R3GRENLYLLLLLDCSOSVSENDFI.TFKESASI.MUDDIECEST
1	J i		NVSVALITEASEPKVLMSVLNDNSRDMTEVISSI.ENANVVDUDA
ŀ	1		I GIGINIYAALNSVYLMMNNOMRIJGMETMAW\OFTDUXTIII\ m
ļ			I LGK \SHWGGSPKTAVDHIRETINTNOKPNDVIDTVATCUCKI DI
1	ļ i		DWRELDSLGSKKDGERHAFILODTKALHOVERUMLDVCVI MDmt
	1 1		1 CGVGNMSANASDOERTPWHVTIKPKSOET\C\DCALICDOMER
	1		AAHCERDGNDHSLWRVNVGDPKSOWGKERI.TEVAVIGDCRDVD
1			LOUNGELD EFYGD DIALL KLAOKVKM STRCOGREGED COME
Í			\EARLGFLRETFKGSTCR\DHENET./WNKOGW\DAUB\WAY\\
1	1		GSKLEHLTLRMGVEWTSCCRGLSPKKKTM\FPNLT\DVRE\VVT
1	1		D\QFL\CS\GPQEDESP\CK*E\SGGA\VFLERRFRLSAGGVWC
			SWGL\YNP\CT.GSA\DKNSPKKGPSVAKVPPPTR/DFHIN\LFP
1 .	!		Q*SPWLRQHPGGMS*IFLPLLANGHLSPFACPARICRPLHFLPS
			EWATLETL EWATLETL
5864	173	1013	PLISVPQSLISLPQPLLCFPGGQEPSAPSPCLYSFLWACSFTMG
			KLPPSIPPSSPLACVLKNLKPLQLTPDLKPKCLIFFCNTAWPQY
1 1			KLDNDSK*PENGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S
i	ľ	ſ	HWSLPSLCSQC/GLIPNLSSFSPFCSFG/PPPQVPSP/TESFFS
			MDSSDLPPSPOAA PROAFROANTING A CARPANTING A C
1	j.		MDSSDLPPSPQAAPRQAEPGPNSHLASAPPPYNPFITSPPHTWS
	i		SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPFSLSQIR*RL GSFSSNIKIQPSSWLIWQQP
5865	568	1684	CLPGPPWGFGWDAGUTTVGGT
j	1		CLPGPRWGEGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC
1 1	1	1	LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTREHAC
1 1	ŀ	j	ACTRV*VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA*AC
i f		ł	TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI
1 1		ł	/CVYVCVLCVWACMRMSTCVWLVYG*ACTCVWMHM/CSCTCR/C
1 1	i i	I	VHVCCMSMHACECLCVYLHICGCAGTRRWAGSARGSRSCSRLP
] [i i		CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEARLGEHRGW
1 1	1	J	GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC
5866	98		GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK
]	30	3197	ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL
1			KKEVAMTEHKMSVEEVCRKYNTDCVOGLTHSKAORT LARDEDNA
i i			DIPPPITPEWVKFCROLFGGFSILLWIGATI.CELAYCIOACUBD 1
1	į		DPSGDNLYLGIVLAAVVIITGCFSYYOEAKSSKTMFSFKNMADO
	ľ	1	QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADI.PITCAUGG
1		· · · · · · · · · · · · · · · · · · ·	KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNTTEPSNMEUPOUR
- 1		1.	KGVVVATGDRTVMGRIATLASGLEVGKTPTATETPHETOLTDGT
			AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV
j		1.	CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM
J		1 :	TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC
ı	1	1 1	NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE
1	[1 i	RNKKVABIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD
		[]	RCSTILLQGKEQPLDEEMKEAFQNAYLBLGGLGERVLGFCHYYL
J	-	1 7	PEEOPPKGFA FOCODIVIDENT OF STATE OF STA
<u> </u>		1 :	PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG
		<u></u>	KCRSAGIKVIMVTGDHPITAKAIAKGVGIIFEGNETVEDIAARL

			I - I
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	I=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence	\=possible nucleotide insertion)
	sequence		NIPVSQVNPRDAKACVIHGTDLKDFTSEQIDEILQNHTEIVFAR
		ļ	
		1	TSPQQKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGI
	Į.	Ļ	AGSDVSKQAADMILLDDNFASIVTGVEEGRLIFDNLKKSIAYTL
	Į.		TSNIPEITPFLLFIMANIPLPLGTITILCIDLGTDMVPAISLAY
	1		EAAESDIMKRQPRNPRTDKLVNERLISMAYGQIGMIQALGGFFS
	ł	i	YFVILAENGFLPGNLVGIRLNWDDRTVNDLEDSYGQQWTYEQRK
	1	1	VVEFTCHTAFFVSIVVVQWADLIICKTRRNSVFQQGMKNKILIF
	Į.	1	GLFEETALAAFLSYCPGMDVALRMYPLKPSWWFCAFPYSFLIFV
	1		YDEIRKLILRRNPGGWVEKETYY
		1	LPGRRARGGRGLGWPPAQALDGSRMGKAKVPASKRAPSSPVAKP
5867	3	1485	LPGRRARGGRGLGWPPAQALDGSRFGRARVPASRRAPSSEVARP
1	1	1	GPVKTLTRKKNKKKKRFWKSKAREVSKKPASGPGAVVRPPKAPE
ı	ļ	1	DPSQNWKALQEWLLKQKSQAPEKPLVISQMGSKKKPKIIQQNKK
	1	1	ETSPQVKGEEMPAGKDQEASRGSVPSGSKMDRRAPVPRTKASGT
	1	1	EHNKKGTKERTNGDIVPERGDIEHKKRKAK\GQPQPHPPR/IDI
ļ	1	1	WFDDVDPADIEAAIGPEAAKIARKQLGQSEGSVSLSLVKEQAFG
1	1	}	GLTRALALDCEMVGVGPKGEESMAARVSIVNQYGKCVYDKYVKP
1	1	1	TEPVTDYRTAVSGIRPENLKQGEELEVVQKEVAEMLKGRILVGH
1	{	1	ALHNDLKVLFLDHPKKKIRDTQKYKPFKSQVKSGRPSLRLLSEK
i	•	1	ALMNDERVE EDAPERRE ROLL WANTE WANTE WAS TO BE TO
1		1	ILGLQVQQAEHCSIQDAQAAMRLYVMVKKEWESMARDRRPLLTA
l	į.	ļ	PDHCSDDA+QSCPAAAAPLQRQCDQSQGQITSPQSGNSGETFS
5	Į		ESWQRGVAWCY
5868	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
1	1	1	AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
ļ	i	1	TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
i	1	•	LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH
			IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
l	1	1	CCLPVCAVNFKCLHELVKHEENGLVFEDSBELAAQLQMLFSNFP
i	j.	}	
i .	1		DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5869	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
1	1	1	AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
l	1	I	TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
Į.	1	1	LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH
ł		1	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
}	1	1	CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP
	1	1	DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
			LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
5870	2122	833	DIAGASHIQUASQSISAKIFAAAQHIJ CUMUCBEDADQEDEDDU
1			AVTVYDKPASPFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
}	i	1	TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
	i i		
l		1	LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH
1			IOVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
			IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP
			IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNOFRKNLRESQQLRWDESWVQTVLPLVMDT
F021		3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNOFRKNLRESQQLRWDESWVQTVLPLVMDT
5871	. 3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS
5871	3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL+LSLRRL+LEPTI+NGLLT+CSRLSVFRFLKV\GSVYEP
5871	3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT
5871	3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLKLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDOKAKIODSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI
5871	. 3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNOFFKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMROADKVQQFKQDPRPTTCLHSVFNVHTGDELLS
5871	. 3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLOINAVSLYLLYLVEWISSGLQIIYNTDEVSFIQNLVF
5871	3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ
5871	3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KOFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR
5871	. 3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KOFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR
5871	3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR
5871	3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSIYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG
5871	3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNOFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLROGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVOEYODLLTPVLHHTTEGYPVVPKYYYVPADFVEYE
5871	. 3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPIRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSOKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI
5871	3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSGLDLPMKVVDMFG CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNOFFKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVORYVPLKDORNVSMRFSNQGPLENDLVVHVALIAESQRLQV
5871	. 3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTT*CLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELLSPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIOTOTPOOVEPIQIWPQQELVKAYLQLGINEKLGLSGR
5871	3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHMRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFFSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID
5871	. 3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHMRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFFSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID
5871	. 3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSIYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVXRPV\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALOFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA
5871	. 3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEELPEFKS
5871	. 3	3465	IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG CCLPVCAVMFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFFFLKV\GSVYEP LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS YEEYGHLQINAVSIYLLYLVEMISSGLQIIYNTDEVSFIQNLVF CV\ERVXRPV\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID DIKNALOFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peotide
NO:	nucleotide '	location	(A=Alanine, C=CVSteine, D=Aspartic Acid P
j	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
- 1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	1	Codon, /=possible nucleotide deletion, \-possible nucleotide insertion)
		 -	AGSQKLWSVVRRAASLLSKVVDSLAPSITNVLVQGKQVTLGAFG
1		•	HEEEVISNPLSPRVIQNIIYYKCNTHDEREAVIQQELVIHIGWI
			ISNNPELFSGTLKIRIGWIIHAMEYELQIRGGDKPALDLYQLSP
			SEVKQLLLDILQPQQNGRCWLNRRQIDGSLNRTPTGFYDRVWQI
1			LERTPNGIIVAGKHLPQQPTLSDMTMYEMNFSLLVEDTLGNIDQ
- 1			PQYRQIVVELLMVVSIVLERNPELEFQDKVDLDRLVKEAFNEFQ
	i	1	KDQSRLKEIEKQDDMTSFYNTPPLGKRGTCSYLTKAVMNLLLEG
		i	EVKPNNDDPCLIS
5872	68	665	VQGYMYRFVIKINSCYSEKTSICRHRCCPELPATQPWPTPTVFF
j	1		NIAIDSESLGCI\SFKLFADKV/PKRWKKNFVI.I.NTGPVVI.GDV
İ			GPCFYRIIPG\LCQGGDFTHHNGTGGKSLYSKEFDDENET/LVU
j	j	}	TAPGVLSTANAGPTTNGSQFFICTAKTEDG*OHWVFGKVKDGMS
5873			IVEALERSGSRNGKTSKKITAANCGOL
36/3	2240	506	RRPPEGGSGGGRRTRARMPLPWSLALPLLLSWVAGGEGNAASAD
			HHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCEATCERGCVE
	1		GECVGPNKCRCFPGYTGKTCSODVNECGMKPPPCOUPCUMTUGG
1			YKCFCLSGHMLMPDATCVNSRTCAMINCOYSCEDTEEGPOOLGD
ľ	1		SSGLKLAPNGRDCLDIDECASGKVICPYNRRCVNTRGGVVCVC
i	Ì		IGFELQYISGRYDCIDINECTMDSHTCSHHANCENTOGSEKCKC
1	1		KQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMK
ļ	1		KKAKIKNVTPEPTRTPTPKVNLQPFNYEEIVSRGGNSHGG\KKG
1	1		NEEKMKEGLEDEKREEKALKD*HRRERPFRG\DVFFPKVNEAGE
	1		FGLIL\VQRKALTSKLEHKADLNISVDCSFNHG\ICDW\KQDR\
	1 1		EDDFDW\NPADR\DNAI\GFY\MAVPGLWQGHK\KDIGRLKLLL
1	1 1	ł	PDLQPQSNFCLLFDYRLAGDKVGKLRVFVKNSNNALAWEKTTSE DEKWKTGKIQLYQGTDATKSIIFEAERGKGKTGEIAVDGVLLVS
	<u>l</u>		GLCPDSLLSVDD
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD
ŀ	l i		AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD
			VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGDSFDSSMDSTenn
1]]	}	SYFRKECGRDLEFSHSNSRDOVIGHRK; GHFDSODWKFALDGEN
1	1		EQDFGHPVSQESSWSOEYSFGPSAVIGDFGGGDI.TEVECTEVEL
	1		SEDYDVDHSG\EA\DSVLRGS\SOVOA\RGRAINTVDORGELLG
		ŀ	. KGETUGLLTAKGGVGKLVTLRNVSTKKIPTVNRTTPKTOGTMOT
1	! !		QKNTPSPDVTLGTNPGTEDIOFPIOKIPIGIDI,KNI,DI,DDDVMC
1	1 1	į	FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSOLFOTLERLER
1	1 1		ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL
1	<u> </u>		NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC
			NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS
[1	SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL
	1		VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN
1 1	1	1	SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV
1 1		1	RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR
ŀ]	1.	APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP
1	1		QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE
			KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK
, ,		[.	FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSOFSBUDIME
1 1		1 1	GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGEEAPA\ BGBC
1 1		1 .	GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLOVTCEREC
ļ Ì	İ	1.	RGPSSKSLKVGMIPAPKRVCLIOEPKVHEPVPTAVDPDBCDDMC
[[1	KKKKPKDLDFAQQKL\TDK\NLGFO\MLOKMGWKEGHGLGSIGV
	1	1	GIR \SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWOL.
5875	296		IFVF
		1848	LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA
	1	(4	LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVVKNDDSDD
1		į v	NLTCSCQGMLTCVGVGDVCNKGKNLLVAVSARGWFHI.FDI.TPAK
	.	'	LDASGHHETLIGEEQRPVFKOHIPANTKVMLISDTDGDGCRFT.
	·	1.	VGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEGQVDSLS
	j		TLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS
			SGDPSCPRRGAAPDIWPYPQQECLHSPNWQHQT\SHGTESSGS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	1	•	Codon, /=possible nucleotide deletion,
	amino acid	sequence	Codon, /=possible nucleocide delecton,
	sequence		\=possible nucleotide insertion)
			GLFALCTLDGTLKLMEEMEEADKLLWSVQVDHQLFALEKLDVTG
	1		NGHEEVVACAWDGQTYIIDHNRTVVRFQVDENIRAFCAGLYACK
	1	i	EGRNSPCLVYVTFNQKIYVYWEVQLERMESTNLVKLLETKP\ST
		l .	TACCRSWAWILTTSL*LVPCFTKRSTIQTSHHSVLPQASRIPPS
	1	İ	WTCLIAGEGFF*TPTLPPKGVFGSHCAAAGSITKQ
5026	1122	224	HLPLGVPSKVAGAAAMEPQEERETQVAAWLKKIFGDHPI?QYEV
5876	1122	223	NPRTTEILHHLSERNRVRDRDVYLVIEDLKQKASEYESEAKYLQ
	1	1	DLLMESVNFSPANLSSTGSRYLNALVDSAVALETKDTSLASFIP
	Ì	1	DPTWE2ANE2AUP221G2K1 INVENTABLE MAINTENED CEDA
	1	1	AVNDLTSDLFRTKSKSEEIKIELEKLEKNLTATLVLEKCLQEDV
	1		KKAELHLSTER\AKVDNRRQNM\DFLKAKSEEFRFGIQAAGEQL
	j	1	SARGQ\DAFSVPIQSLVALIRENWPRLKQQTIPLK\KKLESYLD
			LMP\NPSHCSK*RIEEAK\RELA\SIEAELTRRVS\MMEL
5877	2030	1907	GTLGKMAASSSGEKEKERLGGGLGVAGGNSTRERLLSALEDLEV
30,,		1	LSRELIEMLAISRNQKLLQAGEENQVLELLIHRDGEFQELMKLA
	1	İ	LNQGKIHHEMQVLEKEVEKRDSDIQQLQKQLKEAEQILATAVYQ
			AKEKLKSIEKARKGAISSEEIIKYAHRISASNAVCAPLTWVPGD
]	1	ĺ	PRRPYPTDLEMRSGLLGQMNNPSTNGVNGHLPGDALA/RRKIAR
1	ì		
	!		CPCSTVS/NGSQMTCR*INIILILQKSVCEL
5878	950	2113	GLWKCMQLQGPHTHRVQP*PTPRQQGPQ\VPVAVIAGNRPNYLY
ì	1	1	RMLRSLLSAQGVSPQMITVFIDGYYEEPMDVVALFGLRGIQHTP
1	1]	ISIKNARVSQHYKASLTATFNLFPEAKFAVVLEEDLDIAVDFFS
ì	1	1	FLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLYRVETMPG
	1		LGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECII
1	1	Į.	PDVSRSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDSL
1	ŧ	1	KKEAYEVEVHRLLSEAEVLDHSKNPCEDSFLPDTEGHTYVAFIR
1	i		MEKDDDFTTWTQLAKCLHIWDLDVRGNHRGLWRLFRKKNHFLVV
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i			GVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT
5879	3	981	RLTEAAAAGSGSRAAGWAGSPPTLLPLSPTSPRCAATMASSDED
		1	GTNGGASEAGEDREAPGKRRRLGFLATAWLTFYDIAMTAGWLVL
ì		1	AIAMVRFYMEKGTHRGLYKSIQKTLKFFQTFALLEIVHCLIGIV
1		1	PTSVIVTGVQVSSRIFMVWLITHSIKPIQNEESVVLFLVAWTVT
	1		EITRYSFYTFSLLDHLPYFIKWARYNFFIILYPVGVAGELLTIY
İ	1	\	AALPHVKKTGMFSIRLPNKYNVSFDYYYFLLITMASYIPLFPQL
ì	Ì		YFHMLRQRRKVLHG\G*L*KRMIK*SLQTRCFFQNNQDYLSPSF
1	1	1	NNKNKQLCEISWIVWFLKI
	1138	1324	SLWCLVAGGLGLGPSSQNPLQRAGILARPREARGTFSALTACSA
5880	1120	1324	SVTSKGKSSSGMWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD
1		1	*KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARAASDVL
l	1	1	
1	1		CRSLANETHOLRRILTATAHMCQHLAKCLDERQHAQRNVGERSP
1		1	DQSEHTDGHTSVQSVIEKLQEENRLLKQKVTHVEDLNAKWQRYN
I	1	1	ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC
1	i		AEVKQELAASRTARDAALERVQMLEQQILAYKDDFMSERADRER
}	1		AQSRIQELEEKVASLLHQVSWRQDSREPDAGRIHAGSKTAKYLA
	j	1	ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH
1	1	1	CLOCFSDEQGEELLRHVAECCQ
L	 	 	GGIHPSPTEAPRAQHLTMDCTWRILFLVAAATGTHAQVQLLQSG
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Ì	1	ĺ	SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE+MGPFD
}	1	1	LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSSLRSEDTAV
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i	1	· I	RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR
1	1	Ì	HYSKQVELELQQIEQKSIRDYIQESENIASLHNQITACDAVLER
1	Į.	l	MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG
}	1		ELVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE
1	t	i	
ļ	1	}	ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ
1		1	IPQTALLKYRFFYQFLLGNERATAKEIRDEYVETLSKIYLSYYR
l	1		SYLGRLMKVQYEEVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF
Į.	İ	}	TLGTRGSVISPTELEAPILVPHTAQRGEQRYPFEALFRSQHYAL
1	İ		LDNSCREYLFICEFFVVSGPAAHDLFHAVMGRTLSMTLKHLDSY
1	1		LADCYDAIAVFLCIHIVLRFRNIAAKRDVPALDRYWEQVLALLW
ı	1	Ī	

SEQ	Predicted	Predicted end	1 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phonel-1
ı	location		
i	corresponding	corresponding	
	Corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	Paproline O classification Na Asparagine,
l	amino acid	residue of	
[residue of	amino acid	I=Inreonine V-V-1:
1	amino acid		I "-12 ypcopnan. V=Trroction v re-1
	sequence	sequence	
	sequence	_1_	\=possible nucleotide insertion)
			PPERITURNITY OF THE PROPERTY O
	ŀ	1	PRFELILEMNVQSVRSTDPQRLGGLDTRPHYITRRYAEFSSALV
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	{	1	PPFGGLVAFVKEAFALTERCONTENT DEPT DENARTQEFTEELLS
	1		PPFGGLVAFVKEAEALIBRGQAERLRGEEARVTQLIRGFGSSWK
		1	
5883	2	1374	I
		1 13/4	EFFGRRFRAVMEAGAGAGAGAGWCCDCDCDCDC
	ł	1	CERKKGORWGSLERRGMQAMEGEVLLPALYEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE
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Í			TNOFPSDAPLEEARQFAAQTVGNTYGNFSLATMFPRREFTKEDY
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ľ	l		
- 1			SSKSEKREPVRKRVLEKRGDDFKKEGKIYRLRTQDDGEDENNTW
5885			NGNSTQOM
2003	900	467	AAGGCPPCPI CPCHPMGPCHC
ł	i		AAGGGRRSRLSRSWPTGPSKSPSGVRCCG\RR\AWEDKDEFLDV
- 1	1		
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5886	86		
	**	1341	PFRGRALTLKKQPRPGVAPPSLGTCHKSDPGRPAAQSQPPSPGS GTFGLLSFPM/PTXTTTL KYGITCHKSDPGRPAAQSQPPSPGS
i			GTEGLI SEPREDENCE OF THE STREET CHKSDPGRPAAQSQPPSPGS
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- 1	i		DDDAGE EI VUPIRKVAAKRI, KECDTMMCOOTTE TO THE
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1	I	1	COLLEGE COVER CONTRACTOR CONT
1	ł	ł	KVVGAVGSDEKVAVLOKLOPDIA
1	i	1	KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLBETLKKASPDGY
			TOTAL STATE OF THE
1			FEBLULY OET RMEARIAVENOCONNOCONNOCON
			TRWQGDARQKALKDLLKWVT.RT.DVERT
		1	PPEIGIYQELRMEAFVYYRWQGDARQKALKDLLKWVLELPYFVI D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIOVKEYIIDON
887	1035		NMPAAFMGMLKGDNLGKTIVKA
887	1937		NMPAAFMGMLKGDNLGKTIVKA
887	1937	104	NMPAARMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSIGDEAADGDAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
887	1937	104	NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLLGLRE RPDRCHPGGDDRGPOLHRGSPG/SPGRI GDDRGP
887	1937	104	NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLLGLRE RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAOCHIMGGED
887	1937	104	NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLLGLRE RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAOCDLMCGCDD
887	1937	104	NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLLGLRE RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSOFCSOKAVIVSLWTANDDODDCSSVDFSVFS
887	1937	104	NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLIGLRE RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCIHITN*NLHYPLLIOKYL/NRNNEDTLMKKESPG
887	1937	104	NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLLGLRE RPDRCHPGGDDRGPQLHRGSPG/SPSBLSRRPGPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCIHITN*NLHYPLLIQKYL/NENNFDTIMKTSDGFTLNAESY VSFTTKLDIPTAAKYEYGVPLOTEDSPLPERGCUTSCS
887	1937	104	NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLIGLRE RPDRCHPGGDDRGPQLHRGSPG/SFSELSRRPGPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCIHITN*NLHYPLLIQKYL/NENNFDTIMKTSDGFTLNAESY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP AAFLVNQAVKCTRKINLEGCEFTBJLSMAEVG
887	1937	104	NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLIGLRE RPDRCHPGGDDRGPQLHRGSPG/SFSELSRRPGPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCIHITN*NLHYPLLIQKYL/NENNFDTIMKTSDGFTLNAESY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP AAFLVNQAVKCTRKINLEGCEFTBJLSMAEVG
887	1937	104	NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLIGLRE RPDRCHPGGDDRGPQLHRGSPG/SFSELSRRPGPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCHIIN*NLHYPLLIQKYL/NENNFDTIMKTSDGFTLNAGSY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK
887	1937	104	NMPAARMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLIGLRE RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCHIIN*NLHYPLLIQKYL/NENNFDTIMKTSDGFTLNAESY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK CVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV
887	1937	104	NMPAAMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLIGLRE RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPORVFELVDQINPSI FCHITN*NLHYPLLIQKYL/NENNFDTIMKTSDGPTLNAESY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK CVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ
887	1937	104	NMPAAMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLIGLRE RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLMFTANPPQRVFELVDQINPSI FCHITN*NLHYPLLIQKYL/NENNFDTI_MKTSDGFTLNAESY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK CVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ LMTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLTI LHSTTEQDCLALEGVRTPVLFGYTMOSGCKLITT
887	1937	104	NMPAAMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLIGLRE RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLMFTANPPQRVFELVDQINPSI FCHITN*NLHYPLLIQKYL/NENNFDTIMKTSDGFTLNAESY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDMNP AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK CVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ LNTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLTI LHSTTEQDCLALEGVRTPVLFGYTMOSGCKIIR TEXT
887	1937	104	NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLIGLRE RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSGFCSQKAVIYSLMFTANPPQRVFELVDQINPSI PCHITN*NLHYPLLIQKYL/NENNFDTIMKTSDGPTLNAESY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTTSLCTDNNP AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK CVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ
887	1937	104	NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLLGLRE RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCHITIN'*NLHYPLLIQKYL/NENNFDTIMKTSDGFTLNAESY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK CVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLTI HSTTEQDCLALEGVTPVLFGYTMQSGCKLRLTGALPCQLVAQ CVSLLWGQGFPDYVAPFGNSQGP/ADMLDWVPIHFITQSFNRK SCQLPGALVIEVKNTKYGSILNPOAKYLDNUTANY
887	1937	104	NMPAAMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLIGLRE RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLPGLQGPP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLMFTANPPQRVFELVDQINPSI FCHITN*NLHYPLLIQKYL/NENNFDTIMKTSDGFTLNAESY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK CVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ LMTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGOLTI LHSTTEQDCLALEGVRTPVLFGYTMOSGCKIIRT TON

			Y
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	1	sequence	\=possible nucleotide insertion)
	sequence		LLCRTPGVAMQRADSEQPSKRPRCDDSPRTPSNTPSAEADWSPG
5888	375	2302	
İ	1		LELHPDYKTWGPEQVCSFLRRGGFEEPVLLKNIRENEITGALLP
Ì		ł	CLDESRFENLGVSSLGERKKLLSYIQRLVQIHVDTMKVINDPIH
1	1	l .	GHIELHPLLVRIIDTPQFQRLRYIKQLGGGYYVFPGASHNRFEH
!	1	1	SLGVGYLAGCLVHALGEKQPELQISERDVLCVQIAGLCHDLGHG
1	ì	ſ	PFSHMFDGRFIPLARPEVKWTHEQGSVMMFEHLINSNGIKPVME
1	ì	ļ	QYGLIPEEDICFIKEQIVGPLESPVEDSLWPYKGRPENKSFLYE
1	i	ļ	IVSNKRNGIDVDKWDYFARDCHHLGIQNNFDYKRFIKFARVCEV
l	f	i	DNELRICARDKEVGNLYDMFHTRNSLHRRAYQHKVGNIIDTMIT
ļ	1		DNELKICARDKEVGREIDMFHIRMSHIRMSTYMVICTORIES
	1	ì	DAFLKADDYIEITGAGGKKYRISTAIDDMEAYTKLTDNIFLEIL
[Į.	YSTDPKLKDAREILKQIEYRNLFKYVGETQPTGQIKIKREDYES
1	1	1	LPKEVASAKPKVLLDVKLKAEDFIVDVINMDYGMQEKNPIDHVS
Į.	1	ì	FYCKTAPNRAIRITKNQVSQLLP\EKFAEQ\LIRVYCKKVDRKS
1	•	1	LYA\ARQYFVQW\CADR\NFT\KPQDGRCY*PPTP*HPQKKGW\
ļ			NDSTFSPKIPTRLPRRLPKSRV\QLFKDDPM
	1831	731	LPAACGRPVTARPRQAPEGRSGRPRDLDPYPPQVFPPRPDRVAI
5889	1921	1 '31	VTGGTDGIGYSTAKHLARLGMHVIIAGNNDSKAKQVVSKIKEET
1		1	LNDKET*VLLCCPGWLCLWNSSDPPTSASRGAGTTGVHHHFLLK
İ	ļ	•	LNDKET VILCCPGWICLWASSDEF SASKOAST TOWNKI DEK
ì		1	FGIFIL\DLASMTSIRQFVQKFKMKKIPLHVLINNAGVMMVPQR
1	l .	•	KTRDGFEEHFGLNYLGHFLLTNLLLDTLKESGSPGHSARVVTVS
i	i	1	SATHYVAELNMDDLQSSACYSPHAAYAQSKLALVLFTYHLQRLL
	i		AAEGSHVTANVVDPGVVNTDLYKHVFWATRLAKKLLGWLLFKTP
1		ł	DEGAWTSIYAAVTPELEGVGGRYLYNKKETKSLHVTYNQKLQQQ
	Ī		LWSKSCEMTGVLDVTL
5890	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
5830	1322	200	GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
{	l .		LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
1	1	1	ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
1		ł	TLEREGPREE REGISTRIVOVAPERATITATION CARREST I
l	1	į.	PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
1	1	i ·	RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
ì		1	KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
 		1	AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH
ļ	i	1	LVRQIP\NTAIMMATYELVVYLLNG
5891	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
			GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
į	i		LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
1		1	ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
1		[PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
l		1	RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
1			KWEARROAKAIOIDADAGIRES COMMISSIONIS SAMON, I ISAMOI
1	1	1	KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
I			AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH
1		1	LVRQIP\NTAIMMATYELVVYLLNG
5892	1764	379	VVLRVCGRLSVNSAVSSRTGGWSAGLTCAMQRLQVVLGHLRGPA
1	1	,	DSGWMPOAAPCLSGAPHASAADVVVVHGRRTAICRAGRGGFKDT
1		1	TPDELLSAVMTAVLKDVNLRPEQLGDICVGNVLQPGAGAIMARI
1	[J	AQFLSDIPETVPLSTVNRQCSSGLQAVASIAGGIRNGSYDIGMA
1		1	CGVESMSLADRGNPGNITSRLMEKEKARDCLIPMGITSENVAER
1]	1	FGISREKQDTFALASQQKAARAQSKGCFQAEIVPVTTTVHDDKG
1	1	1	LOTOKEVÖNTAMPÖÖVANAVÖOVOCLÄVETALATTAMPING
1	1	1	TKRSITVTQDEGIRPSTTMEGLAKLKPAFKKDGSTTAGNSSQVS
1			DGAAAILLARRSKAEELGLPILGVLRSYAVVGVPPDIMGIGPAY
1	1	1	AIPVALQKAGLTVSDVDIFEINE\AFASQAAYCVEKLRLPP*EG
1			*TPLGGASGP*GHPLGLHWGHVQVITLAQ*S*SARGKRAYRSGC
1	1	Į.	PCAIGSWNGSPLPVFEYPWGT
5893	3	1653	ILSKRRCQKAKTKELMAKKVAVIGAGVSGLISLKCCVDEGLEPT
3033	,	1033	CFERTEDIGGVWRFKENVEDGRASIYQSVVTNTSKEMSCFSDFP
1	1	•	MPEDFPNFLHNSKLLEYFRIFAKKFDLLKYIQFQTTVLSVRKCP
1	İ		DFSSSGQWKVVTQSNGKEQSAVFDAVMVCSGHHILPHIPLKSFP
[1	1	DFSSSGQWKVVTQSNGKEQSAVFDAVMVCSGRITDERTEDASFP
1	1	1	GMERFKGQYFHSRQYKHPDGFEGKRILVIGMGNLGSDIAVELSK
1	1	F	NAAQVFISTRHGTWVMSRISEDGYPWDSVFHTRFRSMLRNVLPR
1	1		TAVKWMIEQQMNRWFNHENYGLEPQNKYIMKEPVLNDDVPSRLL
i			CGAIKVKSTVKELTETSAIFEDGTVEENIDVIIFATGYSFSFPF
	_ t		

Desiming nucleotide location corresponding to first amino acid amino acid amino acid amino acid amino acid sequence Secure	SEQ	Predicted	Predicted end	
No: nucleotide location corresponding to first amino acid traids and acid residue of amino acid residue of amino acid sequence se	ID			
Cocration corresponding to first mains acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid acid acid acid acid acid acid acid	NO:	nucleotide		M=Aranine, C=Cvsteine D=Aconseid Acid =
corresponding to first amino acid amino acid sequence service of amino acid sequence	ł	location	ľ	Graduate Acid, F=Phenylalanine C-Cluster
to first amino acid residue of securing the confidence of confidence of confid	1		to first	haristidine, I=Isoleucine, K=Lysine,
amino acid sequence GUENCE, SEGUENC				P-Proline O Glaranine, N=Asparagine,
maino acid and acid aequence Perprepalan. Y-Tyrcohan. X-Dixnown, *=stop codon, /=possible nucleotide solded diction /=possible nucleotide solded diction /=possible nucleotide solded diction /=possible nucleotide solded diction /=possible nucleotide solded dic	l	amino acid		S-Serine, Wellutamine, R-Arginine,
amino acid sequence Codom. /=possible nucleotide nucleotion /=possible nucleotide nucleotide -possible nucleotide nucle	1	residue of		W-Trantonham v. G.
Sequence	İ	amino acid	1	Codon (X=Tyrosine, X=Unknown, *=Stop
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DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLKRGFVI.QD TVEQLRCEHCARF\LADRFVEGVCPFCGYEBARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAOLOLPPPACSILLTNFI-CTLPAGHOCTOWED	1	ı	ł	RIPOWNTI VI COMPEYORA MERICA TO A STATE OF THE STATE OF T
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NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL PGSDWTPNAGFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVMEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAOLOLPPPACSILLTNELGTLPAGHOTGTWED	ì	ŧ		TVEOLECEHCAPE/ LADDENEGUCDEGUCDEGUCDEGUCDEGUCDEGUCDEGUCDEGUCD
FGSDWTPNAOFTTPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVMEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAOLOLPPPACSILLITELGTLPAGHOTGTWER	1	ļ	<u>}</u>	NAVELKKPOCKYCPSCPMOSSON FIRE DE PER PRODUCTION DE LA COMPANION
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FSWTDLLLKNNS\ELLANLGNFINRA\GMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAOLOLPPPACSILLTNFI-CTLPACHOLTUSER	1		1	K\FSKSRGVGVFRDM\AHDTGTDDDTGDEVT\TVTDTG
GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAOLOLPPPACSILLTNELCTLPAGHOTCTUSER	1		ĺ	FSWTDLLLKNNS\ELLNNIGNETNER\CMETATER\DSA
GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAOLOLPPPACSILLTNELCTLPAGHOTCTUSER	.]		1	LTPDDORLLA\HVTLEIOHYHO\ LT ENDERDY DOST
UPIMPTVSATIQAOLOLPPPACSILITNELCTLPACUOTCTUSE	1	ŀ	1.	GNOYI OVNEPW KRIKGSEADBODAGTTON
	- 1	İ	17	OPYMPTVSATIOAOLOLPPDACSTI TOUR COMPANIALLSVML
LFOKLENDOTEST.POPECCOARTEDVALUE				LFOKLENDOIESLRORFGGGQAKTSPKPAVVETVTTAKPQQIQA
AOI OO OO WALL SEAFAVA TA				AOLOGORALISEAPAVOLIVITARPOOLOA

	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ	1 .		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Asparcic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	N=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of		Codon, /=possible nucleotide deletion,
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	<u></u>	\=possible nucleotide insertion)
			LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
ļ		Ī	KPPEAPKGKKKK
	2067	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
5897	2967	, 65	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
]	ļ	1	
Ì	İ		RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
1	1	1	EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
!	Į		RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
		1	FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
i	i		EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ
}			NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
I	I	1	MAADEAWGEKMADI I DADEL AMMA EUROMI I GOADOWA LAKID
Į.		1	RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
1			DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
i	Į.		TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI
Į.			NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
1		1	PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
1			GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
1			DE DAY A LA MEDALIGITATION DAY AND
[FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
1	1	ł	K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
Į.	l		FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
i		1	LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
1			GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
ł	i .	Į.	QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP
Į.	1	Ì	LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
1	j	1	
ł	i .) ·	LMDEVTKQGNIVRELKAQKADKNEVAAEVAKI.LDLKKQLAVAEG
1	Į.		KPPEAPKGKKKK
5898	2967	86	HPSTLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
		į	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
	1	1	RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
}	į.		EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
[i	RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
	1	1	FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
1	1	1	
i	1	1	EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPQQ
1		1	NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
i .		1	RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
İ	1	1 .	DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
l	1		TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI
1	[1	NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL
1	I		PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
1	İ		FOODWIENWOLD MICHIGAN COMPANY AND COMPANY
1	I	}	GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
ı			FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
1	1	1	K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
1	l .		FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
I	1	1	LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
i	1		GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
į.	1		QPYMPTVSATIQAQLQLPPPACSILLINFLCTLPAGEQIGTVSP
i		1	
I	I		LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
I	1	1	LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
1	1	1	KPPEAPKGKKKK
5899	326	1078	NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ
1	1	1	EANEKAEBIDAKAEBEFNIEKGRLVQTQRLKIMEYYEKKEKQIE
1	f .	1	QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP
1	1		EVYQGLLDKLVLQGLLRLLEPVMIVRCRP\QDLLLVEAAVQKAI
Ī	1	1	EAT GOTTO TO A TO CONTRACT AND THE SALL AND
1	ı		PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN
1	i		TLESRLDLSAKQKMPEIRMALFGANTNRKFFI
5900	64	1409	KAASRDSPCLEFCPLCGVSSHDLQHRMWYHRLSHLHSRLQDLLK
1	1		GGVIYPALPQPNFKSLLPLAVHWHHTASKSLTCAWQQHEDHFEL
1		1	KYANTYMRFDYVWLRDHCRSASCYNSKTHQRSLDTASVDLCIKP
ł	1		NIAN I VEKTUI VMUKUNCKSASCINSKINGKSUSCOVOSITORT
1	İ	1	KTIRLDETTLFFTWPDGHVTKYDLNWLVKNSYEGQKQKVIQPRI
i		1	LWNAEIYQQAQVPSVDCQSFLETNEGLKKFLQNFLLYGIAFVEN
Į	1		VPPTQEHTEKLAERISLIRETIYGRMWYFTSDFSRGDTAYTKLA
1	1	i .	LDRHTDTTYFQEPCGIQVFHCLKHEGTGGRTLLVDGFYAAEQVL
	4		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ΙĎ	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
-	amino acid	residue of	S=Serine, T=Threonine, V=Valine
	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion
	Sequence		\=possible nucleotide insertion)
1			QKAPEEFELLSKSAI\KHEYIEDVGECHQPHDWDWAQS*ISTHG
l			/YKELYLIRYNNYDRAVINTVPYDVVHRWYTAHRTLTIELRRPE
1	1		NEFWYKLKPGRYLFIDNWRYLHGRECFTGYRQLCGCYLTRDDVL NTARLLGLOA
5901	1	2121	VAIEQTSLKMMQAVGGAPARPTGEYICNQCGAKYTSLDSFQTHL
[KTHLDTVLPKLTCPQCNKEFPNQESLLKHVTIHFMITSTYYICE
	(SCDKQFTSVDDLQKHLLDMHTFVFFRCTLCQEVFDSKVSIQLHL
	1		\AVKHSNEKKYYRCTSCNWDFRNETDLQLHVKHNHLENQGKVHK
	1		CIPCGESFGTEVELQCHITTHSKKYNCKFCSKAFHAIILLEKHL
			REKHCVFETKTPNCGTNGASEQVQKEEVELQTLLTNSQESHNSH
1			DGSEEDVDTSEPMYGCDICGAAYTMETLLQNHQLRDHNIRPGES
į.			AIVKKKAELIKGNYKCNVCSRTFFSENGLREHMOTHLGPVKFYM
			CPICGERFPSLLTLTEHKVTHSKSLDTGNCRICKMPLOSEEEFI.
İ			EHCQMEPDLRNSLTGFRCVVCMQTVTSTLELKIHGTFHMOKTGN
			GSAVQTTGRGQHVQKLYKCASCLKEFRSKQDLVKLDINGLPYGL
l i			CAGCVNLSKSASPGINVPPGTNRPGLGQNENLSAIEGKGKVGGL
			KTRCS*LATFKF*VLKVELPEPHPKPFHRGVSRPDSNSTQLKTP
1			QVSPMPRISPSQSDEKKTYQCIKCQMVFYNEWDIQVHVANHMID
			EGLNHECKLCSQTFDSPAKLQCHLIEHSFEGMGGTFKCPVCFTV
			FVQANKLQQHIFSAHGQEDKIYDCTQCPQKFFFQTELQNHTMTQ HSS
5902	712	209	LKNRRRSRPSIRQSIGSTSVSRWLTSLFTYLDHTADVQ*V*REF
1 1			IPLKPRQ*ED*MFQSWLHAWGDTLEEAFEQCAMAMFGYMTDTGT
			VEPLQTVEVETQGDDLQSLLFHFLDEWLYKFSADEFFIP WGE
			EFSLSKHPQGTEVKAITYSAMQVYNEENPEVFVIIDI
5903	2106	735	DTPGPSLPSTTAPFSLRSLSFPSRPSYLLPGDPOPLOGRGLPTT
			PALFALSAVPGGAASPMPPSGLRLLPLLLPLLWLLVLTPGRPAA
			GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSOGEVPPGP
1. 1			LPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVET
1 1			HNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL
1 1			KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV
1 1	j		RQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGR\RGDL ATIHGMNRPFLLLMATPLERAQHLQS\SRHRQAL\DTNY\CFSF
1]		HGGRNCLRC/VHC+HLIFRKDL\GW\KWI\HE\PKGYHANFC\L
1	İ		GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\
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5904	3	1126	MMEEIENAINTFKEEQRLIYEELIKEEKTTNNELSAISRKIDTW
	ļ	1	ALGNSETEKAFRAISSKVPVDKVTPSTLPEEVLDFEKFLQQTGG
			RQGAWDDYDHQNFVKVRNKHKGKPTFMEEVLEHLPGKTODEVOO
1			HEKWYQKFLALEERKKESIQIWKTKKOOKREEIFKLKEKADNTP
			VLFHNKQEDNQKQKEBQRKKOKLAVEAWKKOKSIEMSMKCASOT.
1 }	j		KEEEEKEKKHQKERQRQFKLKLLLESYTQQKKEQEEFLRLEKEI
1 1			REKAEKAEKRKNAADEISRFQERDLHKLELKILDRQAKEDEKSQ
1			KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW
5905	287	2912	ATSTYPT*GYSNLETRNTEKSMR
1		2722	MAS FPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR
1	1		QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPBKQSRCVNIEWH
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i i	i	i	SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS
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1 1		1	WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVOK
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1]	LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKMVKF*FIEM
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j f			QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK
1			REGGL*YLTLF1SVYFS*LVFG1NGFQYSFVVKLHCLYFMFRL1
			FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIIYNA*
			YNLN*I*QF*YKMCHFVLCMSE*SYNICLFIAGF\LWNMDKYTM

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amino acid sequence should residue of amino acid sequence wheregrophan, Y-Tyrosine, X-Muknown, **stop Codon, /-possible nuclectide deletion, choses sequence residue of the property of the control of th		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
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HEILLTRALPPI/VSSPIYDNRAPHTAELRYCRVINKOSSWGG DEIFLLCDRWQDDIERRYFUNDERAGIFSQADVHEQVALUPK TEPLCLCRWQDDIERRYFUNDERAGIFSQADVHEQVALUPK TEPLCCRWGDIERRYGLOPHERRYFUNDERAGIFSGADVHEQVALUPK KARKKETLIFORLCOHWEITEFBRUDGGLELLTSCOPPTLAS QSAGITVNFPERRREGLIGSIGERYFKEPBLESHEDAYVEBMP TOVSQADAS TYPSEPEPT SSCILLERSAND.PESSWSAVHPTPE SONTBILGSFTERTLPERSGOIPPTLAS GNAFTULGSFTERTLPERSGOIPPTLAS ADDIVOMASSMERBALDYCLIPDRWLSINGSWAVHPTTSSDSMEST DWFRILGHRILENPSCHSVLDFRULEGILGHOMSSSSMAGANSHT VEYGGDAFFGGDFSCADMSHINESGPSNSTMPSHVYOUGGY SGIGSMARREGLDSFFTEFFOV 1873 TILLSSWSF*REDJSFTERSOWYRKKISWFYPQFAKOMA KATSKVPSAHPVHENDHAMREGAELKKKUWERMERKQAARSOE ROKRETIESVCODVLRRGEFFHKEEVLOELHMFFOLDBARK KATSKVPSAHPVHENDHAMREGAELKKKUWERMERKQAARSOE ROKRETIESVCODVLRRGEFFHKEEVLOELHMFFOLDBARK KULVLANKILLYPREVVERWILDYLANSLEPTVAFKASTOKYONAL NECSYPVOQASSELLKSKACFGARBHARVLGHCEWETHIR VGYVGLPRVGKSSLINSLKRSGRCSVGAVFGITKFMOEVYLDKF RILDAFGIVFORNSEVSTLIKTCHVOKALDAYOCKLOEWETHIR VGYVGLPRVGKSSLINSLKRSGRCSVGAVFGITKFMOEVYLDKF RILDAFGIVFORNSEVSTLIKTCHVOKALDAYOCKLOEWETHIR VGYVGLPRVGKSSLINSLKRSGRCSVGAVFGITKFMOEVYLDKF RILDAFGIVFORNSEVSTLIKTCHVOKALDAYOCKLOEWETHIR VGYVGLDRVGKSGLINSTYLDPATHLAFHLSAEILKKROGLVSGOAK AVLADAVUSGKISTYIP PATHLYFHLSAEILKKRAGLVSGOAK AVLADAVUSGKISTYIP PATHLYFHLSAEILKKRAGLVSGOAK AVLADAVUSGKISTYIP PATHLYFHLSAEILKKRAGLVSGOAK AVLADAVUSGKISTYIP PATHLYFHLSAEILKKRAGLVSGOAK AVLADAVUSGKISTYIP PATHLYFHLSAEILKKRAGLVSGOAK AVLADAVUSGKISTYIP PATHLYFHLSAEILKKRAGLVSGOAK AVLADAVUSGKISTYIP PATHLYFHLSAEILKKRAGLVSGOAK AVLADAVUSGKISTYIP PATHLYFHLSAEILKKRAGLVSGOAK AVLADAVUSGKISTYIP PATHLYFHLSAEILKKRAGLVSGOAK AVLADAVUSGKISTYIP PATHLYFHLSAEILKKRAGLVSGOAK AVLADAVUSGKISTYIP PATHLYFHLSAEILKKRAGLVSGOAK AVLADAVUSGKISTYIP PATHLYFHLSAEILKKRAGLVSGOAK AVLADAVUSGKISTYIP PATHLYFHLSAEILKRAGLVSGOAK AVLADAVUSGKISTYIP PATHLYFHLSAEILKKRAGLVSGOAK SSENSHABLLGRAGAAAAAACKAGCRMSKYLQKAKKMOKAAAAA AVLADAVUSGKISTYIP PATHLYFHLSAEILKEA SSENSHABLLGRAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		l .	1	A\IITR\IKAGINPFDVP*KOLNDIEDCDLDVVRLWFRVFLPDG
DEIFLICDKYQKDDLEVRFVLNDMEAKGIFSQADVERGY TPPYCKATTEPVTVKNOKURRSSOLGWESSMOFRYLDDECDTYGN KAKKKRTILIFORLCODHVETGRPHUDGDGLELTSGPPTLAS QSAGITVMFDESPROPIGISGGENFYKEDPLESHDAVVREMP TOVSQADSYYPEDGDISGGENFYKEDPLESHDAVVREMP TOVSQADSYYPEDGDISGGENFYKEDPLESHDAVVREMP TOVSQADSTYYPEDGDISGGENFYKEDPLESHDAVVREMP TOVSQADSTYYPEDGDISGGENFYKEDPLESHDAVVREMP TOVSQADSTYYPEDGDISGGENFYKEDWINDANASNACIYNN ADDIVGMEASSMPEADLYGIDPPMLSNCSVMMMTTSDSMEET DMPRILEMNILEMNSCHSDIPPLRQLHQMSSSSMSAGANSNTT VEVSQSDAFSSTSTCADNSNINESGORSTNIPNSHVFYQDSQY SGIGSMQNEQLSDSFYKEPGV 1873 1873 1873 1873 1873 1874 1871LLSSMSS*** NILDFIKIKSQVKYFKGHKKISMPYPQFAKQNGK KATSKVPSAPHFYHNDDHANERAELKKKWEEMBEKQAARSQUE RQKRETIESVCQOVLRRQBEFEHKEEVLQELMMFPQLDDEATRK AYYKEFRKVUEYSDVILEVLDARDPJGCRCCQMEEBAURAQONK KLULVINKILDVPKEVVEKMUDVLREUELGUNFPQLOBEATRK AYYKEFRKVUEYSDVILEVLDARDPJGCRCCQMEEBAURAQONK KLULVINKILDVPKEVVEKMUDVLREUELGUNFPQLOBEATRK AYYKEFRKVUEYSDVILEVLDARDPJGCRCCQMEEBAURAQONK KLULVINKILDVPKEVVEKMUDVLREUELGUNFPQLOBEATRK AYYKEFRKVUEYSDVILEVLDARDPJGCRCCQMEEBAURAQONK KLULVINKILDVPKEVVEKMUDVLREUELGUNFPQLOBEATRK AYYKEFRKVUEYSDVILEVLDARDPJGCRCCQMEEBAURAQONK KLULVINKILDVPKEVVEKMUDVLREUELGUNFTAMSTCHQVKINL NRCSVFUQAGSESLINSKACFGARNILMRVICHYCCTGVATHA NRCSVFUQAGSESLINSKACFGARNILMRVICHYCCTGVATHAT VERGVSSSINKAKATRSRACSGAAPGTGTKFMQEVYLDKY INKEINTYYKIGDLTGYCTTPNNHQMGMAKNINUHERFKRSNSWIVVC SVDRRSVLORIMSTDDLQGQALASALKKKKMQKRADKIASKL SDEMMSALDLSGNADDGVGD 2477 975 HCCIKKRGEGSGFSPSPSGGFOLGCI) PSHSLPSEETHHTTA HTTILATILTRIPHSHSTRILRFPHPLDGDGGLASWK/PMRER* GWRPAKAAGASLGVAATGKRGCMSKRILLISPPHKKADAL HTTILLSHMPSSTRILRFPHPLDGDGGLASWK/PMRER* GWRPAKAAGASLGVAATGKRGCMSKRILLISPPHKKADAL VKCSCFPGQVAGTTRABPSCVDASIVEQGCARACLCGARAPP VKCSCFPGQVAGTTRABPSCVDASIVEQGCARACLCGARACLCARAPP VKCSCFPGQVAGTTRABPSCVDASIVEQGCARACLCGARACLCARAPP VKCSCFPGQVAGTTRABPSCVDASIVERGCKRNKIEBERGC VKCSCFPGQVAGTTRABPSCVDASIVERGCKRNKIEBERGC SSILRADSSANHKAAHVKTGTEVVALARCCKNKIEBERGC GRIQUITHDLTHINDKEGUNGGSPBLISFSLS SSILRADKRFRICHGARGSTAVTHRUTGLAAAACGCARACLCARACL GRIGUITHDUNGACFSFFYTYSGODO SSILRADKSPAUCHURTGTAVATGRACHERGERGKSK ILMTUNDI		1	}	
TPPYCKAITEPUTVKNOLRRPSDQEVSESMOFFYLPDEEDTYGN KAKKKTLIFOKLCOMPVETGRHUNDGELLTSGOPPTLAS QSAGITVAFPERPRPGLIGSIGEERYFKKEPNLFSIDAVREMP TOVSQARSTYPEPOPISIGESIGEERYFKKEPNLFSIDAVREMP TOVSQARSTYPEPOPISIGESIGHERAMADLESSWSSVAHPTPR SGNTMPLSSTSTETLDSNGQIIPPIRTIVONDLARACIYNN ADDIVGHEASSMERADLYGISDPNULSNCSVMMMTTSSDSMGET DMPRILSHRILENESCNSVILDPRIDARQLIGMSSSSMSAGANSNTT VFVSQBOAFESSDFSCANNSHINESGPSNTNYRSHIVFYQDSQY SGIGSMQNEQLSDSFYPEFTQV TVLLSSWSS**INLDTKIKSQVKVYRKGHKKISWFYFQPAKQNGK KANSKVPSAHPFYHNDNIAMREALLKKKVWSENREKQQAAREQE RQKRETISSYQDVLARGESFEHKERVLQELMMPFQDLADEATRK AYNEFRKVVSTSDHUNDLARPLIGGCRQMEEAVLRAQGNK KLVLVIANKIDLVPKEVVEKWLDVLARRELETVAFKASTQHOVANL NRCSVPVDQASESLLKSKACGRANLMRVCRGLGEVATHIR VGVVGLPWVGKSSLINSLKRSRACSVGAVPGITFMGVVLDKF IRLIDAPGIVGPSMSEVGITLENCVYVQLADPTPVETILOR NLEISNYYGVSGGOTTERFILTAVARRLIKKKKGLVSQDQAK AVIADWVSGKISFYIPP PATHILPHILSSKYKGGLVSGDQAK AVIADWVSGKISFYIPP PATHILPHILSSKYKSMSMVDVC SVDRRSVLGRIMSTDFLQGQALASALKNKKMGKRADKIASKL SDSMSADLDSGNADDGVGD SVDRRSVLGRIMSTDFLQGQALASALKNKKMGKRADKIASKL SDSMSADLDSGNADDGVGD TOTTURKKVVSSANHIKKHHVKNOTCEVVALHRCCKNKNIEGRSGY VKCSCPEQCVGGTTRARBSCVDASIVVGARTKGCHLISTIFIT VTIMGKVVSSANHIKKHHVKNOTCEVVALHRCCKNKNIEGRSGV VKCSCPEQCVGGTTRARBSCVDASIVVGARTKGCCHLISTLITIFI VTIMGKVVSSANHIKKHHVKNOTCEVVALHRCCKNKNIEGRSGV VLEDRKGSUSGONSKVKTTRVTH SSILRADRSHICAQRARAGKLIYHRPLGILANAAPPSENSGSLRR CKSPITYSYNEDOFNMDLRGGFBOVTITRRSTSDTDLVTSDR STIMGRSSYNSINGRSGGSTFSTSDTDLVTSDLS RTIMGTSSYNSINGRSGGSPSTSSTSDTDLVTSDL SSILRADRSHICAQRARAKNIYHRPLGILANAAPPSENSGSLRR CKSPITYSYNEDOFNMDLRGGFBOVTTLGRLFFFVHGOGRRSK IGNTVNT HUNDACFSFSTVLTDLLETVENDERGORRSK IGNTVNT HUNDACFSFSTVLTDLETVENDERGORRSK IGNTVNT HUNDACFSFSTVLTDLETVENDERGORRSK IGNTVNT HUNDACFSFSTVLTDLAGGGRBSKEGGEGGUSTLEGG GKLGMASVKRKRR CGLAGRESUKEGGEGGFGSTSTSTST SSSKWPRQLLEGRSVDPRORGSTLSFFLEDDLITHAGDGGFRIST IGNTVNT HUNDACFSFSTVLTDLETVENDSKENDGLGFRFFILT TSSHHDDEETSISTSTPEGAGOTOSSPMINESGSGPRSEAPE SSSKWPRQLEGRSVDPRORGSTLSFFLEDDLITHAGGGGRGSK IGNTVNT HUNDACFSFSTVTSNGOD GEGENALFERSTVOSNGOS ELLSFRAEGAULIEGERGKVTSCOD GEGENALFSSPROGGHARGECHARGSCSPCTSSSCYSTSCYS SCYSASCYSDSCYN		1	(
KAKKQKTTLLFQRLCQDHVETGFRHVDQDGLELLTSGPPTLAS QSAGITVNPLSGISGEGRYFKENFSIDAVVRAM TOYSQAESYYPSDGD I SEGLISHHASMAPLESISAWSVAHPTFR SQRTHPLLSSTSTETLT_BANGQI PPFERIP UVONDLINASNACIVNN ADDIVGMEASSMESADLYGISDPMM_SNCSVMMTTSDSMGET DNPPLLSHNLENSCNSVLDPDRLDQLIGHGSSSMSAGANSHT VPVQQDDAFSGSDFSCADNSNINSSGPSNSTNPNSHVFVQDSQY SGIGSMQNEQLSDSFPYEFFQV TYLLSSWSS**RLDTKIRSQVKV/FKGHKKISWYPQPAKQMSK KATSKUPSAPHFVHENDHAMREAELLKKKWISEMPEKQAARCQE RQKRETIESVCQOVLRRQSBEFEKKEKVLQELMMFPQLDDEATRK AYYKEFRKVVEYSDVILLEVLDARDPLGCRCCYMEESAKURQANK KLVLVINNLDVPKEVVEKMUDVLRREUPTVAFKASTORQVRNL NRGSVPVQASSELLLKSKACFGARMLMRVLGNYCRLGEVETHIR VGVVGLPNVGKSSLINSLKRSRACSGAMPGTIKFMQEVYLDK IRLDAPGIVVGNDSEVGTILRNCVHYQKLADPVTUDETILCRC NLESISNYYGVGGFOTTERFLTTAVARELGKKKKGGLYSQGOAA AVLADWSGKISFYIDPPATHTLPTHLSAEIVKEMTEVPILDT EQANBOTMECLATGESDELLGDTDPLEMERIKKKKGGLYSQGOAA AVLADWSGKISFYIDPPATHTLPTHLSAEIVKEMTEVPILDT EQANBOTMECLATGESDELLGDTDPLEMERIKKKKGGLYSQGOAA AVLADWSGKISFYIDPPATHTLPTHLSAEIVKEMTEVPILDT EQANBOTMECLATGESDELLGDTDPLEMERIKKKKGGLYSQGOAA AVLADWSGKISFYIDPPATHTLATHLLKHSPMTKIADAI ENNTTYVKIGDLTGVCTHPNHHQMGMAKNNUHBPYKBASHVDVC SURRSVLQR HEMTDELQGGALASALKNKKMQKRADKIASKL SDSMSSALDLSGNSADDGVGD FOR IKKERGSGSSPSPASGFOLLGCQI PEPSIPSEEETTIPHTRA HTRILATITREPPSHSTRIRFPRPLDCCGCLASWK/PMRR* GWRFRAKAGAGSI/GVAATGKRCGNSKRYLQACATGKILLI IIFI VTILKGIKVUSSANIHKAHHVKTGTCEVVALHRCCNKNKI EERSQT VKCSCFPGQVAGTTRABPSCVDASI VEQXWMCHQPCLEGEBECK VKCSCFPGQVAGTTRABPSCVDASI VEQXWMCHQPCLEGEBECK CKEPIRYSYNDOCPHMDLRGGEBEGVTTPRSTSDTDLVTSDSR STILMGRSSYTSYIGHSGDLVIHDLKEUDOGGSRALISFSLS DPQAMCLKGMFRNDDVYLKIS IQDGKHSI FPALPHGGRRISK IGNTYNDT PUQAROFSFEVLPPULEIEVKDKFAKSRPI IKKPI GKLSMPVQRLLERHAI GDRVVSYTIGRILPTOHVSGGSRFLISFSLS DPQAMCLKGMFRNDDVYLKIS IQDGKHSI FPALPHGGGRRISK IGNTYNDT PUQAROFSFEVLPPULEIEVKDKFAKSRPI IKKPI GKLSMPVQRLLERHAI GDRVVSYTIGRILPTOHVSGGSPRABE SSENKKPQLGPGSVPDPRONGS IELSPABERALLLE DGSAPASTKEBEPLISEBATTYRSGQOSARLISFSLS DPQAMCLKGMFROSCOSARLITSFSLUD SSENKERDQLGESSPYGNGGRRISTFSLANGAQDLGDT HFSTSEEDSSPRGGGBBESTJSTSTPGSGGSFTSCYSSCYSTSCYS SCYSSCYNGNRFRASKTPSSUDSAKIESFTVFSGOD BEGENSAFFSVPOSMOS PELDPE		Į.	1	DETAPPEDKAČKODIEAKLAPNOMENKOTŁOĆNOMENKO
QSAGITVNFPERREPGLIGSIGERYFKKEPNLFSHDAVVREMP TOVSQAGAS YPPSPEGI IS GEGLSHHASMAP SSSWSSVANHPTER SONTMPLSSTSTETLDSNSQGI PPFARI PVONDIANACITYNN ADDIVOMRASMPSADLVGISDPMLSSICSVANMITTSSDSMGET DNPFLLSHNLENPSCNSVLDPRDLRQLHQMSSSSMSAGANSNTT VFVSQSDAFESGDFSCADNSMINESGFSNSTNPNSHVFVQDSQY SGIGSMQMEQLSDS PYEFFQV TVLSSWSS ** NLDTKIKSQVV/REGHKKISWPYPQDAKQMSK KATSKVPSAPHFVHNDHANNEAELKKKWVEEMBEKQQAAREQE RQKRETIESVCQDVLRRQEBFEHKERVLQELMMPPQDAKARQCE RQKRETIESVCQDVLRRQEBFEHKERVLQELMMPPQDAKARQCE RQKRETIESVCQDVLRRQEBFEHKERVLQELMMPPQTDLDEATRK AYYKEFRKVVSTSDULLEVLDARDFLGGCCYQMEBAVLRAQGNK KLVLVLINNIDLVPKEVVERWLDVLRRELDTVAFKASTGHQVKNTL NRCSVPVDQASBELLKSKAGGABN.MRVLGNYCRLGEVATHIR VGVVSLPWGASSLINSLKRSRACSVGAVPGITKFMGVYLDKF IRLIDAPGIVGPGNSEVGITLRNCVVVDKTLBWTDFVDFITLDKF MLEISNYYGVSGGOTTERFILTAVAIRLGKKKKGGLVSQGQAAK AVVLANWSGKISTYFDPDATHTLFHILSAVHYEMTEVPDIEDT EQANEDTMECLATUSEDBLLGDTDPLEMEIKLLISPMTKIADAI ENNTTVYKICDLTGYCTNPNNRQMGMAKRNVDHPKSNSNSVVC SVDRRSVLQRIMSTDPLQQGQALASALNKKKMQKRADKIASKL SDSMMSALDLSGRADDGVGD VSVDRRSVLQRIMSTDPLQQGQALASALNKKKMQKRADKIASKL SDSMMSALDLSGRADDGVGD VKCSCPPGQVGGTTRARDFSVLDKATKGCMSKRKYPORRSKL/PMRFK GRKPAKAAGASLGVAATVKRGCCMSKRK/PMRFKSL GRKPAKAAGASLGVAATVKRGCMSKRK/PMRFKSL GRKPAKAAGASLGVAATVKRGCMSKRK/PMRFKLISH TVTLMGRVVSSANHIKKAHHVKTOTCEVVALHRCCKNNKIERSQOT VKCSCPPGQVGGTTRARDFSCVDASIVGEVMCMQPCLEGBECK VLDDRKGNSCSSGNKVKTTRVTH 5909 1 5002 PATGSTI INFQGSSARADGRIGSLPSDSQAPGALCGRAPP SSNLRADRSMICAQARAGKNI,YMRRLGLAAMAPPSBNSQSLRR CKSPIRYSYNPDGYMMDLRGGPHDGVTIPRSTDDTULTSDS STIMERSSYYSIGHSQDLVIHWDLKEVDAGDWIGMYLIDEVLS ENFLDVKNRGWGNGSHGQI INKIDASSYPVEETKI CFRKYTHGV SGALATTYPSTVTWNSAABATKSGGABPRSDSGOLFRFETI TSSHHDDDEFSIJSTEPEBAGI FOSGMRALIFSBD GCKLGRAFVKRKRRPCLIPVSLETVLKKAKSRSPI IKKFL GKLSMPVQRLLERRAIGDRVVSYTIGRRLPTHVHSGGGEPRSEADE SSSWMPQQLLEGSVDPRRGNGSTLSFREDEDONTLEGG GGLQLRASYKRRRRPCLIPVSLETVLKSAGAGDETTRTHYIT HTHLHISMPSAGGGSARAEBEGGARESTLKNSSEKDGLSEVDTV AADPSALEEDBEFEBGGTFGTAHBFGHSGGHFBLAALLE DGRAPATKEEPLEEETSTTSDFDLASSSECVASSCSSCYTSCYS SCYSASCYSSCYNGNRFASHTRFSSVDSAKISESTVFSSQOD BEEENSAFESVPOSMGS PELDPESTNAGAGAQDGCDT THETTHLHISMPSAG			1	TPPYCKATTEPVTVKMQLRRPSDQEVSESMDFRYLPDEKDTYGN
TOUSQABSYTPSGFISGLSHIASWAPLPSSWSSVAHPTFR SCHTMPLESFSTRTLEPSNGQIPPPLYURDINLANSHACTYNN ADDIVGMEASSMPSADLYGISDPNALSHCSVNMMTTSSDSMGST DNPPLLSHWILENPSCHSVALDPDIALGHQMSSSMSAGANSHTT VFVSQSDAFEGSDFSCADNSMINESGPSNSTNPNSHVFVQDSQY SGIGSMQMEQLSDSFPYEFFGV TYLLSSWSS**NLDTIKSQVKV/PKGHKKISWPYPQPAKQMGK KATSKVPSAPHFVHPMDHANREALKKKWVERMERQQAAREQE RQKRFTISSYCQDULRQEEFEHKEVLQELMHFPQLDDEATRK AYYKEFRKVVPYSDVILEVLDARDPLGCRCPQMEERAVLRAQGMK KLUVLNKILULDVREVVEKNLDYLLENPAPKASTOHQVNL NRCSVPVDQASESLLKSKACFGABRIMRVLGNYCRIGEVETHIR VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIR VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIR VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIR VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIR VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIR VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIR VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIR VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIL VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIL VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIL VGRUFUNGSSLIKMSLKKSRACFGABRIMRVLGNYCRIGEVETHIL VGRUFUNGSSLIKMSLKKSRACFGABRIMRVLGNYCRIGETHILD RENATTYVKICSTGYTTHPLTAVAHRLGKKKKGGLYSGOAARA AVIADWYSGKLSFYTIPPARTHLJSELVKKKGGLYSGOAARA AVIADWYSGKLSFYTIPPARTHLJSELVKKKGGLYSGOAARA SUNDRSSLLGNADOVGD SUNDRSSLLGNADOVGD 100000000000000000000000000000000000		1		KAKKQKTTLLFQKLCQDHVETGFRHVDQDGLELLTSGDPPTLAS
TOUSQABSYTPSGFISGLSHIASWAPLPSSWSSVAHPTFR SCHTMPLESFSTRTLEPSNGQIPPPLYURDINLANSHACTYNN ADDIVGMEASSMPSADLYGISDPNALSHCSVNMMTTSSDSMGST DNPPLLSHWILENPSCHSVALDPDIALGHQMSSSMSAGANSHTT VFVSQSDAFEGSDFSCADNSMINESGPSNSTNPNSHVFVQDSQY SGIGSMQMEQLSDSFPYEFFGV TYLLSSWSS**NLDTIKSQVKV/PKGHKKISWPYPQPAKQMGK KATSKVPSAPHFVHPMDHANREALKKKWVERMERQQAAREQE RQKRFTISSYCQDULRQEEFEHKEVLQELMHFPQLDDEATRK AYYKEFRKVVPYSDVILEVLDARDPLGCRCPQMEERAVLRAQGMK KLUVLNKILULDVREVVEKNLDYLLENPAPKASTOHQVNL NRCSVPVDQASESLLKSKACFGABRIMRVLGNYCRIGEVETHIR VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIR VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIR VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIR VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIR VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIR VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIR VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIR VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIL VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIL VGWUGLPHWGSSLILMSLKKSRACFGABRIMRVLGNYCRIGEVETHIL VGRUFUNGSSLIKMSLKKSRACFGABRIMRVLGNYCRIGEVETHIL VGRUFUNGSSLIKMSLKKSRACFGABRIMRVLGNYCRIGETHILD RENATTYVKICSTGYTTHPLTAVAHRLGKKKKGGLYSGOAARA AVIADWYSGKLSFYTIPPARTHLJSELVKKKGGLYSGOAARA AVIADWYSGKLSFYTIPPARTHLJSELVKKKGGLYSGOAARA SUNDRSSLLGNADOVGD SUNDRSSLLGNADOVGD 100000000000000000000000000000000000		1	1	QSAGITVNFPERPRPGLLGSIGEGRYFKKEPNLFSHDAVVREMP
SOMTHPLSSTSTETLPSNOGG PPPLRIPUGNIANSNACTYNN ADDIVGMEASHMEASHMEADLYGISDPMIANSNACTYNN ADDIVGMEASHMEADLYGISDPMIANCS NOWMITTSSDSMET DNPRLISMNLENPSCNSVLDPBDLRQLEGMESSSMSAGANSNTT VEVSGSDAFEGSDFSCADNSMINESGPSNTNPNSHVFVQUSQY SGIGSMQMEQUSDSFP YEFFQV TYLLSSWSS**NLDTKIKSQUKK/RKGHKKISWPPQPAKQNGK KATSKUPSAPHFVHPBUHANREAELKKKWUEMMERQQARAEQE RQKRRTISSYCODVLRRQEFFEKKEVLQELNHFPQLDDEATRK ATYKEFRKYVSYSDVILLBULDARDPLGGCFQOMEBAULRAQGNK KLVLVLINKIDLVPKEVVEKWLDYLENBLPTVARKAGONK KLVLVLINKIDLVPKEVVEKWLDYLENBLPTVARKAGONK KLVLVLINKIDLVPKEVVEKWLDYLENBLPTVARKAGONK KLVLVLINKIDLVPKEVVEKWLDYLENBLPTVARKAGONK KLVLVLINKIDLIVPKEVVEKWLDYLENBLPTVARKAGONK KLVLVLINKIDLIVPKEVVEKWLDYLENBLPTVARKAGONK KLVLVLINKIDLIVPKEVVEKWLDYLENBLPTVARKAGONEVALD NRCSVPVDQASESLLKSKAGGRGHKEVKAGOLVSQCQAAK AVLADWSGKISFYIDPPNSEVGTILENCHVQKLADPVTVETTILQE GNAEDTHEELATTGESDELLGOTDPLEMELKLLHSPMTKIADAI ENKTTYVKIGGLTGVCTNPNRHGMWAKRAVUHAPKRTADAI ENKTTYVKIGGLTGVCTNPNRHGMWAKRAVUHAPKSMSLVC SVDRRSVLQRIMETDPLQGQALASALKNKKMGKRAKKASKL SDSMMSALDLSGNADDOVGD SVDRRSVLQRIMETDPLQGQALASALKNKKMGKARKASKL SDSMMSALDLSGNADDOVGD 400 HCCIKKRGEGSGSFSPASGGFQLGCQI PEPSLIPSEETHDHTRA HTRILRATLTRRPPRSHSTTRLRFPPRLDGOGLASMK/PMRER* GWRPAKAAGASLOVAATGRGGCRSKKYLQKATKGKLLI IIFT VTLMGKVVSANHHKAHNVETGCSVHGCCNKKKLEERSQT VKCSCPFQGVAGTTRAAPSCVDASIVECKWNCHMPCLEGEECK VLEDBRGMSCSSGNKVTTFVTH 5909 1 5002 PAIFGSTI IWAFGSHSAARADGCHGSLPSOSQARGALCGARAPP SSHLRADRSMCSGAGNKVTTVTH SSHLRADRSTYSIGHSQDLVIHMDIKEEVDAGOUHGMYLLDBVLS STLMGRSSYSTIGHSQDLVIHMDIKEEVDAGOUHGMYLLDBVLS STLMGRSSYSTIGHSQDLVIHMDIKEEVDAGOUHGMYLLDBVLS STLMGRSSYSTIGHSQDLVIHMDIKESVDAGOURGYLLTBDLTSDR STLMGRSSYSTIGHSQDLVIHMDIKESVDAGOURGYLLTBDLTSDR STLMGRSSYSTIGHSQDLVIHMDIKESVDAGOURGYLLTBCS SGCAGALATTTSVTVKNSAAPIFKSIGADETVQSQCSRRLISFSLS DFQMGLKKKISMPVARDYLKISIGNGSHGGORSKILTSFSLS SGCAGALTATTSVTVKNSAAPIFKSIGADETVGNSGGRBTLTSFGG GRADATAGAGGSTABEETTGGGRGCHSCCGASCCSPSCYSSCYSTSCYS SSCSSASCYSPSCVNGMRFASHTRPSSVDSAKISESTPPSTAY AADPSALEEDGRSSPARGGGBHSGCGASCCSPSCYSSSCYSTSCYS SSCYSASCYSPSCVNGMRFASHTRPSSVDSAKISESTVPSGOOL HPSTGSESDSSRGGGDHSCGCCASCCSPSCYSSSCYSTSCYS SSCYSASCYSSCVNGMFAS		1		TGVSSOAESYYPSPGPISSGLSHHASMAPLPSSSWSSVAHPTPR
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				ALQIDI I DEP/ICEVVNYNKI LTVFLTKSVLEI*KPIHTPQTYR				

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	location	to first	LaLeucine, Mamethionine, NaAsparagine,
	corresponding	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	to first	residue of	g-gerine T=Threonine, V=Valine,
	residue of	amino acid	W-Truntophan, Y=Tvrosine, X=Unknown, *=Stop
	amino acid	sequence	codon. /=possible nucleotide deletion,
	sequence	boquosio	_nossible nucleotide insertion)
	Sequence		3*NDFFGIKEVYVSRRLRKTSF/RLAVTFLEQAVVSKECVPVDQ
		ļ	FMEHLLPSLLSLASDPVPNVRVLLAKALRQMLLBKAYFRNAGNP
		1	HLEVIEETILALQSDRDQDVSFFAALEPKRRNIIDTAVLEKQN
5918	13	1247	EGAQVARRRSRRQWRAGRCGRGRGGRRAERTGGRGPPGRPRPLP
3,10		}	PGPARRGRRRMETPFYGDEALSGLGGGASGSGGTFASPGRLFPG
	į		APPTAAAGSMMKKDALTLSLSEQVAAALKPAPAPASYPPA\ADG
			APSAAPPDGLLASPDLGLLKLASPELERLIIQSNGLVTTTPTSS
	1		QFLYPKVAASEEQEFAEGFVKALEDLHKQNQLGAGRAAAAAAA AGGPSGTATGSAPPGELAPAAAAPEAPVYA\NLSSY\AGGCRGL
			RGGAT\VAFAAEPVPFPPPPPPPGALGPRRP/RLALQGRRPQTV
•			PDVP\SFGESP\PLSPIET\DTPRRI\KAKRKRL\RNPQIRAPK
	Ì	Ì	PASRKLGAQSRALERESEDPS*SPEHGSLASTASLLREQVAQLK
	1	1	PASRKLGAQSKALEKESEDPS SPERGSBASTADDANSQ VAQST
		<u> </u>	TSVQGDSQGTPTSSQGSINMBHWISQAIHGSTTSTTSSSSTQSG
5919	1	4254	CCCDAHRIADVMAOTHIENHSAPPDVTTYTSEHSIQVERPQGST
-	1		CCPTADKYGNARIMETGDGVPVSSRVSAKIQQLVNTLKRPKRPP
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}		l	QKVCQYKAKVACVKSRDMHWALVAHRDQRDINLSSLRMLIVADG
ł		}	ANPWSISSCDAFLNVFQSKGLRQEVICPCASSPEALTVAIRRPT
		1	DDSNQPPGRGVLSMHGLTYGVIRVDSEEKLSVLTVQDVGLVMPG AIMCSVKPDGVPQLCRTDEIGELCVCAVATGTSYYGLSGMTKNT
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}	1		VAEQRPDSTEEDSFQWMSRVLQAIDSIHQVGVYCLALVPANTLP
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1			PEIGPASVMVGNLVSGKRIAQASGRDLGQIEDNDQARKFLFLSE
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1		į	FKDLGLHPRAVSTSFGCRVNLAICLQGTSGPDPTTVYVDMRALR HDRVRLVERGSPHSLPLMESGKILPGVRIIIANPETKGPLGDSH
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5920	1381	1499	UPPDUMPREPAHISSVROASTOVPRTVPHTQRVANIGTQTTGP
1			SCUCCCTPGRPLLPCKCSSAAHSTYRVQEPAVHIPGQEPLTASM
1			LAAAPIHEOKOMIGERLYPLIHDVHTQLAGKITGMLLEIDNSEL
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	ł	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	<u> </u>	sequence	_1	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
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1	1		l i	SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL
<u></u>			·	OTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
ĺ	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
ļ	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ	residue of	amino acid	Codon, /=possible nucleotide deletion,
l .	amino acid	sequence	Codon, /=possible nucleotide defection,
1	sequence		\=possible nucleotide insertion) LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
}			AIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLETEILQEPS
1	ŧ	1	GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG
		1	VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSE
1	1		HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG
1			LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI
ł	1		EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYS
l			EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
ł	Į.	İ	GEIASECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKAIHE
]	}	}	DEDENIEICSKIVÇNILGNEHQHLYAKILHLVMADGAYQEDNDE
ļ	<u> </u>		DEDENTETCSKIVCNILGNEAGABIAKIANDAVA DOSA KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA
5928	4146	1248	YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR
1		}	YKKYGDKKLHEKKPLQKAKQAHQIPEKKVNIGEBRAKTOBBAAK KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG
1		1	WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ
1			WRNVLSAGGSGEVKAPFLGSGGITAPSSFSSKGQIAMITTE OF MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR
1		1	MQQQRAEDNEAKWKREIIGRGIDEKQRGIDAVIRGEKPRIKEEEV KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRIKEEEV
Ì		Ĭ	YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
1	ł		RRKK/IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV
j			AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS
1			SLTDTRETSEEMQKTNNAISSKREILRRLNENLKAQEDEKGKQN
1	}		LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL
1	İ		DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE
1	1	l l	LOLOTE-JENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
}	1	į.	ATVIDSPVETKSPEFSEASPOMSLKLEGNLEEPDDLETEILQEPS
ļ			GTNKDE\SI.PCTTTDVWISEEKETKETQSADRITIQENEVSEDG
ı		}	VSSTVDOLSDIHIEPGTNDSOHSKCDVDKSVQPEPFFHKVVHSE
i i	Í		HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG
1	}	į	LEDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI
1			EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYS
			EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
ì			GETASECECDSVFNHLEELRLHLEQEMGFEKFFEVYEKIKAIHE
	Į.		DEDENTETCSKIVONILGNEHOHLYAKILHLVMADGAYQEDNDE
5929	3	1558	LDESMTTOLPAYVAILLEYVSRASCODTFTAAVYEHAAILPNAT
5929	3	2000	1.TPVSREEALALMNRNLDILEGAITSAADQGAHIIVTPEDAIYG
1	1		WNFNRDSLYPYLEDIPDPEVNWIPCNNRNRFGQTPVQERLSCL\
	1		AKNINGTYVVANIGDKKPCDTSDPQCPPDGRYQYNTDVVF\DSQG
1		1	KLVARYHKONLFMGENOFNVPKEPEIVTFNTTFGSFGIFTCFDI
	1	ì	LEHDPAVTLVKDFHVDTIVFPTAWMNVLPHLSAVEFHSAWAMGM
1			RVNFLASNIHYPSKKMTGSGIYAPNSSRAFHYDMKTEEGKLLLS
1	}	1	OLDSHPSHSAVVNWTSYASSIEALSSGNKEFKGTVFFDEFTFVK
ł		1	T TOTA CHIVETICOVEL CCHI. SYKMSENI PNEVYALGAFEGLHTVE
1		1	GRYVIOICTLLKCKTTNLNTCGDSAETASTRFEMFSLSGTFGTQ
}		1	YVFPEVLLSENOLAPGEFQVSTDGRLFSLKPTSGPVLTVTLFGK
ŀ	1	1	LYEKDWASNASSGLTAQARIIMLIVIAPIVCSLSW
5930	113	6082	RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK
1 3330	1		KIJWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ
1	1		KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF
İ	1		CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM
	l l	1	LODREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN
1			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV
	1		TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL
}	1	1	KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG
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ł	1		CHILGMNVMEFTRAILTPRIKVGRDYVÇKAQTKEQADFAVEALA
}	}	1	KATVERI.FRWI.VHRINKALDRTKROGASFIGILDIAGFEIFELN
1	Ì	1	SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL
		1	DLOPCIDLIERPANPPGVLALLDEECWFPKATDKTFVBKLVQEQ
	1	1	GSUSKFOKPROLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
- [Ĭ	1	MUATILHOSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT
		1	WEGNER TUGOLYKESLTKLMATLRNTNPNFURCI I PNHEKRAGK
	ļ		LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP
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SEO	Predicted		
ID	beginning	Predicted end	Amino acid segment contrain
NO:	nucleotide	nucleotide	Amino acid segment containing signal peptid (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Dhopula
	location	location	Glutamic Acid F-Phonel-1
		corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine M-Mothierine, K=Lysine,
İ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	
İ	residue of	amino acid	
	amino acid	sequence	I "= ** IPCODIAN. Y='N/Mocine v
	eedneuce	1	
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		NC.	OTKVEGELEEMERKHOOLLEEVILLE FOLLOWARDEELLKVK
		NC. EK	OTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEBM
		NC EK RAI DLI	OTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RLAAKKQELEEILHDLESRVBEEEERNOILQNEKKKMQAHIQ EEQLDEEEGAROKLOLEKYTABALKOOLOGI
		NC EK RAI DLI IKI	OTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RLAAKKQELEEILHDLEESRVBEEEERNQILQNEKKKMQAHIQ EEQLDEEEGARQKLQLEKVTAEAKIKKMEEILLLEDQNSKF
		NC EK RAI DLI IKI RLI	OTKVEGELEEMERKIIQOLLEEKNILAEQLQAETELFAEAEEM RLAAKKQELEEILHDLEERVIBEEEERNOILQNEKKKMQAHIQ EEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF KKLMEDRIAECSSQLAEEEEKAKLAKIRNKQEVMISDLEE
		NC EK RA DLI IKI RLI AKF	OTKVEGELEEMERKIIQOLLEEKNILAEQLQAETELFAEAEEM RLAAKKQELEEILHDLEERVIEEEEERNOILQNEKKKMQAHIQ EEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF KKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE KKEEKTRQELEKAKKLDGETTDLQDQIAELQAQIDELKLQL
		NC EK RAI DLI IKI RLI AKI EKF	OTKVEGELEMERKIIQULEEKNILAEQLQAETELLKVK RLAAKKQELEEILHDLESKVEEEEERNOILQNEKKKMQAHIQ EEQLDEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF KKKIMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE KKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL LEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES
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		NC EK RAI DLI IKI RLIH AKH EKP QEV	OTKVEGELEMERKIIQULEEKNILAEQLQAETELFAEAEEM RLAAKKQELEEILHDLESRVEEEEERNOILQNEKKKMQAHIQ EEQLDEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF KKKIMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE KKEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL GEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES LSRNKAEKQKRDLSELEALKTELEDTLDTTAAQQELRTKRE
		NC EK RAI DLI IKI RLI AKH EKI QEV FKA	OTKVEGELEEMERKIIQQULEEKNILAEQLQAETELFAEAEEM RLAAKKQELEEILHDLESRVEEEEERNOILONEKKMQAHIQ EEQLDEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF KKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE KKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL GEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES SRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE TAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR
		NC EK RAI DLI IKI RLI AKI EKP QEV FKA	OTKVEGELEEMERKIIQVTRQEEELQAKDEELLKVK RLAAKKQELEEILHDLESRVILEEKNILAEQLQAETELFAEAEEM RLAAKKQELEEILHDLESRVBEEEERNOILQNEKKKMQAHIQ EEQLDEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF KKLMEDRIAECSSQLABEEEKAKNLAKIRNKQEVMISDLEE KKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL GEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES LSRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE AELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR NLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV
		NC EK RAI DLI IKI RLI AKI EKI QEU FKA QEL FAK	OTKVEGELEMERKIIQULEEKNILAEQLQAETELFAEAEEM RLAAKKQELEEILHDLESRVEEEEERNOILQNEKKKMQAHIQ EEQLDEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF KKKIMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE KKEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL GEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES LSRNKAEKQKRDLSELEALKTELEDTLDTTAAQQELRTKRE

			rentide
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
1	location	corresponding	L-Leucine, M=Mcthionine, N=Asparagine,
i	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
1	to first	amino acid	la a m-mbreonine V=Vallne.
l	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
4	residue of	amino acid	Codon, /=possible nucleotide deletion,
1	amino acid	sequence	()
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 			HOROVASNLEKKO\KKFDOLLAEEKSISARYAEERDRAEAEARE
1	1	1	KETKALSLARALEBALEAKEEFERONKOLRADMEDLMSSKDDVG
1	1	1	KETKALSHARADEBADEANCA KNVHELEKSKRALEQQV\EEMRTQLEELEDELQATEDAKLRLEV
1	1	1	NMQAMKAQFERDLQTRDEQNEEKKRLLIKQVRELEAELEDERKQ
1	1	į.	NMQAMKAQFERDIQIRDEQIBANKARDEVIKQLRKLQAQMK RALAVASKKKMEIDLKDLEAQIEAANKARDEVIKQLRKLQAQMK
	1		DYORELEEARASRDEIFAQSKESEKKLKSLEAEILQLQEELASS
	l l		DYORELEEARASRDETFAQUES ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLEE
1	1	- \	EKARRHABQERDELLADER TRATLQVDTLNAELAAERSAAQKSDNAR ELEEEQSNMELLADRFRKTTLQVDTLNAELAAERSAAQKSDNAR
1			QUERQNKELKAKLQELEGAVKSKFKATISALEAKIGQLEEQLE
Ì	t	1	QQLERQNKELKALLQELEGAVICH I FMQVEDERRHADQYKEQMEKA QEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA
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ļ	1	ł	NARMKQLKRQLEEABLEATRALIAGKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
į.		1	
	1		TSDVNETQPPQSE RHLEEICFLFLQKGRKLKLSGPRWEEGKPRGTGGLWVKAEANMG
5932	33	572	RHLEEICFLFLQKGKKLKLEGFKULSCHLYKTCRRPRPV\APP FGATLAVGLTIFVLSVVTIIICFTCSCCCLYKTCRRPRPV\APP
	1		PHPP/PVVHAPYPQPPSVPPSYPGPSYQGYHTMPPQPGMPAAPY
1			PMQYPPPYPAQPMGPPAYHETLAGGAAAPYPASQPPYNPAYMDA
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1			FKAAL GTRKLKMADKTFGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD
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4	1	1	AFSIGKMSTAKRTLSKKEQEEDKKABBIKTUKPSSRFADQKNP SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP
l			SDGNKVKTFVRGGVVNAAKEEHEIDERGKKKKSNLELFKEELKQI PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI
1		į.	PNQSSNERPPSLLVIETKKFFBKASSGORRSMDAPSRRNRSSGVL QEERDERHKTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL
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NO: nucleotide location corresponding to first amino acid serior first amino acid serior a			Predicted end	Amino acid segment containing circuit
Corresponding to first amino acid anino compared to the compared t				(A=Alanine, C=Cysteine, D=A====billing Signal peptide
corresponding to first amino acid amino acid amino acid amino acid complete the com	NO:		location	Glutamic Acid E-Phonesis
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to first amino acid anino rogramme program	Į.	corresponding		, including, leisoleucine vertenine
amino acid amino acid	1			L=Leucine, M=Methionine, N=Nanava=i==
xesidue of anino acid sequence sequ	1			P=Proline, O=Glutamine, P-awaining
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110					acid segment containing signal peptide acid segment containing signal peptide anine, C=Cysteine, D=Aspartic Acid, E= anine, C=Cysteine, D=Aspartic Acid, F=Phenylalanine, G=Glycine, mic Acid, F=Phenylalanine, K=Lysine,
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sequence	amino acid	ustidine, I=Isoleucine, G=Glycine, F=Bhenylalanine, G=Glycine, F=Isoleucine, K=Lysine, F=Clycine, M=Methionine, N=Asparagine, F=Threonine, R=Arginine, T=Threonine, V=Valine, T=Threosine, V=Valine, T=Tyrosine, V=Valine, T=Tyrosine, V=Valine, T=Tyrosine, V=Valine, T=Tyrosine, V=Valine, T=Tyrosine, V=Valine, T=Tyrosine, V=Valine, T=Tyrosine, V=Valine, T=Tyrosine, V=Valine, T=Tyrosine, V=Valine, T=Tyrosine, V=Valine, T=Tyrosine, V=Valine, T=Tyrosine, V=Valine, T=Tyrosine, V=Valine, T=Tyrosine, V=Valine, T=Tyrosine, V=Valine,
Agence	sequence Walt	YPtophan, v-walling, V=Valing,
	\=no	", /=possible Yrosine, X=Unb-
	TENT	ssible nucleotide delet, *=Stop
	I PRACE	- ARCISDED
	I SUPp.	TOP ENDITORS
	IGSPS	CRRKSCGPPPEPFNGWHINTDTQFGKWFSISCLENLVWS PTCLVSGNNVTWDKKAPICEIISCEPPPTISNGDFYSNN CGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQWG HTVQCCTAFPEYENNIKAPICEIISCEPPPTISNGDFYSNN CISTNKCTAPEVENNIKYPCWF
	RTO Tree	SGNN/TEMPORAL TOTOPOGOTO
	SSPPPR	CISTNECTED
	PNINGS	TTCLVSGNNVTWDKKAPICEIISCBPPTUNYSCNEGFRL GTVVTYQCHTGPDGEQUFELVGERSIYCTSKDDQVGVW DTVTVCOTNGRWGPKLPHCSRVCQPPPEILHGEHTLSRCPG DEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPPCMS WWSSUVLPLNLQLGAKVEPU
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	I LACMUS -	THE THE PROPERTY OF THE PROPER
1 1 1	I VCVmon -	TO VEVERATE TO SEVENDE TO TOTAL TOTA
	I PVCN x co-	LINGDUMON I SASHOU
	GFT Down	- LUNGUY LUISEPHONE LUIPIGKE
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	688 GGSSVHPR	FFILLIIFLSWIILKHRKGNNAHENPKEVAIHLHGG
	DK\ 201	THAY GT CITY TO THE MAN I
	I HETTON	- CALLEVECO FD AKUNGST
	GVENSYGEN	TLQTNEENSVLP FLQTNEENSVLP FLAYGISHKAYQIDPDL\RKHREO\LVIE\VGRKL BERTGYFSSTDLGRTASHYIKYNTIETFNEY NULL
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1 1 1	/ VANDE -	+ OR MATRICE - ARRIDOTING - 4ESCOV
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1 1 1	DKPTRHKTYLSSSWAY:	CYLGLDQQYD/NLSQRYTSESFCTGOHQ MAAAEGPVGDGELWQTWLPNHVVFLRLR G\EEDALG
1 1 1	GFDCom- ~~CALPACO	Co. T. SDGELWOTTEN
1 1	LSPTOUTER	THATAGGYGDGELWQTWLPNHVVFLRLR SSLPSSPPPQLLTRNVVFGLGGELFLWD G\EEPALSQYQRLLCINPPLFEIYQVL WYLELPKRWGKNSEFEGGKSTVNCSTTP SLVLNKGPANT
l	VARRENTELLGIKGIM	SUYORT TOTAL
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1	VUOTES - W VAARDATE	DrGPr.
1	ACCEDE TO THE PER	- CLDCIDATE - COEGN/T
1 1	1 DV: 100	_ ~~ ESGMT.
_ 1	TROPING TO TOUR DELON	- "CESKYHOTETTE - TELALKI.
	POUR TOP TOP TO TOP TO THE PROPERTY OF THE PRO	- WACLVEDTT - VGLIWT
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	AAKQLEDLSYCREEPECY	LSTEQKCFVEHILCTKPLEPCROPAP STYBCLIWPLLSTVHPASPPLLCTR EKHLTSILQRSVANPAFLKASEKD MARPLANE
	100	STYRCLIWPLLSTVHPASPPLLCTR EKHIRSILORSVANPAFIKASEKD EQYILKQDLAKEEIQRRVKLLCDQ MAERLADKYEEAKEKQEDIMNRMK
	408	MARQEDIMNRMK

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A-Alanine C-Cysteine, D-Aspartic Acid, E=
ID	beginning	location	Gluramic Acid. F=Phenylalanine, G=Glycine,
NO:	nucleotide	corresponding	H-Histidine I=Isoleucine, K=Lysine,
1	location	to first	L-Leucine, M-Methionine, N-Asparagine,
i	corresponding	amino acid	p=proline, O=Glutamine, R=Arginine,
	to first	residue of	c-coming T-Threoning, V=Valing,
- 1	amino acid	amino acid	W-Truntophan Y=Tyrosine, X=Unknown, *=Stop
i	residue of		Codon
1	amino acid	sequence	\-nossible nucleatide insertion)
	sequence	<u></u>	KLLHSFHSELPVLSDSERDMKKELQLIPDQLRHLGNAIKQVTMK
			KDYQQQKMEKVLSLPKPTIILSAYQRKCIQSILKEEGEHIREMV
			KQINDIRNHVNF FSIATFTDEPEVLTEPPSATTTTTIGISATWTTLAGSHGKRNNT
5944	167	3428	FSIATFTDEPEVLTEPPSATITITIGISATATITAGOSTOCISKS
]	1	ITTTSSKRKNRKNKITPENVQIIFDDPLPISYSQPEKVNGESKS
	l .	l	SSTSESGDSDNMRISSCSDESSNSNSSRKSDNHSPAVVTTTVSS
	ŧ.	ļ	KKQPSVLVTFPKEERKSVSGKASIKLSETISEGTSNSLSTCTKS
	1		GPSPLSSPNGKLTVASPKRGQKREEGWKEVVRRSKKVSVPSTVI
	1	1	SRVIGRGGCNINAIREFTGAHIDIDKQKDKTGDRIITIRGGTES
	Į	ł	TROATOLINALIKOPOKEIDELIPKNRLKSSSANSKIGSSAPTT
	l .	l	TO ANTIS MCTKMTTVALSSTSOTATALTVPAISSASTHKTIKNP
		,	INVESTIGATION OF THE PROPERTY
			UPCCTERRACSTEGREDVRPLSPARATINSPKPHMVPRHSNQNSS
		 	GCOUNG ACCUMES DETERMINED TO SELECT THE SECOND OF THE SECO
		1	1 VARIALVERNATEPTENTETTA SNINTAPTNATYPMPTAKEHYPVSSP
	-	į .	CCDCDDAODCGVSDNSDLDCGSASPNKVASSSEQEAGSPPVVEI
	1	1	I MATTER DINESCES CASCAHONO OPPGSVSOEPRPPLQQSQVPPP
	1		DIMMTUDDI ATGGA DVAVPSTAPVTYPMPOTPMGCPQPTPKMET
	1		TATER DEDUCTTA PHYNSASVONSSVAVLSVNHIKRPHSVPSSVQ
	į		T DETT STOSACONSVHPANKPIAPNFSAPLPFGPFSTLFENSPI
	1	1	SAHAFWGGSVVSSQSTPESMLSGKSSYLPNSDPLHQSDTSKAPG
	j	}	FRPPLQRPAPSPSGIVNMDSPYGSVTPSSTHLGNFASNISGGQM
		İ	YGPGAPLGGAPAAANFNRQHFSPLSLLTPCSSASNDSSAQSVSS
		1	GVRAPSPAPSSVPLGSEKPSNVSQDRKVPVPIGTERSARIRQTG
	1		GVRAPSPAPSSVFLGSERPSNVSQDARVTVTVDWCNPGMGNPM TSAPSVIGSNLSTSVGHSGIWSFEGIGGNQDKVDWCNPGMGNPM
			TSAPSVIGSNLSTSVGHSGINSFEGIGONQDAY HIGHER IHRPMSDPGVFSQHQAMERDSTGIVTPSGTFHQHVPAGYMDFPK
	ł		IHRPMSDPGVFSQHQAMERDSTGTVTFSGTTMQTVTTA
	į	1	VGGMPFSVYGNAMIPPVAPIPDGAGGPIFNGFILADIGAGG
	1		MVSSSTENNGPQTVWTGPWAPHMNSVHMNQLG
5945	1461	197	GVTHLFLFGKRKLRNGIAEDLKGQADFFFLLVSEAVVATGSPRA
33 13			WLTCLILPLPGIIFSVLPKAMSRPLLITFTPATDPSDLWKDGQQ
	l .	i	QPQPEKPESTLDGAAARAFYEALIGDESSAPDSQRSQTEPARER
	1	1	KRKKRRIMKAPAAEAVAEGASGRHGQGRSLEAEDKMTHRILRAA
	Ī	1	QEGDLPELRRLLEPHEAGGAGGNINARDAFWWTPLMCAARAGQG
	1		AAVSYLLGRGAAWVGVCELSGRDAAQLAEEAGFPEVARMVRESH
	1		GETRSPENRSPTPSLQYCENCDTHFQDSNHRTSTAHLLSLSQGP
	. [ODDAY DI CUDICEDCEKI, I.I.RGGWEPGMGLGPRGEGKANPI PI V
	1		LKRDOEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW
		1	DEEDDER VERAMERDI.RTYMNLEF
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			Larama ovo vystvi myro a ono hy a t.VI.WGPGAAW \YPQLQKKKU
	1		TENTE TO CHAPTEN I ELITE THE TENTE T
			VEOVERDEWIKTEDT.ATHT.EDKCSGVVLIKAQISELAFFIIASV
			TATAL MARKET RESTREET, DNTVVTGCAKCGLERET DENKLINGER
l	į		COLDERANCE TAVORDAL MEDICARDOCIRVES KLIEKILLINISA
l	1		DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVI
l	1		DENSYPLQQDFSLLDFYPDIVKHGANARL
1	1		DENSYPLQQDFSLLDF1PDTVKHGARVKC RG1PDRRRRGP1GRVNMDLENKVKKMGLGHEQGFGAPCLKCKEF
5947	3	1317	RGIPDRRRRGPIGRVNMDLENKVKANGLGHEQGICAL CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDI
]	\		CEGFELHFWRKICRNC\NVAKKSM/IVDLSNEEBKKVOKSI
1	1		KYTTLIAKLKSUGI PMI KKNVPILITAS VAAKAT OTTA TI TEMP
i			PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHI
1			QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQC
l			PKQMNI PGGDRSTPAAVGAMEDKSAEHKRTQYSCYCCKLSMKEC
1]	DDA TVA EDAGYDKI WHPACFYCSTCHELLVDMIYFWKNBKLIYC
}	l	i	DIVIDE EVEN CAGCIELITES NEYTO A ENONWHLKH FCCFDCDS.
1			I DOET VIMINDEPUCKPCYVKNHAVVCQGCHNAIDPEVQRVIII
1	1]	NEGWIA STECELCSCCSKCLIGOKEMPVEGMVFCSVECKKRMS
		3330	- UPPRINGUECESVI.PSALEVCWDFLSGLTEGSLLPEGFFSGPIDG
5948	3 3 9	3370	OWN OWED CHECKED ARTHUS SPCSVKHSPTRETLIYAQAQAD
1	1	1	I TO THE OF THE PROPERTY OF TH
	i	1	PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRIVE
1	l l		DIGITETEPHKNNRVKKKNEALPSAHGTPASASALPEPKVKIVE

SEO	Predicted		
ID	beginning	Predicted en	
NO:	nucleotide	nucleotide	
1	location	location	
ł	corresponding	corresponding to first	
	to first	amino acid	I TO COULTED DENDETO ON INC. NO NO.
1	amino acid	amino acid	1 * = * = * = * = * * * * * * * * * * *
1	residue of	residue of	1 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	amino acid	amino acid	Welfyptophan, Yetvroetho V.R.
1	sequence	sequence	
	Doquence		I /-E
1	1		SPPSAPRRPPVYYKFIEKGARFI DNEVEVENDA
1	l		KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGEQQSLIDED
j	1		VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC
1			RAHCLOSRARPADCYL CONVCCA PARTICIPATION OF THE PROPERTY OF THE
Į.	,]	RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\I
	1		E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGAC
l	1	1	QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKT
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	1		WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL
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	1 39 1	3370	YRERY PVSGGSVLRSALRVCWDELSCI TRCCL L DECCE
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	l i		
	1		PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRIVEY SPPSAPPRPDDIVVERTEES
]		SPPSAPRRPPVYYKFIEKSAEELDNEVEYDMDEEDYAWLEIVNE
	·]		KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGEQQSLIDEDA
			VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/
	1		RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP
I			E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI
- 1	}		QCHKANCYTAFHUTCAOVACI VANCUER (CNLCKEKGR/VGACI
- 1			QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA
	1		YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR KKAKKAKKALAFBCAH PERIOD
J	j		KKAKKAKALAEPCAVLPTVCAPYIPPQRLNRIANQVAIQRKKQ
- 1			FVERAHSYWLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM KAAKEKLKYWODLBUDLEDA
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- 1	l	i	TOTAL TEREPORT OF THE PROPERTY
	İ		TOTAL VETOT TOTAL
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]	=	-	ESRS_ITMSTSQPGACPCQGAASRPAILYALLSSSLKAVPRPRSR
ļ	Ī	The state of the s	TOTAL TOTAL
	j	1	- ANGROS DE LIGITA()DAVABLEMADA DINDOLI MILLE
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951	7/2		
	143	5449	WNVKPSLLVVQLFKFSDKEEHEQNDSISGKTGETGVEEMIATRK
1		j .	VEODSKETVKLSHEDDHILEDAGGGSTGETGVEEMIATRK
	1	. 1.	VEQDSKETVKLSHEDDHILEDAGSSDISSDAACTNPNKTENSLV
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-	ļ		SOUTH AND A TOTAL WOUNTER AND LONG AND ASSESSMENT OF THE PROPERTY OF THE PROPE
- 1	[, ,	QLNAIESTKIESHETANLQDDRNSQSSSVSYLESKSVKSKHTKP VIHSKQNMTTDAPKKIVAAKYEVIHSKTKVNVKSVKRNTDVPES
	I		Y THE RESERVE THE PROPERTY OF
			OONFHR PVKVRKKQ I DKBPKIQSCNSGVKSVKNQAHSVLKKTLQ

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
_	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	nucleotide		Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	location corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L-Leucine, M=Methionine, N=Asparagine,
I	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	} -	\=possible nucleotide insertion)
	 		DOTLVOIFKPLTHSLSDKSHAHPGCLKEPHHPAQTGHVSHSSQK
		j	OCHKPOOOAPAMKTNSHVKBELEHPGVEHFKEEDKLKLKKPEKN
1			LOPRORRSSKSFSLDEPPLFIPDNIATIRREGSDHSSSFESKYM
[WTPSKQCGFCKKPHGNRFMVGCGRCDDWFHGDCVGLSLSQAQQM
į.	1		GEEDKEYVCVKCCAEEDKKTEILDPDTLENOATVEFHSGDKTME
1		Į	
			CEKLGLSKHTTNDRTKYIDDTVKHKVKILKRESGEGRNSSDCRD
	Ĭ	1	NEIKKWQLAPLRKMGQPVLPRRSSEEKSEKIPKESTTVTCTGEK
1	1	[ASKPGTHEKQEMKKKKV\EKGVLNVHPAASASKPSADQIRQSVR
ļ	1	j	HSLKDILMKRLTDSNLKVPEEKAAKVATKIEKELFSFFRDTDAK
1			YKNKYRSLMFNLKDPKNNILFKKVLKGEVTPDHLIRMSPEELAS
]	1	ļ	KELAAWRRRENRHTIEMIEKEQREVERRPITKITHKGEIEIESD
i	1	ļ	APMKEOEAAMEIOEPAANKSLEKPEGSEK\RKEEVDSMSKDTTS
1			OHROHLFDLNCKICIGRMAPPVDDLSPKKVKVVVGVARKHSDNE
l	1	Ī	AESIADALSSTSNILASEFFEEEKOESPKSTFSPAPRPEMPGTV
1	ŀ	•	EVESTFLARLNFIWKGFINMPSVAKFVTKAY2VSGSPEYLTEDL
i	1	1	
1	1	1	PDSIQVGGRISPQTVWDYVEKIKASGTKEICVVRFTPVTEEDQI
		1	SYTLLFAYFSSRKRYGVAANNMKQVKDMYLIPLGATDKIPHPLV
1		1	PFDGPGLELHRPNLLLGLIIRQKLKRQHSACASTSHIAETPESA
		1	PPIALPPDKKSKIEVSTEEAPEEENDFFNSFTTVLHKQRNKPQQ
}	į.	1	NLQEDLPTAVEPLMEVTKQEPPKPLRFLPGVLIGWENQPTTLEL
1	İ	İ	ANKPLPVDDILQSLLGTTGQVYDQ\AQSVMEQNTVKBIPFLNEQ
1	ļ.	ļ.	TNSKIEKTONVEVTDGENKEIKVKVDNISESTDKSAEIETSVVG
1		}	SSSISAGSLTSLSLRGKPPDVSTEAFLTNLSIQSKQEETVESKE
1		1	KTLKRQLQEDQENNLQDNQTSNSSPCRSNVGKGNIDGNVSCSEN
		1	LVANTARSPQFINLKRDPRQAAGRSQPVTTSESKDGDSCRNGEK
ľ	1		HMLPGLSHNKEHLTEQINVEEKLCSAEKNSCVQQSDNLKVAQNS
1		l	PSVENIQTSQAEQAKPLQEDILMQNIETVHPFRRGSAVATSHFE
			VGNTCPSEFPSKSITFTSRSTSPRTSTNFSPMRPQQPNLQHLKS
1		1	
j.		}	SPPGFPFPGPPNFPPQSMFGFPPHLPPPLLPPPGFG\FA\QNPM
1]	Ī	VPWPPVV\HLP\GQPQRMMGPLSQASRYIGPQNFYQVKDIRRPE
1	Ì	1	RRHSDPWGRQDQQQLDRPFNRGKGDRQRFYSDSHHLKRERHEKE
ı			WEQESERHRRRDRSQDKDRDRKSREEGHKDKERARLSHGDRGTD
]		i	GKASRDSRNVDKKPDKPKSEDYEKDKEREKSKHREGEKDRDRYH
	1	1	KDRDHTDRTKSKR
5952	3226	639	PPARRSARDLPRALSMEAARPSGSWNGALCRLL\LVTL\AFLIF
i		1	ASDACKNVTLHVPSKLDAEKLVGRVNLKECFTAANLIHSSDPDF
i		i	QILEDGSVYTTNTILLSSEKRSFTILLSNTENQEKKKIFVFLEH
1		§	QTKVLKKRHTKEKVLRRAKRRWAPIPCSMLENSLGPFPLFLQQV
1		1	QSDTAQNYTIYYSIRGPGVDQEPRNLFYVERDTGNLYCTRPVDR
1		1	EQYESFELIAFATTPDGYTPELPLILIKIEDENDNYPIFTEET
1	}	1	YTFTIFENCRYGTTYGOVCATDKDEPDTMHTRLKYSIIGOVPPS
			1
		}	PTLFSMHPTTGVITTTSSQLDRELIDKYQLKIKVQDMDGQYFGL
1		1	QTTSTCIINIDDVNDHLPTFTRTSYVTSVEENTVDVEILRVTVE
Į		1	DKDLVNTANWRANYTILKGNENGNFKIVTDAKTNEGVLCVVKPL
]	1	l	NYEEKQQMILQIGVVNEAPFSREASPRSAMSTATVTVNVEDQDE
		Į.	GPECNPPIQTVRMKENAEVGTTSNGYKAYDPETRSSSGIRYKKL
		1	TDPTGWVTIDENTGSIKVFRSLDREAETIKNGIYNITVLASDQG
}		I	GRTCTGTLGIILQDVNDNSPFIPKKTVIICKPTMSSAEIVAVDP
1	1	I	DEPIHGPPFDFSLESSTSEVQRMWRLKAINDTAARLSYQNDPPF
1	1	i	GSYVVPITVRDRLGMSSVTSLDVTLCDCITENDCTHRVDPRIGG
Į	1	1	GGVCLGKWAILAILLGIALFFCILFTLVCGASGTSKQPKVIPDD
		1	LAQONLIVSNTEAPGDDKVYSANGFTTQTVGASAQGVCGTVGSG
			IKNGGQETIEMVKGGHQTSESCRGAGHHHTLDSCRGGHTEVDNC
1			
			RYTYSEWHSFTQPRLGEESIRGHTLIKN
5953	330	811	PLLCNPDPGWYWWVKQESEISKESQEMDARPKLDLGFKEGQTIK
l			LCIGNITNKKGGASKPRTARGGGLSLLPPPPGGKVTIPPPSS/V
		1	KLPSTNHVTPPSIPKSNHGGSDADILLDLDSPAPVTTPAPTPVS
ļ	L .	L	VSNDLWGDFSTASSSVPNQAPQPSNWVQF
5954	32	2130	PPPPPPKLANMADLEAVLADVSYLMAMEKSKATPAARASKRIVL
1		I	PEPSIRSVMQKYLAERNEITFDKIFNQKIGFLLFKDFCLNEINE
i		1	AVPQVKFYEZIKEYEKLDNBEDRLCRSRQIYDAYIMKELLSCSH
t	L		

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	The state of the second of the
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, O=Glutamine, R=Arginine
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine
1	residue of	amino acid	Warryptophan, Yarrysine, Xalinknown tasken
	amino acid sequence	sequence	Codon, /=possible nucleotide deletion
	sequence	ļ <u>.</u>	\=possible nucleotide insertion)
ł	i	1	PFSKQAVEHVQSHLSKKQVTSTLFQPYIEEICESLRGDIFQKFM
i			ESDKFTRFCQWKNVELNIHLTMNEFSVHRIIGRGGFGEVYGCRK
			ADTGKMYANKCLNKKRIKMKQGETLALNERIMLSLVSTGDCPFI
			VCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSBKEMRFYA
1		1	TEIILGLEHMHNRFVVYRDLKPANILLDEHGHARIS\DLGLACD
		1	FSKKKPHASVGTHGYMAPEVLQKGTAYDSSADWFSLGCMLFKLL RGHSPFRQHKTKDKHEIDRMTLTVNVELPDTFSPELKSLLEGLL
1			QRDVSKRLGCHGGGSQEVKEHSFFKGVDWQHVYLQKYPPPLIPP
		}	RGEVNAADAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERW
1			QQEVTETVYEAVNADTDKIEARKRAKNKQLGHEEDYALGKDCIM
ļ	1		HGYMLKLGNPFLTQWQRRYFYLFPNRLEWRGEGESRQNLLTMEO
]		ILSVEETQIKDKKCILFRIKGGKOFVLOCESDPEFVOWKET.NE
5955	1706		TFKEAQRLLRRAPKFLNKPRSGTVELPKPSLCHRNSNGT
ددور	1726	444	KREREFRLAVCPLRYPSAYESSPGTELRECGLCRSGORFADCPD
ļ			PANRQDVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFTHUPRO
			VWKRCINIWRDVGLFGVLNEIANSEEEVFEWVKTASGWALALCR
]			WASSLHGSLFPHLSLRSEDLIAEFAQVTNWSSCCLRVFAWHPHT
Ì			NKFAVALLDDSVRVYNASSTIVPSLKHRLQRNVASLAWKPLSAS
	1		VLAVACQSCILIWTLDPTSLSTRPSSGCAQVLSHPGHTPVTSLA WAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLLW
1	1		SPDGSKILATTPSAVFRVWEAQMWTCERWFTLSGRCQTGCWSPD
1			GSRLLFTVLGEPLIYSLSFPERCGEGKG\ALEVQSQQRLWQICL
- FOE -			RQQYRHQMVRRGLGERLTPWSGTPVGNVWLCL
5956	1705	139	GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAOKPEGA
1			TYVWSSIINTLQTOVEVKKRRHRLKRHNDCEVGSEAVDVIRGI
ı			IQNKYFGDVDIPRAKVVRVCOALMDYKVFEAVPTKVEGKDKKDT
ł			FEDSSCSLYRPTTIPNQDSQLGKENKLYSPARYADALFKSSDIR
	1. 1		SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL
1	1		LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK AYSDSQEDEWLSAAIDCSEYLPDQMVVEISRSFPEQPDRTDLVK
			ELLFDAIGRYYSSREPLLNHLSDVHNGIAELLVNGKTEIALEAT
			QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK
1			RIFSKAIVDNKNLSKGKTDLLVLFL\MDHOKDVFKIDGTI\UVI
			VS\VK\LMAIQNGRDPNRDAGYIYCORIDORDYSNNTEKTTYDE
5957	1400		LLNLLKTLDEDSKLSAKEKKK\LLGOFYKCHPDIFIEHEGD
3337	1479	451	ELQVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENTKNAMT.TV
1		1	GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDOTSI.EFF
}			SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIFIGTENEV
}			SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG
			PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE
]			LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKKNISHD TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPAERITEDHEKKS
			KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL
5958	. 1	3138	AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD
	1		ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPARGSACCPOIDE
į 1	1		DTTNNRKIRVNGTKEPIEFKSNOWFG\ATVKA\HKGKSCGDVAB
			LLFTWRNFLKPTPEKGPVGTCYVAIONFSAYAEFSPCGNSNADD
1		1	EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWOGOVITASVADITA
ľ			NYSFKDILRKLAGEKQTEVAPASYDDSYLGYSVAAGEFTGDSOO
j	1	1	ELVAGIPRGAQNFGYVSIINSYDMTFIQNFTGEQMASYFGYTVV
		1	VSDVNSDGLDDVLVGAPLFMEREFESNPREVGOIYLYLOVSST.I.
l		!	FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD
I	J	j	QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD
i		f	SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN
1			LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD
			ETEFROKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE
- 1	j		QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR
j			NEGEGAYEAELFYMIPEEADYVGIERNNKGFRPLSCEYKMENVT
		1	RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLOIRSS
			NKDNPDSNFVSLQINITAVAQVEIRGVSHPPQIVLPIHNWEPEE
		-	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence	\=possible nucleotide insertion)
	sequence		EPHKEEEVGPLVEHIYELHNIGPSTISDTILEVGWPFSARDEFL
	1	ì	
	[}	LYIFHIQTLGPLQCQPNPNINPQDIKPAASPEDTPELSAFLRNS
	[1	TIPHLVRKRDVHVVEFHRQSPAKILNCTNIECLQISCAVGRLEG
ı		ĺ	GESAVLKVRSRLWAHTFLQRKNDPYALASLVSFEVKKMPYTDQP
		l.	AKLPEGSIAIKTSVIWATPNVSFSIPLWVIILAILLGLLVLAIL
	1		TLALWKCGFFDRARPPQEDMTDREQLTNDKTPEA
5959	1	1166	GTSGYAAQQLPSLLKEREFHLGTLNKVFASQWLNHRQVVCGTKC
3939	1 -	1	NTLFVVDVOTSQITKIPILKDREPGGVTQQGCGIHAIELNPSRT
	1		LLATGGDNPNSLAIYRLPTLDPVCVGDDGHKDWIFSIAWISDTM
	1	I	AVSGSRDGSMGLWEVTDDVLTKSDARHNVSRVPVYAHITHKALK
l	İ		
ļ	1		DIPKEDTNPDNCKVRALAFNNKNKELGAVSLDGYFHLWKAENTL
ĺ	1	1	SKLLSTKLPYCRENVCLAYGSEWSVYAVGSQAHVSFLDPRQPSY
İ	Į.	1	NVKSVCSRERGSGIRSVSFYEHIITVGTGQGSLLFYDIRAQRFL
			EERLSACYGSKPRLAGENLKLTTG\KGWLNHDETWRNYFSDIDF
	1		FPNAVYTHCYDSSGTKLFVAGGPLPSGLHGNYAGLWS
5960	2853	870	FVWSDGGPRPRRGPAVGAGAAHLSDPWAMTPGTANRATNPLNKE
2,500	1 2000	1	LDWASINGFCEQLNEDFEGPPLATRLLAHKIQSPQEWEAIQALT
	İ		VLETCMKSCGKRFHDEVGKFRFLNELIKVVSPKYLGSRTSEKVK
l			NKILELLYSWTVGLPEEVKIAEAYQMLKKQG\IVKSDPKLPDDT
1			
		•	TFPLPPPRPKNVIFEDEEKSKMLARLLKSSHPEDLRAANKLIKE
	Į.	ł	MVQEDQKRMEKISKRVNAIEEVNNNVKLLTEMVMSHSQGGAAAG
	l		SSEDL\MKEL\YQRCERMRPTLFPTGRVDTEDND\EALAEILQA
	I		NDNLTQVINLYKQLVRGEEVNGDATAGSIPGSTSALLDLSGLDL
l	•	Į	PPAGTTYPAMPTRPGEQASPEQPSASVSLLDDELMSLGLSDPTP
1	ļ	1	PSGPSLDGTGWNSFQSSDATEPPAPALAQAPSMESRFPAQTSLP
1	1	ł	ASSGLDDLDLLGKTLLQQSLPPESQQVRWEKQQPTPRLTLRDLQ
ŧ .		ì	NKSSSCSSPSSSATSLLHTVSPEPPRPPQQPVPTELSLASITVP
ł	-]	1	LESIKPSNILPVTVYDQHGFRILFHFARDPLPGRSDVLVVVVSM
ł	1		LSTAPQPIRNIVFQSAVPKVMKVKLQPPSGTELPAFNPIVHPSA
1	j.	ŀ	ITOVLLLANPOKEKVRLRYKLTFTMGDQTYNEMGDVDQFPPPET
ł		1	-
	<u> </u>	<u> </u>	WGSL
5961	198	3147	SGEPRPEPGNMATCIGEKIEDFKVGNLLGKGSFAGVYRAESIHT
ļ			GLEVAIKMIDKKAMYKAGMVQRVQNEVKIHCQLKHPSILELYNY
[1	FEDSNYVYLVLEMCHNGEMNRYLKNRVKPFSENEARHFMHQIIT
1	ì	İ	GMLYLHSHGILHRDLTLSNLLLTRNMNIKIADFGLATQLKMPHE
1	1	1	KHYTLCGTPNYISPEIATRSAHGLESDVWSLGCMFYTLLIGRPP
}	1	1	FDTDTVKNTLNKVVLADYEMPTFLSIEAKDLIHQLLRRNPADRL
l	1	1	SLSSVLDHPFMSRNSSTKSKDLGTVEDSIDSGHATISTAITASS
i	1	1	STSISGSLFDKRRLLIGQPLPNKMTVFPKNKSSTDFSSSGDGNS
			FYTOWGNOETSNSGRGRVIQDAEERPHSRYLRRAYSSDRSGTSN
[SOSOAKTYTMERCHSAEMLSVSKRSGGGENEERYSPTDNNANIF
1	1	1	NFFKEKTSSSSGSFERPDNNQALSNHLCPGKTPFPFADPTPQTE
	1	[TVOOWFGNLQINAHLRKTTEYDSISPNRDFQGHPDLQKDTSKNA
	į.	I	WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF
1		i	GSDPLSEQSKTRGMEPPWGYQNRTLRSITSPLVAHRLKPIRQKT
l		1	KKAVVSILDSEEVCVELVKEYASQEYVKEVLQISSDGNTITIYY
]		1	PNGG/RGFPLA/DRPPSPT/DNISR/YSF/DNLPEKYWRKYQYA
l		1	SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVWFYDGVKI
l		ļ	HKTEDFIQVIEKTGKSYTLKSESEVNSLKEEIKMYMDHANEGHR
1		1	ICLALESIISEEERKTRSAPFFPIIIGRKPGSTSSPKALSPPPS
1			VDSNYPTRDRASFNRMVMHSAASPTQAPILNPSMVTNEGLGLTT
Į			TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGWATQ\LTSGAVW
f		1	VQFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENEKLPDYIKQ
ł		1	
		<u> </u>	KLQCLSSILLMFSNPTPNFH
5962	20	2447	RVCSSSASTASQAVMADAWEEIRRLAADFQRAQFAEATQRLSER
ļ	1	i	NCIEIVNKLIAQKQLEVVHTLDGKEYITPAQISKEMRDELHVRG
l	1	1	GRVNIVDLQQVINVDLIHIENRIGDIIKSEKHVQLVLGQLIDEN
1		1	YLDRLAEEVNDKLQESGQVTISELCKTYDLPGNFLTQALTQRLG
Į.		1	RIISGHIDLDNRGVIFTEAFVARHKARIRGLFSAITRPTAVNSL
1	1	1	ISKYGFQEQLLYSVLEELVNSGRLRGTVVGGRQDKAVFVPDIYS
[Ţ	RTQSTWVDSFFRQNGYLEFDALSRLGIPDAVSYIKKRYKTTQLL
I.	1	i.	*** *** * * * * * * * * * * * * * * *

	SEQ	Predicted	Predicted end	Dring
	αı	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
٠		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
		amino acid	residue of	S=Serine, T=Threonine, V=V=line
ı		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Ctom
ı		amino acid	sequence	Codon, /=possible nucleotide deletion
ł		- seducince		\=possible nucleotide insertion)
1			ļ	PLKAACVGQGLVDQVEASVEEAISSGTWVDIAPLLPTSLSVEDA
- 1				AILLQQVMRAFSKQASTVVFSDTVVVSEKF\INDCTELFRELMH
-				QKAEKEMKNNPVHLITEEDLKQISTLESVSTSKKDKKDERRRKA
ı				TEGSGSMRGGGGGNAREYKIKKVKKKGRKDDDSDDESQSSHTGK KKPEISFMFQDEIRDFLRKHIQDAPEEFISELAEYLIKPLNKTY
١				LEVVRSVFMSSTTSASGTGRKRTIKDLQEEVSNLYNNIRLFEKG
-				MKFFADDTQAALTKHLLKSVCTDITNLIFNFLASDLMMAVDDPA
-1				AITSEIRKKILSKLSEETKVALTKLHNSLNEKSIEDFISCLDSA
1		1		AEACDIMVKRGDKKRERQILFQHROALAEOLKVTEDPALTLHLT
1				SVLLFQFSTHSMLHAPGRCVPOI IAFLNSKIPEDOHALLVKVOC
1				LVVKQLVSQSKKTGQGDYPLNNELDKEQEDVASTTRKELOELSS
ŀ	5963	62		SIKDLVLKSRKSSVTEE
		"2"	1130	PWNPQDFPGNRGLMG\QKGEIGPP\GQQGKKGAPGMP\GLMGSN
1		1		GSPGQPGTPGSKGSKGEPGIQGMPGASGLKGEPGATGSPGEPGY
-			•	MGLPGIQGKKGDKGNQGEKGIQGQKGENGRQGIPGQQGIQGHWG AKGERGEKGEPGVRGAIGSKGESGVDGLMGPAGPKGQPGDPGPQ
				GPPGLDGKPGREFSEQFIRQVCTDVIRAQLPVLLQSGRIRNCDH
1		,		CLSQHGSPGIPGPPGPIGPEGPRGLPGLPGRDGVPGLVGVPGRP
				GVRGLKGLPGRNGEKGSOGFGYPGEOGPPGPPGPEGPGTCVPG
				PPGDPGLPGKDGDHGKPGIQGQPGPPGICDPSLCFSVIARRDPF
+	5964	3		RKGPNY
1	2204	3	2147	SCRTRGRLSPLQPREAGSSRGSRARSEPPRFGGMEEACQVQTTK
1				RGDPHELRNIFLQYASTEVDGERYMTPEDFVQRYLGLYNDPNSN
				PKIVQLLAGVADQTKDGLISYQEFLAFESVLCAPDSMFIVAFQL
1				FDKSGNGEVTFENVKEIFGQTIIHHHIPFNWDCEFIRLHFGHNR KKHLNYTEFTQFLQELQLEHARQAFALKDKSKSGMISGLDFSDI
				MVTIRSHMLTPFVEENLVSAAGGSISHQVSFSYFNAFNSLLNNM
				ELVRKIYSTLAGTRKDAEVTKEEFAQSAIRYGQATPLEIDILYQ
1				LADLYNASGRLTLADIERIAPLAEGALPYNLAELOROOSEGICE
				PIWLQIAESAYRFTLGSVAGAVGATAVYPIDIVKTRMONOPGSG
	ſ			SVVGELMYKNSFDCFKKVLRYEGFFGLYRGLTPOLTGVARRYAT
1		1		KLTVNDFVRDKFTRRDGSVPLPAEVLAGGCAGGSOVTETMDLE:
1	1			VKIRLQVAGEITTGPRVSALNVLRDLGIFGLYKGAKACFLRDIP
ı	1	1		FSAIYFPVYAHCKLLLADENGHVGGLNLLAAGAMAG\VPAASLV TPADVIKTRLQVAARAGQTTYSGVIDCFRKIL\REEGPSAFWKG
1				TAARVFRSSPQFG\VTLVTYELLQRGPYIDFGGLKPAGSEPTPK
1	ļ			SRIADLPPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPSVA
L				VVQPKAAVAATQ
	5965	1	1498	MVTWLYRFLPTSNMAAKLRSLLPPDLRLQFWLHARLQKCFLSRG
	l			CGSYCAGAKASPLPGKMAMGLMCGRRELLRLIOSGRRVHSVAGD
	j	ľ		SQWLGKPLTTRLLFPAAPCCCRPHYLFLAASGPRSI.STSATERA
		J		EVQVQAPPVVAATPSPTAVPEVASGETADVVOTAAEOSFAFI.GI.
	1		ı	GSYTPVGLIQNLLEFMHVDLGLPWWGAIAACTVFARCLIFPLIV
	l	1	ł	TGQREARIHNHLPEIQKFSSRIREAKLAGDHIEYYKASSEMAL YQXKHGIKLYKPLILPVTQAPIFISFFIALREMANLPVPSLQTG
ĺ	İ			GLWWFQDLTVSDPIYILPLAVTATMWAVLELGAETGVQSSDLQW
	- 1			MRNVIRMMPLITLPITMHFPTAVFMYWLSSNLFSLVQVSCLRIP
ĺ	1		ĺ	AVRTVLKI PQRVVHDLDKLPPREGFLESFKKGWKNAEMTROT.PF
			İ	REQRMRNQLELAARGPLRQTFTHNPLLOPGKDNPPNIPSS\SSS
\vdash	5966	102		SSKPKSKYPWHDTLG
Ì		102	1925	RSKQVMARLTKRRQADTKAIQHLWAAIEIIRNQKQIANIDRITK
	1			YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGTEOR
				GYWLPGDEIDWETENHDWYCFECHLPGEVLICDLCFRVYHSKCL
	1	Ì		SDEFRLRDSSSPWQCPVCRSIKKKNTNKQEMGTYLRFIVSRMKE
	1	1		RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYEE PKADAOLLLHWTVLFYCADGEOADLADM YVDTGYTT
		ļ		FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC KNCFYLANARPDNWFCYPCIPNHELDWAKMKGFGFWPAKVMQKE
	1	ļ	1	DNQVDVRFFGHHHQRAWIPSENIQDITVNIHRLHVKRSMGWKKA
	1			CDELELHQRFLREGRFWKSKNEDRGEEEABSSISSTSNEQLKVT
]			QEPRAKKGRRNQSVEPKKEEPEPETEAVSSSOEIPTMPOPTEKV
				SVSTOTKKLSASSPRMLHRSTOTTNDGVCQSMCHDKYTKIFNDF

Deginning nucleotide location corresponding corresponding corresponding corresponding to first amino acid amino acid residue of residue of amino acid amino acid residue of amino acid residue of amino acid residue of residue of amino acid residue of residue o	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO: nucleotide location corresponding to first amino acid amino acid amino acid amino acid apquence property amino acid apquence amino acid apquence amino acid apquence amino acid apquence amino acid apquence amino acid apquence amino acid apquence amino acid apquence amino acid apquence amino acid apquence amino acid apquence amino acid apquence amino acid apquence amino acid apquence amino acid apquence amino acid apquence amino acid apquence amino acid apquence amino acid apposition amino acid acid amino acid acid amino acid acid acid acid acid acid acid acid				(A=Alanine, C=Cvsteine, D=Aspartic Acid F-
corresponding co first amino acid corresponding co first amino acid cesidue of amino acid cesidue of amino acid sequence corresponding co first cesidue of amino acid sequence cocon,	}			
to first amino acid residue of amino acid residue of amino acid sequence Perciane, Oscilutamine, R-Arginine, S-Serine, T-Threonine, V-Valine, amino acid sequence Codon, /=possible nucleotide deletion, -possible nucl				
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid sequence sequenc	1			
amino acid residue of amino acid sequence sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence SEMMASDHAREJERVVERALEKIRSEMEERSGANNKANANNOG EMDRAKGOVERCHERKINSEMEERSGANNKANANNOG SEMMASDHAREJERVVERALEKIRSEMEERSGANNKANANNOG SEMMASDHAREJERVVERALEKIRSEMEERSGANNKANANNOG SERAMYLCONNISYCSIKCOGEMMABHARETCRERK SERAMYLCONNISYCSIKCOGEMMABHARETCRERK SERAMYLCONNISYCSIKCOGEMMABHARETCRERK SERAMYLCONNISYCSIKCOGEMMABHARETCRERK SERAMYLCONNISYCSIKCOGEMMABHARETTARTY YMSRVMGMHARETTRQUSLANKOGLIVETILVUCKGSKAGIFQE SERAMYLCONNISYCSIKCOGEMMABHARETTARTY SEPRALDISSSOMGCVCGSIKKRNINKGEMSTITRFIVSRNKE RAIDLANKORKOKNENDHYMRILMSANGGILVETILVUCKGSKAGIFQE FRADDAGLLIGHTVIFYGADSGADIRGMINSTUTETIVSRNKE SEDEFALBUSSSOMGCVCGSIKKRNINKGEMSTITRFIVSRNKE RAIDLANKORKOKNENDHYMRILMSANGGALIVETILVUSKASSE FRADDAGLLIGHTVIFYGADSGADIRGMINSTUTETIVSRNKEN SETAMYLCONNISYCSIKCOGEMMABHARENGSGRIPMPOPISKY SUSTOTIKKLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKKLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKKLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKKLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKKLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKKLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKKLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKKLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKKLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKKLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKKLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKKLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKKLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKKLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKKLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKCLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKCLSASSPRMLIRSTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKCLSASSPRMLINGTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKCLSASSPRMLINGTOTINDUCCOSMCHDKYTKIFDDY SUSTOTIKCLSASSPRMLINGTOTINDUCCOSMCHDKYTKIFDY SUSTOTICATION SUSTOTICATION SUSTOTICATION SUSTOTICATION SUSTOTICATION SUSTOTICATION SUSTOTICATION SUSTOTICATION				
xesidue of amino acid sequence (Codon, *possible nucleotide deletion) (Codon, *possible nucleotide deletion) (Codon, *possible nucleotide deletion) (Codon, *possible nucleotide deletion) (Codon, *possible nucleotide deletion) (Codon, *possible nucleotide insertion) (Codon, *possible nu	1			
amino acid sequence	1			
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FKELFSSSPSKIYGRALEKCRSHPEVIGYGGEVKGYGEVTRR GRRQHVRFTEYVKDGIKHTCVKFYIEGSEPGKGTVAQVKENP GSGEYDFRYIFVEIESYPRRTIIIEDNRSQDD 5970 316 4712 SQDNIGHRLLQKHGWKLGQGIGKSLQGRTDPIPIVVKYDVMGMG RMEMELDYAEDATERRRVLEVEKEDTEELRQKYKDYVDKEKAIA KALEDLRANFYCELCDKQYQKHQEFDNHINSYDHAHKQRLKDLK QREFARNVSSRSKDEKKQEKALRRLHBLAEQRKQAECAPGSGP MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSFSTDKG GFPTAVQITNTTGLAQAPGLASQGISFGIKNLIHTPLQKLGVSF SPAKKAPVKLESIASVFKDHABEGTSEDGTKPDEKSSDQGLQKV GDSDGSSNLDGKKEDEDPQDCGSLASTLSKLKRMKREEGAGATE PEYYHYIPPAHCKVKPNFPFLLFMRASEQMUGDNTHPKNAPES KKGSSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA GKESQEGPKHPTGFPVLSKDESTALQWFSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE PKKSKEVGGEKLVRSSGGRMDAPAGGSACSGLMKQEFGGSHGSE TEDTGRSLPSKKERSCKSHRHKKKKKKKKSKHKKKATDTEKK SSKAESGEKSKKRKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	5969	1126	503	
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GSGEYDFRYIFVEIESYPRRTILIEDRSQDD 5970 316 4712 SQDNIGHRLLQKHGWKLGGLGKSLQGRTDFIPIVVKYDVMGMG RMEMELDYAEDATERRVLEVEKDTEELROKYKDYVDKEKAIA KALEDLRANFYCELCDKQYQKHQEFDNHINSYDHAHKQRLKDLK QREFARRVSSRSRKDEKKQEKALRRHHBLAEQRKQAECAPGSGP MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSEFSTDKG GPFTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF SPAKKAPVKLESIASVFKDHAEEGTSEDGTKPDEKSSDQGLQKV GDSDGSSNLDGKKEDEDPDQGGSLASTLSKLKRMKREGAGATE PEYYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES KKGSSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA GKESQEGFKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS YSCNPLVFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKERSGKSHRHKKKKKKKSKHKKASKHKADTEEK SSKAESGEKSKKRKKKRKKKKKKKKKKKKSKHKKADTEKK SSKAESGEKSKKRKKKRKRKKKKHKKSSAPADSERGPKPEPPGSGSPA PPRRRRAQDDSQRRSLPAEEGSSGKKDEGGGSSSODHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDDDDASSHRLHQ KSPSQYSEEEEEEDSGSEHSRSRSGRRHSHRSSRSSYSSSS DASSDQSCYSRGRSYSDDS YSDYSDRSRHSKKSHDSDDDSYAS SKHRSKRHKYSSSDDDYSLSCSGSRSRSRHTRERSRSGRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSDRSRTRSPSQRSGR KRSWGHESPEEHISGRRDF IRSKIYRSQSPHYFRSGRGEGFGKK DDCRGDDSKATGPPSQNSNIGTGRGSEEDCSPEDMNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPPLIGKLPATRKPNKCEESGLERGEGQEGSETERGPP GSSDALFGHQPP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG				
SQDNIGHRLLQKHGWKLGQGLGKSLQGRTDPIPIVVKYDVMGMG RMEMELDYAEDATERRRVLEVEKEDTEELRQKYKDYVDKEKAIA KALEDLRAMFYCELCDKQYQKHQEFDHHINSYDHAHKQRLKDLK QREFARNVSSRSRKDEKKQEKALRRLHBLAEQRKQAECAPGSGP MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSEFSTDKG GPFTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF SPAKKAPVKLESIASVFKDHABEGTSEDGTKPDEKSSDQGLQKV GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE PETYHYIPPAHCKVKPNFPFLLFMRASCQMBGDNTTHPKNAPES KKGSSPKPKSCIKAAASQGASKTVSEVSEOPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA GKESQEGFKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE PKKSKEVGGEKIVRSSGGMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKHKKSSKHKRKHKADTEEK SSKAESGEKSKKKRKKKKKKKKKKKKKKKKKKKKKKKKHKADTEEK SSKAESGEKSKKRKKKKKKSSAPADSERGPKPEPPGSGSPA PPRRRRAQDDSQRSLPABEGSSGKKDEGGGGSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSRRSGRRHSSHRSSRSYSSSS DASSDQSCYSRQRSYSDDSYSDVSDRSRRHSKRSHDSDDSDYAS SKHRSKHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSGRSRS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSGRSRS SSCSRSRSKRRSRSTTAHSWQRSRSYSDDRSRTRSPSQRSGSR KRSWGHESPERHSGRRDFIRSKIYRSQSPHYFRSGRGEGFGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGERQSETEEGPP GSSDALFGHQFF\SEETTGPLLDPPPEESKSGEVTADHPVAPLG	1		•	GRRQHVRFTEYVKDGLKHTCVKFYIEGSEPGKQGTVYAQVKENP
REMELDYAEDATERRVLEVEKEDTEELRQKYKDYVDKBKAIA KALEDLRANFYCELCDKQYCKHQEFDNHINSYDHAHKQRLKDLK QREFARNVSSRSRKDEKKQEKALRRLHELAEQRKQAECAPGSGP MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSEFSTDKG GPFTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF SFAKKAPVKLESIASVFKDHAEEGTSEDGTKPDEKSSDQGLQKV GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE PETYHY1PPAHCKVKNPNFPFLLFMRASEQMBGDNTTHPKNAPES KKGSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA GKESQEGPKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE PKKSKEVGGEKIVRSSGGRMDPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKKKKKSKHKKADTEEK SSKAESGEKSKKRKKRKRKKKKKKKKKKKKKKKKHAHADTEEK SSKAESGEKSKKRKKRKRKKKKKKKKKKKKKKKHQEKPEPPGSGSPA PPRRRRAQDDSQRRSLPAEGGSGKKDEGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDASSHRLHQ KSPSQYSEEEEEDGSEHSRSRSRSRRSRSTSSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHISKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRHTRERSRSRSSS SCSRSRSKRRSRSTTAHSWQRSRSYSDDSRSTRSPSQRSGSS KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPBDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEGRGSETEEGPP GSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG			}	GSGEYDFRYIFVEIESYPRRTIIIEDNRSQDD
KALEDLRANFYCELCDKQYQKHQEFDNHINSYDHAHKQRLKDLK QREFARNVSSRSKKDEKKQEKALRIHELAEQRKQAECAPGSGP MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSEFSTDKG GFPTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF SPAKKAPVKLESIASVFKDHAEEGTSEGTKPDEKSSQDQGLQKV GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE PEYTHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES KKGSSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQRVSETQMCESNSSKETSLATPA GKESQEGPKHPTGPFFPVLSKDESTALQWFSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKKKKKSKHRKHKADTEEK SSKAESGEKSKKRKKRKKKKKKKKKKKKADTEEK SSKAESGEKSKKRKKRKKKKKKKKKKKBAPADSERGPKPEPPGSGPA PPRRRRAQDDSQRRSLPAEEGSSGKKDEGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSHRSQPSSGDEDSDDASSIRLHQ KSPSQYSEEEEEDSGSEHSRSRSRRHSSHRSSRSYSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSHTRERSRSRSSS SCSRSRSKRRSRSTTAHSWQRSRSYSDRSRSTTRSPSQRSGR KRSWGHESPEERHSGRRDFIRSKITRSQSPHYFRSGGEGFGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPBKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLDATKRPNKKCESGLERGEDQCGSETEEGPP GSSDALFGHQFP\SEETTGPLLDPPPBERSKSGEVTADHPVAPLG	5970	316	4712	SQDNIGHRLLQKHGWKLGQGLGKSLQGRTDPIPIVVKYDVMGMG
QREFARNVSSRSKKDEKKQEKALRRLHELAEQRKQAECAPGSGP MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSEFSTDKG GPFTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF SFAKKAPVKLESIASVFKDHAEEGTSEDGTKPDEKSSDQGLQKV GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE PETYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES KKGSSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA GKESQEGPKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDARTKGTERPKDIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKKKKSKHKKADTEEK SSKAESGEKSKKRKKRKKKKKKKKKKKKKKKKKKKADTEEK KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDDASSHRLHQ KSPSQYSEEEEEDSGSEHSRSRSRSGRSHSTRSSRSYSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRTHRESRRSRGSRS SCSRSKKRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIVRSQSPHYFRSGREGFGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRVERKPSVSEEVQATPNKAGPKLKDPPQGYFFGFKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEQESTEEGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGVTADHPVAPLG GSSDALFGHQFP\SEETTGPLLDPPPEESKSGVTADHPVAPLG	1	ì	1	RMEMELDYAEDATERRRVLEVEKEDTEELRQKYKDYVDKEKAIA
MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSEFSTDKG GFFTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF SPAKKAPVKLESIASVFKDHAEEGTSEDGTKPDEKSSDQGLQKV GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE PEYYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES KKGSSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSKETSLATPA GKESQEGPKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKHKKSSKHKRHKADTEEK SSKAESGEKSKKKKKKKKKKKKKKKKKSAPADBERGPKPEPPGSGSPA PPRRRRAQDDSQRRSLPAEGSSGKKDEGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSHRSQPSSGDEDSDDASSHRLHQ KSPSQYSEEEEEEDSGSEHSRSRSRSGRRHSSHRSSRSYSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQRRSRSHTRERSRRSRSRS SSCSRSRSKRRSSTTAHISWQRSRSYSDRSRSTRSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGREGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYTGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEBQEQESETEBGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG)	}	1	KALEDLRANFYCELCDKQYQKHQEFDNHINSYDHAHKQRLKDLK
GPFTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF SPAKKAPVKLESIASVFKOHABEGTSEDGTKPDEKSSDQGLQKV GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKMKREEGAGATE PEYYHYI PPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES KKGSSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA GKESQEGPKHFTGPFFPVLSKDESTALQWFSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKKKKSKHKKADTEEK SSKAESGEKSKKKKKRKKKKKKKKKKKKKKKKKKHKADTEEK SSKAESGEKSKKKKKRKKKKKKKSAPADSERGPKPEPPGSGSPA PPRRRRAQDORRSLPAEGSSGKKDEGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHQ KSPSQYSEEEEEEDSGSEHSRSRSGRRHSSHRSSRSSSSSDDMSSDYSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSHTRERSRSRGRSRS SSCSRSRKRRSSSTTAHSWQRSRSYSRDRSRSTRSPSQRSGR KRSWGHESPEERHSGRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEBQEQSETEBGPP GSSDALFGHQFF\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGFVESSL	1	ļ	•	QREFARNVSSRSRKDEKKQEKALRRLHELAEQRKQAECAPGSGP
SPAKKAPVKLESIASVFKDHABEGTSEDGTKPDEKSSDQGLQKV GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE PEYYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES KKGSSPKPKSCIKAAASQGEKTVSEVSEQPKETSMTEPSEPGS KABAKKALGGDVSDQSLBSHSQKVSETQMCESNSSKETSLATPA GKESQEGPKHPTGPPFPVLSKDESTALQWPSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGRMDAPAGGACSGLNKQEPGGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKKKKKKKADTEEK SSKAESGEKSKKKRKRKKKKKKKKKKKKKKKADTEEK SSKAESGEKSKKKRKRKKKKKKKKKKKKKADTEEK KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHQ KSPSQYSEEEEEEDGSEHSRSRSRSGRRHSSHRSSRSYSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHRSDRSYSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSHSHTRERSRSGRSRS SCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRTTSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPGGTGFKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEQEQSETEBGPP GSSDALFGHQFF\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQFGVESSL	İ		\$	MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSEFSTDKG
GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE PEYYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES KKGSSPKPKSCIKAAASQGAEKTVSEVSEDPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA GKESQEGPKHPTGPFFPVLSKDESTALQWFSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKKKKKSSKHKKKADTEEK SSKAESGEKSKKRKKRKKKKKKKKKSSKHKKKADTEEK SSKAESGEKSKKRKKRKKNKSSAPADSERGPKPEPPGSGSPA PPRRRRAQDDSQRRSLPAEGSSGKKDEGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHQ KSPSQYSEEEEEDSGSEHSRSRSGRRHSSHRSSRSYSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHKKSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRHTRERSRRGRSRS SCSRSKRRSSTTAHSWQRSRSYSDRSRSTTSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPBDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEQEQESETEBGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGFVESSL	ŀ		1	GPFTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF
GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE PEYYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES KKGSSPKPKSCIKAAASQGAEKTVSEVSEDPKETSMTEPSEPGS KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA GKESQEGPKHPTGPFFPVLSKDESTALQWFSELLIFTKAEPSIS YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGSHGSE TEDTGRSLPSKKERSGKSHRHKKKKKKKKKSSKHKKKADTEEK SSKAESGEKSKKRKKRKKKKKKKKKSSKHKKKADTEEK SSKAESGEKSKKRKKRKKNKSSAPADSERGPKPEPPGSGSPA PPRRRRAQDDSQRRSLPAEGSSGKKDEGGGSSSQDHGGRKH KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHQ KSPSQYSEEEEEDSGSEHSRSRSGRRHSSHRSSRSYSSSS DASSDQSCYSRQRSYSDDSYSDYSDRSRRHKKSHDSDDSDYAS SKHRSKRHKYSSSDDDYSLSCSQSRSRSRHTRERSRRGRSRS SCSRSKRRSSTTAHSWQRSRSYSDRSRSTTSPSQRSGSR KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPBDKNSVTAKLLL EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS LGNKPVLPLIGKLPATRKPNKKCEESGLERGEQEQESETEBGPP GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGFVESSL	1	1	1	SFAKKAPVKLESIASVFKDHAEEGTSEDGTKPDEKSSDQGLQKV
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1	•		NDKLYLYLQLPSGPTTGDKSSEPSTLSNEEYMYAYRWIRNHLEE
Ì			HTDTCLPKQSVYDAYRKYCESLACCRPLSTANFGKIIREIFPDI
}			KARRLGGRGQSKYCYSGIRRKTLVSMPPLPGLDLKGSESPEMGP
1]		EVTPAPRDELVEAACALTCDWAERILKRSFSSIVEVARFLLQQH
1	1		LISARSAHAHVLKAMGLAEEDEHAPRERSSKPKNGLENPEGGAH
	1		KKPERLAQPPKDLEARTGAGPLARGERKKSVVESSAPGANNLQV
ļ	1		NALVARLPLLLPRAPRSLIPPIPVSPPILAPRLSSGALKVATLP
l	[ĺ	LSSRAGAPPAAVPIINMILPTVPALPGPGPGPGRAPPGGLTQPR
1	1		GTENREVGIGGDQGPHDKGVKRTAEVPVSEASGQAPPAKAAKQD
	1		IEDTASDAKRKRGRPLKKSGGSGERNSTPLKSAAAMESAQSSRL
j	1 1	,	PWETWGSGGEGNSAGGAERPGPMGEAEKGAVLAQG\QGDGTVSK
	1	4	GGRGPGSQHTKEAEDKIPLVPSKVSVIKGSRSQKEAFPLAKGEV
5974	4293	2200	DTAPOGNKDLKEHVLQSSLSQEHKDPKATPP
		2200	LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK\BID
	1 1	Į.	LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRR
		j	TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQONGSV\S
			DISPVQAAKKEFGPPSRRKSNCVKEVEKT OF KREKRRI OOOFI D
			EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPI,TTADPIDEURIC
		i i	VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKOKUDI.TPVT
	1	1	ENQTFRFDYAFDDSAPNEMVYRFTARPLVETTFERGMATCRAVC
	1	į.	QTGSGKTHTMGGDFSGKNODCSKGIYALAARDVFT.MI.KVDNVVV
	1		LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKOOVOVGLOR
	1		REVKCVEDVLKLIDIGNSCRTSGOTSANAHSSRSHAVFOLLER
	1	1	KGKLHGKFSLIDLAGNERGADTSSADROTRLEGAEINKSLLALK
	1	j	ECIRALGRNKPHTPFRASKLTOVLRDSFIGENSRTCMIATISDG
	1	! !	MASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHHPPMOT\ DD
			LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQMVEM

			·
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Sequence	\=possible nucleotide insertion)
	sequence		EEOVVEDHRAVFQESIRWLEDEKALLEMTEEVDYDVDSYATQLE
Ì	1	}	AILEOKIDILTELRDKVKSFRAALQEEEQASKQINPKRPRAL
L			
5975	4293	2200	LGLOMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK\EID
)]	ļ	LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRR
ļ	Į.		TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNGSV\S
ł			DISPVQAAKKEFGPPSRRKSNCVKEVEKLQEKREKRRLQQQELR
	Į.		EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDEHRIC
ì		'	VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDLTRYL
			ENOTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATCFAYG
	1	[OTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKK
Į		1	LELOVYATFFEIYSGKVFDLINRKTKLRVLEDGKQQVQVVGLQE
1			REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR
1	ı	1	KGKLHGKFSLIDLAGNERGADTSSADRQTRLEGAEINKSLLALK
!	l	ļ.	
j .	ĺ	Į.	ECIRALGRNKPHTPFRASKLTQVLRDSFIGENSRTCMIATISPG
1	l .	1	MASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHHPPNQI\DD
	l		LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQMVEM
i	ļ		EEQVVEDHRAVFQESIRWLEDEKALLEMTEEVDYDVDSYATQLE
ì			AILEQKIDILTELRDKVKSFRAALQEEEQASKQINPKRPRAL
5976	20	2949	VHHLHLTRVSVVVNLDIILRIAQQMGIKTLNLVLG\LKRA\LEF
1	(PEVSWMEVKDPNMKGAMLTNTGKYAIPTIDA\EAYAIGKKEKPP
1		1	FLPEEPSSSSEEDDPIPDELLCLICKDIMTDAVVIPCCGNSYCD
1	İ	Į.	BCIRTALLESDEHTCPTCHQNDVSPDALIANKFLRQAVNNFKNE
1		Į.	TGYTKRLRKOLPSPPPPIPPPRPLIQRNLQPLMRSPISRQQDPL
į	1	ł	MIPVTSSSTHPAPSISSLTSNQSSLAPPVSGNPSSAPAPVPDIT
į.	1		ATVSISVHSEKSDGPFRDSDNKILPAAALASEHSKGTSSIAITA
1	ļ	ļ	LMEEKGYOVPVLGTPSLLGQSLLHGQLIPTTGPVRINTARPGGG
(1	1 '	RPGWEHSNKLGYLVSPPQQIRRGERSCYRSINRGRHHSERSQRT
l .	1	-	CGPSLPATPVFVPVPPPPLYPPPPHTLPLPPGVPPPQFSPQFPP
ļ.	1	1	
Į.	1	1	GQP\PPAGYSVPPGFPPAPANLSTPWVSSGVQTAHSNTIPTTQ
	1	1	APPLSREEFYREQRRLKEEEKKKSKLDEFTNDFAKELMEYKKIQ
ł	1	ł	KERRRSFSRSKSPYSGSSYSRSSYTYSKSRSGSTRSRSYSRSFS
1	1	i	RSHSRSYSRSPPYPRRGRGKSRNYRSRSRSHGYHRSRSRSPPYR
ì	1	1	RYHSRSRSPQAFRGQSPNKRNVPQGETEREYFNRYREVPPPYDM
			KAYYGRSVDFRDPFEKERYREWERKYREWYBKYYKGYAAGAQPR
1	1		PSANRENFSPERFI.PLNIRNSPFTRGRREDYVGGQSHRSRNIGS
1	1	}	NYPEKLSARDGHNQKDNTKSKEKESENAPGDGKGNKHKKHRKRR
1		1	KGEESEGFLNPELLETSRKSREPTGVEENKTDSLFVLPSRDDAT
1	1	1	PVRDEPMDAESITFKSVSEKDKRERDKPKAKGDKTKRKNDGSAV
1	1		SKKENIVKPAKGPQEKVDG\DVRDLLDLNL\QLKKPKEETPKDL
1		Ì	TILNHHLPLRRMKKSL\EPP\EKLTLNQQK\TPRNKTSQRGKSE
1		1	EGLFORCOIRKANN
5977	1363	1336	FLEDRGQVLSHFQCLSLHSINHILHPGAGVAAGPATGW/REYLT
33//	1 200	1336	PVLKESKFKETGVITPEEFVAAGDHLVHHCPTWQWATGEELKVK
1		ŀ	AYLPTGKQFLVTKNVPCYKRCKQMEYSDELEAIIEEDDGDGGWV
1		1	
1		l.	DTYHNTGITGITEAVKEITLENKDNIRLQDCSALCEEEEDEDEG
1		1	EAADMEEYEESGLLETDEATLDTRKIVEACKAKTDAGGEDAILQ
i		}	TRTYDLYITYDKYYQTPRLWLFGYDEQROPLTVEHMYEDISQDH
1		1	VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIETVAEGGGEL
1			GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM
5978	160	3213	RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEPAGRQ
1		1	RPRREPEAMDEQSVESIAEVFRCFICMEKLRDARLCPHCSKLCC
1	,	1	FSCIRRWLTEQRAQCPHCRAPLQLRELVNCRWAEEVTQQLDTLQ
1		1	LCSLTKHEENEKDKCENHHEKLSVFCWTCKKCICHQCALWGGMH
ĺ		1	GGHTFKPLAEIYEQHVTKVNEEVAKLRRRLMELISLVQEVERNV
		1	EAVRNAKDERVREIRNAVEMMIARLDTQLKNKLITLMGQKTSLT
1	}	1	EWAKIAWAREKAKETKIANA SEIRI TAKKIDI TAKKISTI TAKAKISTI
1			QETELLESLLQEVEHQLRSCSKSELISKSSEILMMFQQVHRKPM
1		1	ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP
1	1		LQVSGLCWRLKVYPDGNGVVRGYYLSVFLELSAGLPETSKYEYR
1		1	VEMVHQSCNDPTKNIIREFASDFEVGECWGYNRFFRLDLLANEG
1			YLNPQNDTVILRFQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ
1		1	INNLKERLTIELSRTQKSRDLSPPDNHLSPQNDDALETRAKKSA
		1	

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
-	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
			CSDMLLER/GPYSAS/VREAKEDEEDEEKIQNEDYHEELSDGDL
1			DLDLVYEDEVNQLDGSSSSASSTATSNTEENDIDEETMSGENDV
1			EYNNMELEEGELMEDAAAAGPAGSSHGYVGSSSRISRRTHLCSA
	1	ļ	ATSSLLDIDPLILIHLLDLKDRSSIENLWGLQPRPPASLLQPTA
1	1		SYSRKDKDQRKQQAMWRVPSDLKMLKRLKTQMAEVRCMKTDVKN
1	1		TLSEIKSSSAASGDMQTSLFSADQAALAACGTENSGRLQDLGME
1	i	1	LLAKSSVANCYIRNSTNKKSNSPKPARSSVAGSLSLRRAVDPGE
1	1		NSRSKGDCQTLSEGSPGSSQSGSRHSSPRALIHGSIGDILPKTE
ł	i	1	DRQCKALDSDAVVVAVFSGLPAVEKRRKMVTLGANAKGGHLEGL
i			QMTDLENNSETGELQPVLPEGASAAPEEGMSSDSDIECDTENEE
ſ	1.	1	QEEHTSVGGFHDSFMVMTQPPDEDTHSSFPDGEQIGPEDLSFNT
	[DENSGR
5979	212	3665	LPDMTMYLWLKLLAFGFAFLDTEVFVTGQSPTPSPTDAYLNASE
			TTTLSPSGSAVISTTTIATTPSKPTCDEKYANITVDYLYNKETK
1	[LFTAKLNVNENVECGNNTCTNNEVHNLTECKNASVSISHNSCTA
1			PDKTLILDVPPGVEKVPVHCCS\QVEQPDSTIWLKWKNIETSTC
			DTQNITYRFQCGNMIFDNKEIKLENLEPEHEYKCDSEILYNSHK
1	1		FTNASKIIKTDFGSPGEPQIIFCRSEAAHQGVITWNPPQRSFHN
Í			FTLCYIKETEKDCLNLDKNLIKYDLQNLKPYTKYVLSLHAYIIA
1	1		KVQRNGSAAMCHFTTKSAPPSQVWNMTVSMTSDNSMHVKCRPPR
ļ	1		DRNGPHERYHLEVEAGNTLVRNESHKNCDFRVKDLQYSTDYTFK
			AYFHNGDYPGEPFILHHSTSYNSKALIAFLAFLIIVTSTALLIN
	<u> </u>		LYKIYDLHKKRSCNLDEQQELVERDDEKOLMNVEPIHADILLET
1			YKRKIADEGRLFLAEFQSIPRVFSKFPIKEARKPFNONKNEVUD
		•	ILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYTAAOGDD
(i i		DETVDDFWRMIWEQKATVIVMVTRCEEGNRNKCAEYWPSMEEGT
			RAFGECCCKDLTKHKRCP\DYIIOKLNIVNKKEKATGREVTHIO
	1		FTSWPDHGVPEDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGP
1			TGTYIGIDAMLEGLEAENKVDVYGYVVKLRRORCLMVOVEAOVT
			LIHQALVEYNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAR
1			FQRLPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVPLKHE
1			LEMSKESEHDSDESSDDDSDSEEPSKYINASFIMSYWKP\EVMI
	j	•	AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWG
			EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ
1			YTNWSVEQLPAEPKELISMIQVVKQKLPQKNSSEGNKHHKSTPL
			LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP
1 1	'		GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD
1 . 1	1		KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS
5980	3	2363	
1	1		DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PERDLEVOENNEDA AHDLTEL BURNEUL LOUTEVAHQGNWETI
j /			PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQEIQEIRKYFSFP
j l		}	VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN
į į	ľ		CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN
[Į.		LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESIMN
	1		IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP
1	1		VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL
1	1	ľ	ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR
1		1	MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK
l l	1		SICSOFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK
]	[į	DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN
	[WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG
		!	SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL
		1	DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA
	1		MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK
		1	LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG
			DPLKRPLLGIVQPMLQGIMNRLCKS\NSEOPNRGLDDST
5981	1	2519	GRKHSAAMERPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRL
1			DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP
j		1	G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV
		_	ILVLTTFHVPLVIMTFGQSKLYRSEDYGKNFKDITDLINNTFIR
			· · · · · · · · · · · · · · · · · · ·

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
(to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TEFGMAIGPENSGKVVLTAEVSGGSRGGRIFRSSDFAKNFVQTD
ì			LPFHPLTQMMYSPQNSDYLLALSTENGLWVSKNFGGKWEEIHKA
1	}		VCLAKWGSDNTIFFTTYANGSCKADLGALELWRTSDLGKSFKTI
Ì	1	1	GVKIYSFGLGGRFLFASVMADKDTTRRIHVSTDQGDTWSMAQLP
i			SVGQEQFYSILAANDDMVFMHVDEPGDTGFGTIFTSDDRGIVYS
!		1	KSLDRHLYTTTGGETDFTNVTSLRGVYITSVLSEDNSIQTMITF
•			DQGGRWTHLRKPENSECDATAKNKNECSLHIHASYSISQKLNVP
ł			MAPLSEPNAVGIVIAHGSVGDAISVMVPDVYISDDGGYSWTKML
1			EGPHYYTILDSGGIIVAIEHSSRPINVIKFSTDEGQCWQTYTFT
1]	1	RDPIYFTGLASEPGARSMNISIWGFTESFLTSQWVSYTIDFKDI
!			LERNCEEKDYTIWLAHSTDPEDYEDGCILGYKEQFLRLRKSSVC
1			QNGRDYVVTKQPSICLCSLEDFLCDFGYYRPENDSKCVEQPELK
	1		GHDLEFCLYGREEHLTTNGYRKIPGDKCQGGVNPVREVKDLKKK
1			CTSNFLSPEKQNSKSNSVPIILAIVGLMLVTVVAGVLIVKKYVC
1			GGRFLVHLYSVLQQH\AEA\NGVDGVDALDTASHTNKSGYHDDS
			DEDLLE
5982	56	2316	ATRPPRGSSWCRQFSRTASAAPGRSNMLRIPVRKALVGLSKSPK
ł			GCVRTTATAASNLIEVFVDGQSVMVEPGTTVLQACEKVGMQIPR
Ì		Í	FCYHERLSVAGNCRMCLVEIEKAPKVVAACAMPVMKGWNILTNS
İ	-	i	EKSKKAREGVMEFLLANHPLDCPICDQGGECDLQDQSMMFGNDR
1	1	1	SRFLEGKRAVEDKNIGPLVKTIMTRCIQCTRCIRFASEIAGVDD
1	1		LGTTGRGNDMQVGTYIEKMFMSELSGNIIDICPVGALTSKPYAF
i	1	Í	TARPWETRKTESIDVMDAVGSNIVVSTRTGEVMRILPRMHEDIN
1	1		EEWISDKTRFAYDGLKRQRLTEPMVRNEKGLLTYTSWEDALSRV
	İ	1	AGMLQSFQGKDVAAIAGGLVDAEALVALKDLLNRVDSDTLCTEE
ł		1	VFPTAGAGTDLRSNYLLNTTIAGVEEADVVLLVGTNPRFEAPLF
1	1	1	NARIRKSWLHNDLKVALIGSPVDLTYTYDHLGDSPKILQDIASG
i			SHPFSQVLKEAKKPMVVLGSSALQRNDGAAILAAVSSIAQKIRM
Į.	1	1.	TSGVTGDWKVMNILHRIASQVAALDLGYKPGVEAIRKNPPKVLF
1	İ	1	LLGADGGCITRQDLPKDCFIIYQGHHGDVGAPIADVILPGAAYT
l	1	i	EKSATYVNTEGRAQQTKVAVTPPGLAREDWKIIRALSEIAGMTL
1	}	1	PYDTL\DQVRNRLEEVSPNLVRYDDIEG\ANYFQQANELSKLVN
1	1	1	QQLLADPLVPPQLTMKDFYMTDSISRASQTMAKCVKAVTEGAQA
l	1		VEEPSIC
5983	248	1763	EARGDGGRRHRASGRRAGRGEP\AGLKSQGQRAVPKRAVARGG
1	Ì	1	RQ\YSAAIALLEPAGSEIADDLSILYSNRAACYLKEGNCSGCIQ
i			DCNRALELHPFSMKPLLRRAMAYETLEQYGKAYVDYKTVLQIDC
1			GLQLANDSVNRLSRILMELDGPNWREKLSLIPAVPASVPLQAWH
1	1	1	PAKEMISKQAGDSSSHRQQGITDEKTFKALKBEGNQCVNDKNYK
1			DALSKYSECLKINNKECAIYTNRALCYLKLCQFEEAKQDCDQAL
1			QLADGNVKAFYRRALAHKGLKNYQKSLIDLNKVILLDPSIIEAK
1	1	1	MELEEVTRLLNLKDKTAPFNKEKERRKIEIQEVNEGKEEPGRPA
		1	GEVSTGCLASEKGGKSSRSPEDPEKLPIAKPNNAYEFGQIINAL
i		1	STRKDKEACAHLLAITAPKDLPMFLSNKLEGDTFLLLIQSLKNN
			LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL
			SDTPNNHFTLEDIQALKRQYEL
5984	755	1193	SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSFVL
1	1	1	TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG
ı		1	SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVPTMY
1			FHHSLRSISRFSSG
5985	22	1408	RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR
1			RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE
			FAVEYFTRLREARAPASVLPAATPRQSLGHPPPEPGPDRVADAK
1			GDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEEEEDTDPRVI
j		1	HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD
1			EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG
1			ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM
			FESFIESVPLLKSLEVSERMKIVDVIGBKIYKR/DGERIITQGE
			K\ADSFYIIESGEVSILIRSRTKSNKDGGNQEVEIARCHKGQYF
			GELALVINKPRAASAYAVGDVKCLVMDVQAFERLLGPCMDIMKR
1			nishyeeqlvkmfgssvdlgnlgq

_	SEQ	Predicted		
- 1	ID		Predicted end	
- 1	NO:	beginning	nucleotide	I MARKET CECVSCRINE DENOMERO NELL SELLES
- 1	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- 1		corresponding	to first	L-Louging, 1=1Soleucine, K=Lysine,
		to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ı		amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
- 1		residue of		S=Serine, T=Threonine, V=Valine,
		amino acid	amino acid	W=Tryptophan, Y=Tyrosine Y=Unknown + Cha-
- 1			sequence	Couon, /=possible nucleoride deletion
<u> </u>		sequence	_1	\=possible nucleotide insertion)
- '	5986	1806	484	DAWKSTSLTFHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP
- 1			1	SPCCRFDSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPMEED
- 1		J	1	GLEWIT DE COLLEGE DE C
1		I		GLRWTPKSPLDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASI
Ì				LISNVCS IGDHVAQELFQGSDLGMAEEAERPGEK\AGQHSPLRE
			ľ	LHVICVQSILDEFLQT\YGSLIPLSTDEVVEKLEDIEOOFROMD
- 1		İ	i	SKKGLVLQL1QSYQRMPGNAMVRGFRVAVKDHIJT.TMDDI COL VO
		Į		QNNLNDQVMMYGDLVMDTVPEK\WHFRNSFEV\DVI.PTVCVDC
- 1		l	i	VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQ
- 1			}	RTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNN
		1	1	DSDCGAEVI-OYCKULAL CORECTROOPERING TERMVARONN
			Ì	DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL
5	987	1806	484	1 = :
- 1		ŀ	1 ***	DAWKSTSLTFHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP
i			ŀ	SPECKEDSPRGPPPPRLGLLGALMAFDCUPGGDDUPGGDDUPGD
- 1			ļ	GLKWTPKSPLDPDSGLLSCTLPNGFGGOSGPFGFPSLADDDAGT
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-	i	•		LOSVIETDVEGHFILIRELEPLLCHSDNDSOLTWTSGDNADWGN
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		L_		EPVLINPVLADSAAVDPAVVPISDNLPPVDAVPSGPAPVDLALV

No: beginning molectide location corresponding corresp	000	Predicted	Predicted end	Amino acid segment containing signal peptide
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Corresponding to first amino acid amino acid amino acid amino acid sequence P=Proline, Q=Glutamine, R=Asparagine, P=Proline, Q=Glutamine, R=Asparagine, residue of amino acid sequence Codon, /=possible nucleotide deletion, logosable nucleotide insertion) DPVPNDLTPUPPULVKSRPTDPRRGAVSSALGSSAGLIVES:			•	
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maino acid residue of amino acid sequence sequence metryptophan, Y-Tyrosine, V-Valine, wetryptophan, Y-Tyrosine, V-Valknown, *-Stop Codon, /-possible nucleotide deletion, \-possible nucleotide deletion, \-possible nucleotide deletion, \-possible nucleotide insertion) prymblTrypptvDFVLVSRFTDPRRGAVSSALGGSAPOLLVESE, LDPFXTIIPEVKEVVDSLKIESGTSATHEARPRISISEYAR, ROQROAGTERENSQPTPGKWESLPFTFTGLADIPCLVIPPABA KTALQRSPETPLEICLVPVGPSPASPSPEPPVSKDVASSPTEP PSQEMPLLARPSPPVGVSVSPAVPTPSMSAALPFPAGGIGMPP LPPPLQPFSLPLEMGPVLPDPTTYTAPLPSMPYSPTYT GPLGMGPGPGHAPFWSTVPPPLPSMSAALPFPAGGIGMPP LPPPLQPFSLPLSMAPPLSGAVAPPTECAMPPPRAVERPTSCTY GPLGMGPGPGHAPFWSTVPPPLPSSTGRAVPOPKMESRGTP, GPPENVLPLSMAPPLSLGLPGHAPPTEPTKVEVKPVPASPHP KKPLDATKAVPTPRQSTVFKLDAVHPARLAKISFLETPRTOSS DVVQAFISEIGIERSDLSSLLEGPERAKECPPPAPAGSLA GRSGGVDIPQEKRPLDRLQAPPLANVAGLTPPATPHOLWKEL AVSLLAKKSPKSTAGAGGTLKFEGTAHIPAAVRLGEGWHGP RVHVGSGDHDYC\VRSRTPPKK\MPALLIPEVGSRNVKRHGD TITPVLSLGPAAPPPCLAARSFLHFAVRVGLEGWHGP RVHVGSGDHDYC\VRSRTPPKK\MPALLIPEVGSRNVKRHGD SLLSPEASPCRNSRSVSGSNNTSTASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS				h=beucine, m=methionine, n=Asparagine,
residue of amino acid sequence (Codon, 1-possible nucleotide deletion, 1-possible nucleotide deletion, 1-possible nucleotide insertion) ppvprdltpvpptlvkspptpprkspptprapage		1 -		P=Proline, Q=Glutamine, K=Arginine,
amino acid sequence Codon, /-possible nucleotide deletion, /-possible nucleotide insertion) DPVPMDLTPVDPVLVKSPFTDDRRGAVSSALGGSAPOLLVESE LDPPKTIITPEVKEVVDSLKIESGTSATTHEARPRPLSLSEYRM ROQROABTEEMSLOPPIGKWPSLBFTPTGLADIDCLVIPPAPA KTALQRSPETPLEICLVPVGSPSASPSEPBPVSKDVASSPTTGO PSQEMPLLARPSPDVGVSVSPAVPTPSMSAALDFPAGGLGMPP- LPPPLQPFSLPLAMGPVLPDPTTTYAPLSSWPCYPHVSPSGY CLPPPPTVPLVSGTGPGAVAVPTFCSAMPPPAPAVSPYSTGTT GPLGMGGGPGPGMAPWSTVPPDPTKYVEVKPVPSSGTY GPPMAVLPLSMAPPLSLGLDGHGGMAPPPTAVPSFSTYPASPHP RKPPLGTPRPR KPDLPATRAVVPTPQGSTVPKLPAVPPTGVSTVPNSPGTPTRVEVKKPVPASPHP EKVSALVQSPOMKALACVSAEGVTVERPASERLKPETQETPRP KPPLPATRAVVFTPQGSTVPKLPAVPHAPLRKLSFLPTPTTQGS DVVQAFTSEIGIERSDLSSLLEQFEKSEAKKECPPPAPADSLA GMSGGVDIPQEKRPLDRLQAPPLAVMSLTPPATPPHQLWKFL AVSLLAKKSPSSTAGNGSTLKEGEVTSAKHPAVRLLGEVHGP RVHVSSGDHDVC\VRSRTPPKK\MPALLIPEVGSRMVVKRHQD TIKPVLSLGPAAPPPCLAASEFLYAFAVGLEGVHGP RVHVSSGDHDVC\VRSRTPPKK\MPALLIPEVGSRMVVKRHQD SILLSPEASPCRNDMYTTTPPESAKORSMKCYKRACRSASPSS GMGGRGNRSRSVSGSNTSTSASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS			1 -	S=Serine, T=Threonine, V=Valine,
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DEVPNDLTPVDPVLVKSRPTDPRRGAVSSALGGSAPOLLVESE LDPPKTIIPEVKEVVDSLKIEGTSATTHEARPRPLSLSEYRN RQQRQAETEKSPOPPTGKMPSLPETPTGLADIPCLUIPPAPA KTALQRSPETDLEICLVPVGPSPASPSPEPPVSKVASSPTEQ PSQEMPLLARPSPDVQSVSPAVDYTPSMSALLPFPAGGLGMPP LPPPJLQPPSLPLSMSPVLPDFTHYADLPSMPCVPHVSPSGY CLPPPTVPLVSSTGAVAVPPTPSMSALLPFPAGGLGMPP LPPPJLQPPSLPLSMSPVLPDFTHYADLPSMPCVPHVSPSGY CLPPPTVPLVSSTGAVAVPPTPSMSALLPFPAGGLGMPP LPPPJLQPPSLPLSMSPVLPDFTHYADLPSMPCVPHVSPSGY GPLWGPGPQNAPFWSTVPPPPLPPASIGRAVPQPKMSRGTP GPPEWVLPLSMAPPLSLEDEGAPQTEPTKVEVKEVRASPHP HEVSALVQSPQMKALACVSAEGTVEEPASEALKEEPPARASHP KPPLPATKAVPTPRGSTVYKLPAVHPARIKLSFLPTPRTQGS DVQAFISEIGIEABDLSSLLEGPEKSEKKEEPPPAPADSLA GNSGGYDIPQERPLDRLQAPELANVAGITPPATPPHQLWKPL AVSLLAKAKSPKSTAQEGTLKPBGVTSAKHEPAVPHPOLWKPL AVSLLAKAKSPKSTAQEGTLKPBGVTSAKHEPAVPHPOLWKPL AVSLLAKAKSPKSTAQEGTLKPBGVTSAKHEPAVPHQLGEVHOP TIKPVLSLGPAAPPPPCLAASREPLDHRTSSQADPSAPCLAF SLLSPEASPCRNDMINTTPPEPSAKGNSKCYKACKACRSASPSS GMGGRGNNSRSVSGSNRTSEASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS		amino acid	sequence	
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### HEVSALVOS POMKALACVSAECVTVEEPASERLK PETOETRPR KPPLPATKAVPTPRQSTVPKLPAVHPARLRKLSFLPTPRTQGS DVVQAFISETGIERASDLSSLLEQFEKSEAKKECPPPAPADSLA GNSGGVDI PQEKRPLDRLQAPELANVAGLTPPATPPHQLWKPL AVSLLAKAKSPKSTAQEGTLKPEGVTZSKHIPAAVRLQEGVHGP RVHVGSSDHDYC\VRSRTPPKK\MPALLIPEVGSRWNVKRHQD TIKPVLSLGPAAPPPCTAASREPLDHRTSSEQADPSAPCLAP SLLSPEASPCRNDWNTRTPPEPSAKORSWRCYRKACKSASPSS GWQGR:GRNGRSVSSGSNRTSEASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS		1		
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LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFR FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPE				PONLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI
FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPE				LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI
		1		FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG
				RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF
RH		f		
	5004	304	1034	AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL
	コフフセ	374	1734	PRPEIANOPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG
				POPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT
			,	
		•		LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV
				HNEATGKSSWWMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSKA
				PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT
				FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT
				LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS
		1		SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTQVD
		1 .		PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLEAPGPSSLVPTL
		1		SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY
MENLECDMDNI ISDLMDEGEGLDFNFEPDP		1	1	
	5995		2437	RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR
	2233	-	243/	GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAA
		1		AEMMEELHSL\DP\RRQELLEARF\TGLGVSKGPLNSESSNQSL
		1	ł	
LSVGSLSDREVETPERRQNDQRNRARRABPIBISQGR01FRGH		<u> </u>	<u> </u>	CSVGSLSDKEVETPEKKQNDQRNRKRKAEPYETSQGKGTPRGHK

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding	H=Histidine, I=Isolcucine, K=Lysine,
1	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	,	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence	1	\=possible nucleotide insertion)
1			ISDYFERRVEQPLYGLDGSAAKEATEEQSALPTLMSVMLAKPRL
j			DTEQLAQRGAGLCFTFVSAQQNSPSSTGSGNTEHSCSSQKQISI
1	j	1	QHRQT\QSDLTIEKISALENSKNSDLEKKEGRIDDLLRANCDLR
			RQI\DEQQKMLEKYK\ERLNRCFDNEPRNFLIEKSKQEKMACRD
			KSMQDRLRLGHFTTVRHGASFTEQWTDGYAFQNLIKQQERINSQ
ľ]	· ·	REEIERQRKMLAKRKPPAMGQAPPATNEQKQRKSKTNGAENETL
l l		ŀ	TLAEYHEQEEIFKLRLGHLKKEEAEIQAELERLERVRNLHIREL
	1		PTIMEDMOOF PRIDE NORWALL OF GROOM TO THE TENTE OF THE TENTE OF T
1	1	i	KRIHNEDNSQFKDHPTLNDRYLLLHLLGRGGFSEVYKAFDLTEQ
1	ł .		RYVAVKIHQLNKNWRDEKKENYHKHACREYRIHKELDHPRIVKL
}	į.		YDYFSLDTDSFCTVLEYCEGNDLDFYLKQHKLMSEKEARSIIMQ
ľ			IVNALKYLNEIKPPIIHYDLKPGNILLVNGTACGEIKITDFGLS
1			KIMDDDSYNSVDGMELTSQGAGTYWYLPPECFVVGKEPPKISNK
	1		VDVWSVGVIFYQCLYGRKPFGHNQSQQDILQENTILKATEVQFP
			PKPVVTPEAKAFIRRCLAYRKEDRIDVQQLACDPYLLPHIRKSV
5996	1632		STSSPAGAAIASTSGASNNSSSN
3556	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
	1		LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
i i			AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
			FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
			FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAOP
5997	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
1			LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
1			AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
1			FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
			FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5998	1612	981	DQQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
i i			LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
1			AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
			FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
	i		FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP
5999	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP
			GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG
1 1			ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG
1 1			LLQAKLQLITHAYFEEKDFSQISILKELYEHMISSLGGASLEGS
1 1			QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG
1 1			ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD
1 1			FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS
1 ' 1	J	i	KGQEPNDTNQYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE
1 1	i		QLGSDQTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE
1	l		EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI
1 1	ļ		LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL
į į	1		VRHVTENRDDVF'LDGTGWEGGDEWIRAQFAVYIHALLAATLQLV
1 1	1		LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK
1			TA\MSSWLSTFTTSTSQSLTEPPDEKP
6000	101	1561	TEDCOTTA DIACTA TRACENTIANA DESCRIPTION DE LA CONTRACTA DE LA
1 1	·		TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL
1 1	İ		DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR
1 1	ļ		KAEBLIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDK
	į	İ	VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNONERAKVCFEK
]]	1		ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD
1 [NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV
1 1	İ	į	LRSAA\KFYRGKDEPDKAIELLKKALEYIP\NNAYLHCQIGCCY
		1	RAKVFQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR
		ļ	VCSILASLHALADQYEDAEYYFQKEFSKELTPVAKQLLHLRYGN
[1	FQLYQMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRI.
		I	SKNGADSEALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS
			SWNGE
6001	176	1038	AFAHSPSRGHRETHIHTPRHTPRCTMAESHLQSSLITASQFFEI
		1	WLHFDADGSGYLEGKELQNLIQELQQARKKAGLELSPEMKTFVD
	l l		QYGQRDDGKIGIVELAHVLPTEENFLLLFRCQQLKSCE\EFMKT
		İ	WRKYDTDHSGFIETEELKNFLKDLLEKANKTVDDTKLAEYTDLM

SEO	Predicted	Predicted end	Amino soid comment containing ciers montain
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
) NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1		,	
1	corresponding to first	to first amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, O=Glutamine, R=Arginine,
I	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	t .	Codon, /=possible nucleotide deletion,
		sequence	
	sequence		\=possible nucleotide insertion)
1	i		LKLFDSNNDGKLELTEMARLLPVQENFLLKFQGIKMCGKEFNKA
1	ļ		FELYDQDGNGYIDENELDALLKDLCEKNKQDLDINNITTYKKNI MALSDGGKLYRTDLALILCAGDN
6002	0.75	<u> </u>	
6002	977	81	LAPPGGGLHIPPRTPLSHSRPPPSHHAPHPSPLPLPPADLHPHS
1	İ	ĺ	SMAQRSDLLELDCQLTRDRVVVVSHDENLCRQSGLNRDVGSLDF
1	1	ſ	EDLPLYKEKLEVYFSPGHFAHGSDRRMVRLEDLFQRFPRTPMSV
ł	ł	ł	EIKGKNEELIREQ/VLVRRYDRNEITIWASEKSSVMKKCKAANP
1	Ì]	EMPLSFTISRGFWVLLSYYLGLLPFIPIPEKFFFCFLPNIINRT
1	1	1	YFPFSCSCLNQLLAVVSKWLIMRKSLIRHLEERGVQVVFWCLNE
5000			ESDFEAAFSVGATGVITDYPTALRHYLDNHGPAARTS
6003	140	4098	GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFKVP
	[APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA
	İ	ĺ	FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR
	\		SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA
[1	İ	HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII
	ł	ļ	RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEWQTHSLE
1		1	RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY NSLEPSYOKSLOTYLKSSGSVASLPOSDRSSSSSQESLNRPFSS
1		j	KWSTANPSTVAGRVSAGSSKASSLPGSLQRSRSDIDVNAAAGAK
1	ĺ	•	AHHAAGOSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV
	1		RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGSPGRVLT
1]	TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSREASPSRLSV
ļ			ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQPLASRHHSRS
į.			TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVEEA
i	ł	\	VADALLLGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS
1		}	YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGLLGLQN
[LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI
		1	QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES
			FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD
			FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFELNTPE
1	1	1	FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPTP
j	,	}	RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDIYSSLRG
\	ĺ		VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA
1	1	1	GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPYNYSDSIS
		1	PFNKSALKEAMFDDDADQFPDDLSLDHSDLVABLLKELSNHNER
1	,	1	VEERKIALYELMKLTQEESFSVWDEHFKTILLLLLETLGDKEPT
1		l	IRALALKVLREILRHQPARFKNYABLTVMKTLEAHKDPHKEVVR
1	1	i	SAEEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT
1	ł	ĺ	KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVAV
			HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS
1		1	GÖS
6004	140	4098	GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFKVP
ł			APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA
ŀ	j	1	FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR
{	l	i	SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA
1	1		HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII
1	İ		RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEWQTHSLE
	Į.		RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY
1	[NSLEPSYQKSLQTYLKSSGSVASLPQSDRSSSSSQESLNRPFSS
1			kwstanpstvagrvsagsskasslpgslqrsrsdidvnaaagak
1	l		AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV
Ì			RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGSPGRVLT
		1	TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSREASPSRLSV
]		ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQPLASRHHSRS
	1	1	TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVEBA
1			VADALLIGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS
	[1	YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGLLGLQN
1			LLKNORTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI
1			QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES
		ļ	FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD
1		l	FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFELNTPE
L	<u> </u>		

SEQ	Predicted	Predicted end	Amino acid coment
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	ccrresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
<u> </u>	sequence		\=possible nucleotide insertion)
İ	j		FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPTP
-	ļ		RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDIYSSLRG
		}	VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA
İ			GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPYNYSDSIS
. 1	1	ļ	PFNKSALKEAMFDDDADQFPDDLSLDHSDLVAELLKELSNHNER
Ī			VEERKIALYELMKLTQEESFSVWDEHFKTILLLLLETLGDKEPT IRALALKVLREILRHQPARFKNYAELTVMKTLEAHKDPHKEVVR
			SAEEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT
Ī			KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVAV
			HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS
			GQS
6005	133	5955	RSSGRRQEQLGQFPGRERKGMASGLGSPSPCSAGSEEEDMDALL
j			NNSLPPPHPENEEDPEEDLSETETPKLKKKKKPKKPRDPKIPKS
]			KRQKKERMLLCRQLGDSSGEGPEFVEEEEEVALRSDSEGSDYTP
[i	GKKKKKKLGPKKEKKSKSKRKEEEEEDDDDDDDSKEPKSSAQLL
1			BDWGMEDIDHVFSEEDYRTLTNYKAFSQFVRPLIAAKNPKIAVS
			KMMMVLGAKWREFSTNNPFKGSSGASVAAAAAAAAVAVVESMVTA
J	j		TEVAPPPPPVEVPIRKAKTKEGKGPNARRKPKGSPRVPDAKKPK PKKVAPLKIKLGGFGSKRKRSSSEDDDLDVESDFDDASINSYSV
			SDGSTSRSSRSKKLRTTKKKKKGEEEVTAVDGYETDHQDYCEV
			CQQGGEIILCDTCPRAYHMVCLDPDMEKAPEGKWSCPHCEKEGI
]		QWEAKEDNSEGEEILBEVGGDLEEEDDHHMEFCRVCKDGGELLC
1]		CDTCPSSYHIHCLNPPLPEIPNGEWLCPRCTCPALKGKVOKILI
1	1		WKWGQPPSPTPVPRPPDADPNTPSPKPLEGRPEROFFVKWOGMS
Ī			YWHCSWVSELQLELHC\QVMFRNYQRKNDMDEPPSGDFGGDEEK
			S\RKRKNKDPKFAEMEERFYRYGIKPEW\MMIHRILNHSVDKKG
i			HVHYLIKWRDLPYDQASWESEDVEIQDYDLFKQSYWNHRELMRG EEGRPGKKLKKVKLRKLERPPETPTVDPTVKYERQPEYLDATGG
1			TLHPYQMEGLNWLRFSWAQGTDTILADEMGLGKTVQTAVFLYSL
1 .			YKEGHSKGPFLVSAPLSTIIN\WEREFEMWAPDMYV\VTYVGDK
			DSRAIIRENEFS\FEDNAIRGGKKASRMKKEASVKFHVLLTSYE
1	}		LITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQHK
ĺ			LLLTGTPLQNNLEELFHLLNFLTPERFHNLEGFLEEFADIAKED
	İ		QIKKLHDMLG\PHMLRRLKADVFKNMPSKTELIV\RVELSPM\O
1			KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNHPY
1 :			LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEGGH
]			RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGGITGNMRQEAIDR FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQ
1			AFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVV
1 1			RPGLGSKTGSMSKQELDDILKFGTBELFKDEATDGGGDNKEGED
1			SSVIHYDDKAIERLLDRNQDETEDTELQGMNEYLSSFKVAQYVV
1 1			REEEMGEEEEVEREIIKQEESVDPDYWEKLLRHHYEOOORDLAR
			NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNOSDYSVASREGDE
1			DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFNAR
1			QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVSLF
1 1	1		MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKKVQ
1 1	1		EFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDTQP
] 1			NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIECT QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKGKG
] 1	j		AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGETPK
1	ļ	ļ	DINDEROKKNIKORPMFNINDCCFTBLHCLWONEERAATVTKKT
, 1		İ	YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKGEM
{	1		NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDPSH
			PSMALNTRFAEVECLAESHOHLSKESMAGNKPANAVLHKVLKOL
1 i		İ	EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP
6006			EPTPQQVAQQQ
"""	1	965	DNDFLRNTVHRHEPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC
]			GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAAVS
1 1	j	j	ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKVGV
] [CRVDPRGKPCETVFQRLSYNGQSSVVRCRPLTGRTHQIRVHLQF LGHPILNDPIYNSVAWGPSRGRGGYIPKTNEBLLRDLVAEHQAK
			DOMESTIMO PARTICIO PARTICIO DE LA CONTREMINA DE LA CONTRE

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
Į	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
1	to first	amino acid	S=Serine, T=Threonine, V=Valine,
i	amino acid	residue of	Saserine, Tainteonine, Vavaline,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			QSLDVLDLCEGDLSPGLTDSTAPSSELGKDDLEELAAAA\QKME
•			EVAEAAPQELDTIALASEKAVETDVMNQ\RQT\TLCRVPAGATG
	1	}	SLAPRPCDVPTCPTL
6007	 3	2351	HELGQVEYVFTDKTGTLTENEMQFRECSINGMKYQEINGRLVPE
1)	1	GPTPDSSEGNLSYLSSLSHLNNLSHLTTSSSFRTSPENETELIK
ł	1	1	EHDLFFKAVSLCHTVQINNVQTDCTGDGPWQSNLAPSQLEYYAS
ĺ	1	4	SPDEKALVEAAARIGIVFIGNSEETMEVKTLGKLERYKLLHILE
1	}	1	FDSDRRRMSVIVQAPSGEKLLFAKGAESSILPKCIGGEIEKTRI
İ	1	ļ	HVDEFALKGLRTLCIAYRKFTSKEYEEIDKRIFEARTALQQR\E
1	1	1	EKLAAVFQFIEKDLILLGATAVEDRLQDKVRETIEALRMAGIKV
		ļ	WVLTGDKHETAVSVSLSCGHFHRTMNILELINQKSDSECAEQLR
1		1	QLARRITEDHVIQHGLVVDGTSLSLALREHEKLFMEVCRNCSAV
1	1		LCCRMAPLQKAKVIRLIKISPEKPITLAVGDGANDVSMIQEAHV
	Ì		GIGIMGKEGRQAARNSDYAIARFKFLSKLLFVHGHFYYIRIATL
1		!	VQYFFYKNVCFITPQFLYQFYCLFSQQTLYDSVYLTLY\NICFT
1	1		SLPILIYSLLEQHVDPHVLQNKPTLYRDISKNRLLSIKTFLYWT
1	1		PURTUE I STRUKTUR AND
		1	ILGFSHAFIPFFGSYLLIGKDTSLLGNGQMFGNWTFGTLVFTVM VITVTVKMALETHFWTWINHLVTWGSIIFYFVFSLFYGGILWPF
1		1	VITVIVKMADETHEWIWINHDVIWGSIIFIFVFSBFIGGIBHEF
1	1	1	LGSQNMYFVFIQLLSSGSAWFAIILMVVTCLFLDIIKKVFDRHL
1		1	HPTSTEKAOLTETNAGIKCLDSMCCFPEGEAACASVGRMLERVI
1			GRCSPTHISRSWSASDPFYTNDRSILTLSTMDSSTC
6008	4554	1089	AGVRRAGARRGPGRALFAGATAVPPPSARRRRRCPAPEHAGPAR
i	ì	Ì	ASRPSQETMFQLPVNNLGSLRKARKTVKKILSDIGLEYCKEHIE
}	1		DFKQFEPNDFYLKMTTWEDVGLWDPSLTKNQDYRTKPFCCSACP
1	i	1	FSSKFFSAYKSHFRNVHSEDFENRILLNCPYCTFNADKKTLETH
1	1		IKIFHAPNASAPSSSLSTFKDKNKNDGLKPKQADSVEQAVYYCK
1	Ì		KCTYRDPLYEIVRKHIYREHFQHVAAPYIAKAGEKSLNGAVPLG
1		į	SNAREESSIHCKRCLFMPKSYEALVQHVIEDHERIGYQVTAMIG
1	1	1	HTNVVVPRSKPLMLIAPKPQDKKSMGLPPRIGSLASGNV\RSLP
	1	ł	SQQMVNRLSIPKPNLNSTGVNMMSSVHLQQNNYGVKSVGQGYSV
1	\	i	GQSMRLGLGGNAPVSIPQQSQSVKQLLPSGNGRSYGLGSEQRSQ
	,	1	APARYSLQSANASSLSSGQLKSPSLSQSQASRVLGQSSSKPAAA
1	1	1	ATGPPPGNTSSTQKWKICTICNELFPENVYSVHFEKEHKAEKVP
1	1	1	AVANYIMKI:HNFTSKCLYCNRYLPTDTLLNHMLIHGLSCPYCRS
1	1	,	TFNDVEKMAAHMRMVHIDEEMGPKTDSTLSFDLTLQQGSHTNIH
1	1	ł	LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQPKVQEKADIPVKS
i	1	•	SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ
		}	TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN
1	1		GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP
			SFFEEKPEEPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP
1			TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL
1		į.	LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN
1	ļ	1	LGKEDDSSSDSFENLEEESNESGSPFDPVFEVEPKISNDNPEEH
			VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS
1			EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDE
1		1	SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD
ì		[QSQW:NASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP
	1	1	
1	1	l .	I MRGSTAGVKUSSCOA
6009	4050	1574	MHGSLAGVKLSSQQA
1	4272	1534	CHGLOHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC
1	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKS1C*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW
1	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKS1C*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHOHWNMFP1QRPPLVMKGRRIMCGKCEKG*VSDSVTGG
	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKS1C*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFP1QRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL
	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKS1C*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFP1QRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGF1V1GK1QSLEAKVPLPVNGQTGERASPG
	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNNFFIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA
	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLOKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL
	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWMMFPIQRPPLVMKGRRIMGGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FYLAPODGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP
	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMGGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN
	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMGGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAPLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*KNGGTTLHQLFAEVN AVTRGSAVORRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG
	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAPLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP
	4272	1534	CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMGGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAPLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*KNGGTTLHQLFAEVN AVTRGSAVORRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG

SEQ	Predicted	Predicted end	l mine
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	corresponding	to first	<pre>II=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,</pre>
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	_	\=possible nucleotide insertion)
			I**RGRLSGEWGCGLGRGELFQVSIGIGVSIVHIGQGDHEV
ļ	İ	1	AGLVERGALHATGQGVEALVQQLLDVGPAGALGLCDGAALF
	1	1	GRVGQLPAEGLQVCITLVAQWRMHDGRELGGAEWPWQALHGA
		İ	CGVGGAILLKALSQYFLKGG*RLWCARGQ*PVKKRQRRWRG*TR
ļ		}	R*NGLTIHCFN*LI*GAVCCRLVILRWCGLLEVHGVYGT*IHCL
	1		GSFPGRLWP+PFISQERPNGHCQWEFRLAVPSWKCRWSRWRVRG
İ			TWRYGNPLLNLL*GAWLGGAACGGQQGGPLSTWQACTGPGQAAF
		ŀ	LPPFQGACRPRTQRCRTWVCPIAWRQLLAYTRD
6010	1	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM
1		ĺ	AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIFD
		ļ	PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSAA
1			TIVAKHTSALCNACRIASSKTANPVAKRHFVOSAKEVANSTANL
1			VKTIKALDGDFSEDNRNKCRIATAPLIEAVEN TAFASNPEFVS
	ł		IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP
İ	1		PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC
			IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP
ļ			IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM
			TVLDQTKTLAESALQMLYAAKEGGGNPKAOHTHDATTFZACI.MK
1			EAVDDIMVTI NEAASEVGLVGGMVDAIAEAMSKI DEGTDDEDKG
			TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPREIGGLASOMTSD
1			YGHLAFQGQMAAATAEPEEIGFOIRTRVODLGHGCTFLVOKAG\
1			ALQVCPTDSYTKRELIECARAVTEKVSLVLSALOAGNKGTOACT
			TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENTI.KTA
1			KALVEDTKLLVSGAASTPDKLAQAAQSSAAT!TOLAEVVKLGAA
1			SLGSDDPETQVVLINAIKDVAKALSDLISATKJAASKPVDDPSM
			YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTPALEATIRCIKO
1 1			ELTVFQSKDVPEKTSSPEESIRMTKGITMATA :: AVAAGNSCRQE
			DVIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRFGTEC
			TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA
1 1			EAMRGTEWVDPBDPTVIAETELLGAAASIEAAAKKLEOLKPPAK
			PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK
			VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGHA
1 1	i		SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV
1 1			KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM
6011	446	1835	LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
1 1		4033	LLQPAMRKSPGLSDCLWAWILLLSTLTGRSYGQPSLQDELKDNT
1	i		TVFTRILDRLLDGYDNRLRPGLGERVTEVKTDIFVTSFGPVSDH
1			DMEYTIDVFFRQSWKDERLKFKGPMTVLRLNNLMASKIWTPDTF
1			FHNGKKSVAHNMTMPNKLLRITEDGTLLYTMRLTVR\AECPMAF
j (į		GRDFPM\D\AHACPLKFGSYAYTRAEVVYEWTREPARSVVVAED GSRLNQYDLLGQTVDSGIVQSSTGEYVVMTTHFHLKRKIGYFVI
]	ĺ	i	QTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLSIS
1 1			ARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGYA
	İ		WDGKSVVPEKPKKVKDPLIKKNNTYAPTATSYTPNLARGDPGLA
1 1		İ	TIAKSATIEPKEVKPETKPPEPKKTFNSVSKIDRLSRIAFPLLF
1			GIFNLVYWATYLNREPQLKAPTPHQ
6012	351	5013	PAELFQSFAIWHKELYDWRLGPWNQCQPVISKSLEKPLECIKGE
1	i		EGIQVREIACIQKDKDIPAEDIICEYFEPKPLLEQACLIPCQQD
1 1	1		CIVSEFSAWSECSKTCGSGLQHRTRHVVAPPQFGGSGCPNLTEF
	•	j	QVCQSSPCEAEELRYSLHVGPWSTCSMPHSRQVRQARRRGKNKE
1 !	!	}	REKDRSKGVKDPEARELIKKKRNRNRQNRQENKYWDIQIGYQTR
] [j	EVMCINKTGKAADLSFCQQEKLPMTFQSCVITKECQVSEWSEWS
1 1	j	ŀ	PCSKTCHDMVSPAGTRVRTRTIRQFPIGSEKECPEFEEKEPCLS
1 1	l	Į	QGDGVVPCATYGWRTTEWTECRVDPLLSQQDKRRGNQTALCGGG
] [ĺ	IQTREVYCVQANENLLSQLSTHKNKEASKPMDLKLCTGPIPNTT
]		ļ	QLCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRKRRIT
		İ	NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGK
			ECGPGTQVQEVVCINSDGEEVDROLCRDAIFPIPVACDAPCDKD
		1	CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRCP
1	1	1	NSSALQEVRSCNEHPCTVYHWQTGPWGOCIEDTSVSSFNTTTTW
<u>_</u>			NGEASCSVGMQTRKVICVRVNVGQVGPKKCPESLRPETVRPCLL
			The state of the s

	Drodietod	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
NO:	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
1			L=Leucine, M=Methionine, N=Asparagine,
1	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	residue of	amino acid	W=Tryptopnan, Y=Tyrosine, X=Onkhown, -=Scop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	l	\=possible nucleotide insertion)
			PCKKDCIVTPYSDWTSCPS\SCKEGDSSIRKQSRHRVIIQLPAN
ł	i	Į.	GGRDCTDPLYEEKACEAPQACQSYRW\KTHKW\HRCQ\LVP\WS
{	ł	ł	VQQDSP\GAQEGCGPGRQARAITCRKQDGGQAGIHECLQYAGPV
Į.	į.)	PALTQACQIPCQDDCQLTSWSKFSSCNGDCGAVRTRKRTLVGKS
1	1		KKKEKCKNSHLYPLIETQYCPCDKYNAQPVGNWSDCILPEGKVE
1	1	1	VLLGMKVQGDIKECGQGYRYQAMACYDQNGRLVETSRCNSHGYI
i	1	1	EEACIIPCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLREKPYN
ł	i .	Ì	GGRPCPKLDHVNQAQVYEVVPCHSDCNQYLWVTEPWSICKVTFV
	1	1	NMRENCGEGVQTRKVRCMQNTADGPSEHVEDYLCDPEEMPLGSR
ļ	1		VCKLPCPEDCVISEWGPWTQCVLPCNQSSFRQRSADPIRQPADE
1	Ì	1	GRSCPNAVEKEPCNLNKNCYHYDYNVTDWSTCQLSEKAVCGNGI
1 .		1	KTRMLDCVRSDGKSVDLKYCEALGLEKNWQMNTSCMVECPVNCQ
1		1	LSDWSPWSECSQTCGLTGKMIRRRTVTQPFQGDGRPCPSLMDQS
j	1	1	KPCPVKPCYRWQYGQWSPCQVQEAQCGEGTRTRNISCVVSDGSA
1		1	KhChavhCikmõieõmphcõnārāna encoopcoopcou
1		1	DDFSKVVDBEFCADIBLIIDGNKNMVLEESCSQPCPGDCYLKDW
į.	ļ		SSWSLCQLTCVNGEDLGFGGIQVRSRPVIIQELENQHLCPEQML
]	ļ		ETKSCYDGQCYEYKWMASAWKGSSRTVWCQRSDGINVTGGCLVM
İ	İ	1	SQPDADRSCNPPCSQPHSYCSETKTCHCEEGYTEVMSSNSTLEQ
	j	1	CTLIPVVVLPTMEDKRGDVKTSRAVHPTQPSSNPAGRGRTWFLQ
ļ	4		PFGPDGRLKTWVYGVAAGAFVLLIFIVSMIYLACKKPKKPQRRQ
			NNRLKPLTLAYDGDADM
6013	1161	710	GAFIAGVPVQPVLIRYPNSLDTTSWAWRGPGVLKVLWLTASQPC
	1	ł	SIVDVEFLPVYHPSPEESRDPTLYANNVQRVMAQALGIPATECE
ļ	1	i	FVGSLPVIVVGRLKVALEPQL/WGTGKSASEGWAVRWLCGRWGR
ł	1	j	ARPESNDQPGRVCQAATAL
6014	2857	613	EAVAGGMEKSRMNLPKGPDTLCFDKDEFMKEDFDVDHFVSDCRK
1 001#	1 2037	1	RVQLEELRDDLELYYKLLKTAMVELINKDYADF\VNLSTNLVGM
1		1	DKALNQLSVPLGQLREEVLSLRSSVSEGIRAVDERMSKQEDIRK
1	1		KKMCVLRLIQVIRSVEKIEKILNSQSSKETSALEASSPLLTGQI
i		İ	LERIATEFNQLQFHACQSK\GMPLLDKVRPRIAGITAMLQQSLE
		ł	GLLLEGLQTSDVDIIRHCLRTYATIDKTRDAEALVGQVLVKPYI
1			DEVIIEOFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS
1		1	EKGNTVPGYDFLVNSVWPQIVQGLEEKLPSLFNPGNPDAFHEKY
		1	TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI
1	l l	1	RFREIAGSLEAALTDVLEDAPAESPYCLLASHRTWSSLRRCWSD
	1	1	EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE
1	1	[IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV
1		<u> </u>	
1		1	ADLDKLQEQLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS
	1	1	ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS
i			SYVDSALKPLFQLQSGHKDKLKQAIIQQWLEGTLSESTHKYYET
l .	1	İ	VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL
1	1	1	QLALDVEYLGEQIQKLGLQASDIKSFSALAELVAAAKDQATAEQ
ł			P
6015	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC
1	1	1	VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN
1		Į.	RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
ł	į		GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT
1		}	HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR
1		Į	EGIEEEDQEEDKNIVVDDITEQKPEPQDDGKSTESDVKADGDSK
1	1	1	GSEEVDSHCKKALSHKELYERARELLVSYEEEQFTVLEKFRYLP
1	1		KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT
			FEQLAALQIEYEENVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ
1	Í		ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF
1			ALLERMLSELPALGISGIRFIIIRWIVEDIVARIRICANARCI SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII
Ì		1	SAGGMEAKKGMENCOHODMAKMAEOCHGOECMAGEGHALL
1	1		F\KAMGQGLQDE\EQEKLLRICSIYTQSGENSLVQEGSEASPIG
ļ	1		KSPYTLDSLYWSVKPASSSFGSEAKAQQQEEQGSVNDVKEEEKE
1			EKEVLPDQVEEEEENDDQEEEEEDEDDEDDEEEDRMEVGPFSTG
1		1	QESPTAENARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR
1			SRPRTPAELMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL
,	1		\SCGVGS\GNCSNSSSSNFRGAFLLEARGSLH\GL\KTGLQLF
6016.	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC
		,,	

SEQ	Predicted	Predicted end	Draine
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
-	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Ston
[sequence	sequence	Codon, /=possible nucleotide deletion.
			\=possible nucleotide insertion)
1			VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN
1			RITVWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
Í			GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT HKKMPFINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR
İ		l I	EGIEEEDQEEDKNIVVDDITEQKPEPQDDGKSTESDVKADGDSK
			GSEEVDSHCKKALSHKELYBRARELLVSYEEEQFTVLEKFRYLP
i			KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT
ľ			FEQLAALQIEYEENVDLNDVLVPKPFSQFWQPLLRGLHSONFTQ
			ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRE
	1		SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII
1	Ì	•	F\KAMGQGLQDE\EQEKLLRICSIYTQSGENSLVQEGSEASPIG
			KSPYTLDSLYWSVKPASSSFGSEAKACQQEEQGSVNDVKEEEKE EKEVLPDQVEEEEBNDDQEEBEEDEDDEDDEEEDRMEVGPFSTG
			QESPTAENARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR
			SRPRTPAELMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL
6017			\SCGVGS\GNCSNSSSSNFRGAFLLEARGSLH\GL\KTGLOLF
1 801/	203	3469	SHQEIEQNSAMAPRKRGGRGISFIFCCFRNNDHPEITYRLENDS
	,		NFALQTMEPALPMPPVEELDVMFSELVDELDLTDKHREAMFALD
1			AEKKWQIYCSKKKDQEENKGATSWPEFYIDQLNSMAARKSLLAL
			FKEEEEERSKTIESLKTALRTKPMRFVTRFIDLDGLSCILNFLK TMDYETSESRIHTSLIGCIKALMNNSQGRAHVLAHSESINVIAQ
			SLSTENIKTKVAVLEILGAVCLVPGGHKKVLQAMLHYQKYASER
1			TRFQTLINDLDKSTGRYRDEVSLKTAIMSFINAVLSQGAGVESL
			DFRLHLRYE\FLMLGIHPVMDKLRKHENSTLDRHIDPFRMI.DNF
			DELEFAKRFELVHIDTKSATOMPELTRKRLTHSEAYPHFMSTLH
[[HCLQMPYKRSGNTVQYWLLLDRIIQQIVIQNDKGQDPDSTPLEN
			FNIKNVVRMLVNENEVKQWKEQAEKMRKEHNELQQKLEKKEREC
			DAKTQEKEBMMQTLNKMKEKLEKETTEHKQVKQQVADLITAQLHE LSRRAVCASIPGGPSPGAPGGPFPSSVPGSLLPPPPPPPPPLPGGM
1 1			LPPPPPPLPPGGPPPPPGPPPLGAIMPPPGAPMGLALKKKSIPQ
	İ		PTNALKSFNWSKLPENKLEGTVWTEIDOTKVFKILDLEDLERTF
1			SAYQRQQDFFVNSNSKQKEADAIDDTLSSKLKVKELSVIDGRPA
1			QNCNILLSRLKLSNDEIKRAILTMDEOEDLPKDMLEOUKRUPF
1 1			KSDIDLLEEHKHELDRMAKADRFLFEMSRINHYOORLOST.VEKK
1 1			KFAERVAEVKPKVEAIRSGSEEVFRSGALKOLLEVVLAFGNYMN
1	į.		KGQRGNAYGFKISSLNKIADTKSSIDKNITLLHYLITIVENKYP SVLNLNEELRDIPQAAKVNMTELDKEISTLRSGLKAVETELEYQ
1 1			KSQPPQPGDKFVSVVSQFITVASFSFSDVEDLLAEAKDLFTKAV
1 1			KHFGEEAGKIQPDEFFGIFDQFLQAVSEAKQENENMRKKKEEEE
1 1			RRARMEAQLKEQRERERKMRKAKENSEESGEFDDLVSALRSGEV
6018	13	2513	FDKDLSKLKRNRKRITNOMTDSSRERPITKLNF
	-3	2510	TISQSGGIRRRREAVWFEVVNMDFSRLHMYSPPQCVPENTGYTY
1 1			ALSSYSSDALDFETEHKLDPVFDSPRMSRRSLRLATTACTLGD
	ſ	İ	GEAVGADSGTSSAVSLKNRAARTTKQRRSTNKSAFSINHVSRQV TSSGVSYGGTVSLQDAVTRRPPVLDESWIREQTTVDHFWGLDDD
1	1	ļ	GDLKGGNKAAIQGNGDVGAGAATGHNGFFCSNCNMLSERKDVLT
1			AHPAAPGPVSRVYSRDRNOKCDDCKGKRHLDAHPGPAGTI.WUTW
1 1	1		ACAGYFLLQILRRIGAVGQAVSRTAWSALWLAVVAPGKAASGUP
1			WWLGIGWYQFVTLISWLNVFLLTRCLRNICKFIATATTELTAG
[LSLRGQG\NFFSPLPVLNWASMHRTORVDDPODVFKPTTSPLKO
	!	 	PLOGDSEAFPWHWMSGVEQQVASLSGCCHHHCENI.REL.TTLI.OV
		1	LOARVDOMEGGAAGPSASVRDAVGQPPRETDFMAFHQEHEVRMS
	ĺ	İ	HLEDILGKLREKSEAIQKELEQTKQKTISAVGEQLLPTVEHLQL ELDQLKSELSSWRHVKTGCETVDAVQERVDVQVREMVKLLFSED
		į	QQGGSLEQLLQRFSSQFVSKGDLQTMLRDLQLQILRNVTHHVSV
		Í	TKQLPTSEAVVSAVSEAGASGITEAQARAIVNSALKLYSQDKTG
1			MVDFALESGGGSILSTRCSETYETKTALMSLFGIPLWYFSOSDR
i i			VVIQPDIYPGNCWAFKGSQGYLVVRLSMMIHPAAFTLEHIPKTI,
		I	SPTGNISSAPKDFAVYGLENEYOREGOLLGOFTYDODGESLOME
6019	2	_ 1	QALKRPDDTAFQIVELRIFSNWGHPEYTCLYRFRVHGEPVK
		1003	TPNDREPPPQRPPSSRRASHLAQEITSAASLGDQTQILGSLTTA

	D. 37-6-3	Desailated and	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
j	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residuc of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	amino acid	sequence	Codon, /=possible nucleotide deletion,
j	sequence	bequesie	\=possible nucleotide insertion)
<u> </u>	sequence		PVITSAIRSMPGISSQILTNAQGQVIGTLPWVVNSASVAAPAPA
1]		OSLOVOAVTPOLLLNAQGQVIATLASSPLPPPVAVRK\PSTPES
1	1	ļ	LLKSEVOPIKPTPTVPQPAVVIASPAPAAKPSASAPIPITCSET
ł	1	ł	
[1	i	PTVSQLVSKPHTPSLDEDGINLEEIREFAKNFKIRRLSLGLTQT
į	1		QVGQALTATEGPAYSQSAICRFEKLDITPKSAQKLKPVLEKWLN
1	}	i	EAELRNQEGQQNLMEFVGGEPSKKRKRRTSFTPQAIEALNAYFE
ì	1	İ	KNPLPTGQEITEIAKELNYDREVVRVWFCNRRQTLKNTSKLNVF
ì	1		QIP
6020	4953	549	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
0020	,	,	AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
}			QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
1	Į.		RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE
1	[EPONSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
1			GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
i		1	
1	1	1	GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
1		1	FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
1	ì	1	GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
		1	AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
i			LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR
	[l .	RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
1		Į	TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
1	1		YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
Į		1	NPPKVIMELFONDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
ļ	i	1	HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP
	j] .	QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVBCGGERV
1	1	1	ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
i	1	1	FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
i		•	DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV
			DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT
1	1		
	1	1	DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
l l	1		ROFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
		1	KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
Ì	1	ł	TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
1	ſ	}	RDSLR/PTQ/LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
1	1	}	FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP
1	1		NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
1]		NKOKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
1	1	1	SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
ł		1	HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
1	1	1	PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
1	1		KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
1		į.	LFVAVLLYSLPNYLSMKIVKPNV
	 	 	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
6021	4953	549	EATOREVSIGNYGNAPUTTCKPLASTIQISKAVRUGNIIIIDPW
1			AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALKSGI
1			QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
1	1	1 .	RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE
1	1		EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
{	1		GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
1	1	1	GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
[FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
1	1		GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
1	1	l	AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
1	1		LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR
ļ]		RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
1	1	1	
1	1		TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
1	1		YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
1	1	1	NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
l	1	1	HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLYMVP
1		ł	QGIRPVVQLTAIEILANGLRNMKNFQMASITSPSLVVECGGERV
		1	ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
1	1		FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
	<u> </u>	-l	

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	I was actu acqueit confaining cional nontida
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
j	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, O=Glutamine, P-Arginine
	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, Y-Hnknow, 4-35.00
İ	sequence	sequence	Codon, /=possible nucleotide deletion
———	bequence	 	\=Possible nucleotide insertion
- 1			DIVIEMEDTKPLLASKCLSSMSTALSKMASDATIGUTEVERETU
1			DWWSKFYASSGEHEKCGOYIOKGYSKLKIYNCELDANA EZECLO
ı]		DESDIFKLYRGKSDENEDPSVVGEFKGSFRIVDI.DDDGVDADD
İ		1	RQFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
		İ	KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
į	1		TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
			RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
1		1	FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
1	1		NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
İ			SIDOTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
}			HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
			PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
		1	KUDDPHRPETSFLWPTNPCKTMKFIVWRRFKWUTTGLT.FLT.TT.
6022	4953		LFVAVLLYSLPNYLSMKIVKPNV
1	1753	549	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW
1	l I	1	AHTKPVVTLTSYWEDISHRLDAVNTLLAMARRIOTNIFALKSGI
Ì			QGKIPANQLAELWLKLIDEVIEDTRYTI, DI. TEGKANUTUI DTOT
1			RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQLTE
1			EPONSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
l	1		GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
}			FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNESRYP
ì	i l		GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
	1 1		AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
1	}		DIGIASSTAGAMEELQDQEGWEYASLIGWKFHWKODGGDTEDDD
1			RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKOVUGA
ł]		1 TVFGANTPIVSCNFDRDYIYHLRCYVYOARNIJAI.DKDCFCDD
1	1 1		TARICFLIRSKTTEILESTLNPTWDOTTIFDEVETVCEPOTVIO
İ.			NPPRVIMELFDNDOVGKDEFLGRSIFSPVVKINSFMDITTPVI IM
	1 1		APVMINGDRACGDVLVTABLILRGRDGSNI,PTI,DDODADNI VMVD
1			QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV
1	i		ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
1	1		FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPOLKASLLSAPPCR DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEBEIV
			DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT
1 1			DFSDTFKLYRGKSDENEDPSVVGEPKGSFRIYPLPDDPSVPAPP
			ROFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
1	1		ARVIE (DRDHYIPNTLNPVFGRMYELSCYLPOEKDI,KISUVDVD)
] }	1		TFTRDEKVGETIIDLENPF\LSRFG\SHCG\TDRPVCVCCARREN
1 1	1		RUSLR\PTQ\LLONVARFKGFPOPTI.SEDGSDTDVGGDDVGr DD
	1		FEANKILHQHLGAPEERLALHILRTOGI.VDEHVETDTI HETTEOD
[İ		NIS \RYILKVIIWNTKDVILDEKSITGEEMSDIVUVCWIDGARD
i . I			NAQATDVHYRSLDGEGNFNWRFVFPFDVLPAFOLCTVAVVELUE
			SIDGIEFRIPPR\LIIOIW\DNDKFS\LDDVIGEDPTLTCDUTT
		1	HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
			PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP KLDI,PNRPETCEI METNOCKTMVALIA
			KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL LFVAVLLYSLPNYLSMKIVKPNV
6023	102	916	SQELGMFVELNNLLNTTPDRAEQGKLTLLCDAKTDGSFLVHHFL
í			SFYLKANCKVCFVALIQSFSHYSIVGQKLGVSLTMARERGQLVF
1			LEGL/IVCSGR/VFQAQKEPHPLQFLREANAGNLKPLFEFVREA
- 1			LKPVDSGEARWTYPVLLVDDLSVLLSLGMGAVAVLDFIHYCRAT
	!		VCWELKGNMVVLVHDSGDAEDEENDILLNGLSHQSHLILRAEGL
1	ì		ATGFCRDVHGQLRILWRRPSQPAVHRDQSFTYQYKIQDKSVSFF
6024			AKGMSPAVL
0024	3	3260	FLSFLCYPRFRCLFCLQFAIPASRMEQLNELELLMEKSFWEEAE
		1	LPAELFQKKVVASFPRTVLSTGMDNRYLVLAVNTVONKECNGER
[1	KLV1TASQSLENKELCILRNDWCSVPVEPGDITHI.EGDCTCDTW
		ľ	11DADFGYLLLYPDMLISGTSIASSIRCMRRAVI.SETFDSSDDA
		·(<u>'</u>	TROMLIGTVLHEVFOKAINNSFAPEKLOELAFOTIQEIRHLKEM
			. 70

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted		
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į.	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	Begarines		YRLNLSQDEIKQEVEDYLPSFCKWAGDFMHKNTSTDFPQMQLSL
ļ			PSDNSKDNSTCNIEVVKPMDIEESIWSPRFGLKGKIDVTVGVKI
			HRGYKTKYKIMPLELKTGKESNSIEHRSQVVLYTLLSQERRADP
ì	-		
ì	į		EAGLLLYLKTGQMYPVPANHLDKRELLKLRNQMAFSLFHRISKS
1		1	ATRQKTQLASLPQIIEEEKTCKYCSQIGNCALYSRAVEQQMDCS
1	1	[SVPIVMLPKIEEETQHLKQTHLEYFSLWCLMLTLESQSKDNKKN
ļ	i	Į	HQNIWLMPASEMEKSGSCIGNLIRMEHVKIVCDGQYLHNFQCKH
l l	}	i	GAIPVTNLMAGDRVIVSGEERSLFALSRGYVKEINMTTVTCLLD
}	1	1	RNLSVLPESTLFRLDQEEKNCDIDTPLGNLSKLMENTFVSKKLR
1	Į.	l	DLIIDFREPOFISYLSSVLPHDAKDTVACILKGLNKPQRQAMKK
1		j	VLLSKDYTLIVGMPGTGKTTTICTLVRILYACGFSVLLTSYTHS
1	1		AVDNILLKLAKFKIGFLRSR\QIQKVHPAIQQFTEHEICRSKSI
1			KS\LALLEELYTSQLIDATTCMGINHPIFSRKIFDFCIVDEASQ
1		1	· · · · · · · · · · · · · · · · · · ·
1		[ISQPICLGPLFFSRRFVLVGDHQQLPPLVLNREARALGMSESLF
1			KRLEQNKSAVVQLTVQYRMNSKIMSLSNKLTYEGKLECGSDKVA
1	}	1	NAVINLRHFKDVKLELEFYADYSDNPWLMGVFEPNNPVCFLNTD
1	ļ	I	KVPAPEQVEKGGVSNVTEAKLIVFLTSIFVKAGCSPSDIGIIAP
		1	YRQQLKIINDLLARSIGMVEVNTVDKYQD\RDKSIVLVSFVRSN
ļ ·			KDGTVGELLKDNRRI NVAITRAKHKLILLGCVPSLNCYPPLEKL
ļ	1	1	LNHLNSEKLIIDLPSREHESLCHILGDFQRE
6025	3977	89	GGFPAQSDHLPPVFPLRSDLLITMSTLYVSPHPDAFPSLRALIA
1000		1	ARYGEAGEGPGWGGAHPRICLQPPPTSRTSFPPPRLPALEQGPG
	1	1	GLWVWGATAVAQLLWPAGLGGPGGSRAAVLVQQWVSYADTELIP
	Į.	1	AACGATLPALGLRSSAQDPQAVLGALGRALSPLEEWLRLHTYLA
1			GEAPTLADLAAVTALLLPFRYVLDPPARRIWNNVTRWFVTCVRQ
1	i	1	PEFRAVLGEVVLYSGARPLSHQPGPEAPALPKTAAQLKKEAKKR
1	i	1	
i i	ł	İ	EKLEKFQQKQKIQQQQPPPGEKKPKPEKREKRDPGVITYDLPTP
1	1	1	PGEKKDVSGPMPDSYSPRYVEAAWYPWWEQQGFFKPEYGRPNVS
Į.		1	AANPRGVFMMCIPPPNVTGSLHLGHALTNAIQDSLTRWHRMRGE
1	1	}	TTLWNPGCDHAGIATQVVVEKKLWREQGLSRHQLGREAFLQEVW
İ	ì		KWKEEKGDRIYHQLKKLGSSLDWDRACFTMDPKLSAAVTEAFVR
Į.			LHEEGIIYRSTRLVNWSCTLNSAISDIEVDKKELTGRTLLSVPG
į.	}	1	YKEKVEFGVLVSFAYKVQGSDSDEEVVVATTRIETMLGDVAVAV
	1	1	HPKDTRYQHLKGKNVIHPFLSRSLPIVFDEFVDMDFGTGAVKIT
}	1	1	PAHDONDYEVGORHGLEAISIMDSRGALINVPPPFLGLPRFEAR
1	İ		KAVLVALKERGLFRGIEDNPMVVPLCNRSKDVVEPLLRPQWYVR
}	1		CGEMAQAASAAVTRGDLRILPERHQRTWHAWMDNIRE\WCMFPG
	1		KLWWG\HR\IPAYFVTVSDPAVPPGEDPDGRYWVSGRNEAEARE
1			KAAKEFGVSPDKISLQQDEDVLDTWFSSGLFPLSILGWPNQSED
ì			LSVFYPGTLLETGHDILFFWVARMVMLGLKLTGRLPFREVYLHA
1			
1			IVRDAHGRKMSKSLGNVIDPLDVIYGISLQGLHNQLLNSNLDPS
1			EVEKAKEGQKADFPAGIPECGTDALRFGLCAYMSQGRDINLDVN
1			RILGYRHFCNKLWNATKFALRGLGKGFVPSPTSQPGGHESLVDR
1		}	WIRSRLTEAVRLSNQGFQAYDFPAVTTAQYSFWLYELCDVYLEC
}	I		LKPVLNGVDQVAAECARQTLYTCLDVGLRLLSPFMPFVTEELFQ
1			RLPRRMPQAPPSLCVTPYPEPSECSWKDPEAEAALELALSITRA
1			VRP\LRADYNLHPESGPTCFLEVAD\EATGALASAVSGYVQGPG
1	1	1	OAOVVVAVAEPWGLPAP\QGCAVALASDRCSI\HLQLQG\LLDP
1		1	ARELG\KLO\AKRVEAO\ROAO\RLR\ERRA\ASGNPVKVPL\E
ı			VOEADEAKLOOTEAELRKVDEAIALFOKML
6000	1 2634	514	GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAVDKKVDCPRLC
6026	2674	314	TCEIRPWFTPRSIYMEASTVDCNDLGLLTFPARLPANTQILLLQ
1		İ	
ł	1	!	TNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINGKKMPQLLSV
1		1	YLEENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHN
1		1	LLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIKDMNFK
1]	1	PLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPH
i			VALQKVVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPEL
ı		1	ISIDSLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKLESLML
1		1	NSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKTN
1	1		IRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFP
1		1	SNLNVEAGSYVSFHCRATA\EPQPEIYWITPSGQKLLPNT\LTD
L	<u> </u>	J	CHAIN A MIGOT A DE MICHAILE (DE AL MITALE AOSTROLA (MED

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	1 TANAMO GUAG, SEGMENT CONTAINING SIGNS 1 SALLIST
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	ccrresponding	H=Histidine, I=Isoleucine, K=Lysine,
- [corresponding	to first	L=Leucine, M=Methionine N-henaragina
	to first amino acid	amino acid	P=Pro-ine, O=Glutamine, P-appring
	residue of	residue of	S=Serine, T=Threonine, V=Valine
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine Y-Unknown + Char
-	sequence	sequence	Codon, /=possible nucleotide delotion
	1		\=possible nucleotide insertion)
i	1	}	KFYVHSEGTLDINGVTPKEGGLYTCIATNLVGADLKSVMIKVDG
			SFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFVK
ŀ			TENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNR
]			KKCVNVTTKGLHPDQKEYEKNNTTTLMACLGGLLGI IGVICLIS CLSPEMNCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKS
<u> </u>			TSLKVKATVIGLPTNMS
6027	5254	4148	GGRRAPGRPGRSIKDEEEETVFREVVSFSPDPLPVRYYDKDTTK
ł		1	PISFYLSSLEELLAWKPRLEDGFNVALEPLACRQPPLSSQRPRT
			LLCHUMMGGYLDDRFIQGSVVOTPYAFYHWOCTDVFIVEGUUMV
į		1	11PPVGWTNTAHRHGVCVLGTFITEWNEGGRICEAFLACDERCY
			QAVADRLVQIT\RFFRFDGWLINIENSLSLAAVCNMDDET.DVIT
1	1		TQLHRQVPGGLVLWYDSVVQSGOLKWODELNOHNBVERDSCDCR
			I FINYNWREEHLERMLGOAGERRADVYVGVDVFARGNVVGGDEDW
1			DKVGGGFRPRASGPVPPLGPHFLMDLPFPSAPQRNDSSCSSQSG
6028	120	3432	DPVALRNRCPAPAKLCPH
	1	3.32	NCLLLQAKGFHGEIEDLQQWLTDTERHLLASKPLGGLPETAKEQ
1			LNVHMEVCAAFEAKEETYKSLMQKGQQMLARCPKSAETNIDQDI NNLKEKWESVETKLNER\KT\KLEEALNLA\MEFHNSL\QDFIN
]		WLTQAEQTLNVASRPSLILDTVLFQIDEHKVFANEVNSHREQII
			ELDKIGTHLKYFSOKODVVLIKNLIJSVOSPWEKTVORIVEROR
j]		SLUDARKRAKQFHEAWSKLMEWLEESEKSLDSELFTANDDDWIN
Í			TQLAQHKEFQKSLGAKHSVYDTTNRTGRSLKFKTSLADDAT VID
	·		DMLSELRDKWDTICGKSVERONKLEEA\LIFSCOFTDALOALID
i			WLIKVEPQLAEDQPVHGDIDLVMNI,IDNHKAFOKELGKPTGCVO
		•	ALKKSARELIEGSRDDSSWVKVOMOELSTRWETVCATCTCVOTD
į			LEAALRQAEEFHSVVHALLEWLAEAEQTLRFHGVLPDDEDALRT
1			LIDOHKEFMKKLEEKRAELNKATTMGDTVLAICHPDSITTIKHW
			ITIIRARFEEVLAWAKQHQQRLASALAGLIAKQELLEALLAWLQ WAETTLIDKDKEVIPQEIEEVKALIAEHQTFMEEMTRKQPDVDK
1			VTKTYKRRAADPSSLQSHIPVLDKGRAGRKRFPASSLYPSGSQT
			QIETANPAVNLLVSKWOOVWLLALFRERKINDALDDI.PRI DEFA
			NEDFDIWAKKYMRWMNHKKSRVMDFFRRTDKDODGKTTPOPPID
1 1			GILSSKFPTSRLEMSAVADIFDRDGDGYTDVVFFVAALUDNIVDA
1	1		I KPITDADKIEDEVTROVAKCKCAKRFOVEOIGDNKVPERI CNO
1 1		!	FGDSQQLRLVRILRSTVMVRVGGGWMALDERIJVKNDDCDAVCDD
1 1			NMBLREKFILADGASQGMAAFRPRGRRSRPSSRGASPNRSTSVS
i i			SQAAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA
			ECSDFPVPSAEGTPIQGSKLRLPGYLSGKGFHSGEDSGLITTAA ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE
1 1	l	i	IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK
			LDKSSKR
6029	1	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM
ļ	1		AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAOAAVIJGTED
			PNSQAGHQGLVDPIQFARANOAIOMACONI,VDPGSSPSOULSAA
		1	TIVAKHTSALCNACRIASSKTANDVAKRHEVOSAKEVANGTANI
1		1	VKTIKALDGDFSEDNRNKCRIATAPLIEAVENT TAFASNDRBUG
			IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP
ł	j	1	PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC
Į	i		IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHOOOM
	!	!	TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK
į	1		EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG
i	į		TPVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD
1		1	YGHLAFQGQMAAATAEPEEIGFOIRTRVODIGHGCIFI.VOKAC\
}	ļ	ł	ALQVCPTDSYTKRELIECARAVTEKVSLVLSALOAGNKGTONGT
		ł	TAATAVSGIIADLDTTIMFATAGTI.NARNSETFADHDENTI VOD
	ł	·	KALVEDTKLLVSGAASTPDKLAOAAOSSAATITOLAEVOVI CAA
ļ		1	SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKDUDDDEM
İ		i	YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRAI.RATIECTVO
]	i .	ELTVFQSKDVPEKTSSPEESIRMTKGTTMATAKAVAAGNCOPOR
			DVIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRFGTEC

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1		residue of	S=Serine, T=Threonine, V=Valine,
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	residue of	amino acid	
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	l	\=possible nucleotide insertion)
·			TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA
Į	1	1	EAMKGTEWVDPEDPTVIAETELLGAAASIEAAAKKLEQLKPRAK
	Į.	!	PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK
{	1		VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGHA
i	1	1	SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV
1 .	1		KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM
1		1	LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
		<u> </u>	
6030	3	1777	FPGRGSPALQLEVLICLGLMGLERALNVLAPIFYRNIVNLLTEN
1	!		APWNSLAWTVTSYVFLKFLQGGGTGSTGFVSNLRTFLWIRVQQF
	1		TSRRVELLIFSHLHELSLRWHLGRRTGEVLRIADRGTSSVTGLL
1	Į.	1	SYLVFNVIPTLADIIIGIIYFSMFFNAWFGLIVPLCMSLYLTLT
1	ļ		IVVTEWRTKFRRAMNTQENATRARAVDSLLNFETVKYYNAESYE
1	}		VERYREAI I KYQGLEWKSSASLVLLNQTQNLVIGLGLLAGSLLC
l	1		AYFVTEQKLQVGDYVLFGTYIIQLYMPLNWFGTYYRMIQTNFID
J			MENMFDLLKK\ETEVKDLPGAGPFRFQKGRIEFENVHFSYADGR
1	1	ì	BTLODVSFTVMPGQTLALVGPSGAGKSTILRLLFRFYDISSGCI
1			RIDGODISQVTQALFRFSHWELCPKDTVLFNDTIADNIRYGRVT
1	1	1	AGNDEVEAAAQAAGIHDAIMAFPEGYRTQVGERGLKLSGGEKQR
}	1	1	VAIARTILKAPGIILLDEATSALDTSNERAIQASLAKVCANRTT
	\	l .	IVVAHRLSTVVNADQILVIKDGCIVERGRHEALLSRGGVYADMW
i	Į.		
1	l		QLQQGQEETSEDTKPQTMER
6031	160	1694	LRMSENLDKSNVNEAGKSKSNDSEEGLEDAVEGADEALQKAIKS
1	I	ŀ	DSSSPQRVQRPHSSPPRFVTVEELLETARGVTNMALAHEIVVNG
[ì	1	DFQIKPVELPENSLKKRVKEIVHKAFWDCLSVQLSEDPPAYDHA
	1	1	IKLVGEIKETLLSFLLPGHTRLRNQITEVLDLDLIKQEAENGAL
j	1 .	1	DISKLAEFIIGMMGTLCAPARDEBVKKLKDIKEIVPLFREIFSV
,	Į.	.l	LDLMKVDMANFAISSIRPHLMQQSVEYERKKFQEILERQPNSLD
		1	FVTQWLEEASEDLMTQKYKHALPVGGMAAGSGDMPRLSPVAVQN
j	ł.	\	YAYLKLLKWDHLQRPFPETVLMDQSRFHELQLQ\REQLTILGAV
ļ			LLVTFSMAAPGISSQADFAEKLKMIVKILLTDMHLPSFHLKDVL
1	i	1	TTIGEKVCLEVSSCLSLCGSSPFTTDKETVLKGQIQAVASPDDP
			IRRIMESRILTFLETYLASGHQKPLPTVPGGLSPVQRELEEVAI
1			KFARLVNYNKMVFCPYYDAILSKILVRS
6032	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
6032	1 33	1 2413	SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
l l		1	YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK
1	1	1	QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP
1	1		
1.	1		PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS
1	1		SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK
ł	1		SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
1	1		ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
1	1		NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG
			MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAAYGRSPVVGFD
1	1		PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL
1	1		IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
1	l		DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL
1	1		SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
1	Į.		AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS
1	1	į	W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V
l	1	ľ	EVLHYTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
1	1		EAPHALKADKAOPHPWESCAPSPYLAWCGVML (ASTAVDMPTMY
1			w\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\
		J	RATVYEVIY
6033	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
1	1		SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
1	J.		YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK
	1		QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP
i	1		PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS
1		l	SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK
1	1	1	SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
Ì	1		ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
l l	1	Į	NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG
1		1	

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidinc, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion.
<u> </u>	sequence		\=possible nucleotide insertion)
1			MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAAYGRSPVVGFD
1	j		PHHIMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL
			IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
į			DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL
			SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
			AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V
	1		EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
	ļ	1	W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\
1	1		RATVYEVIY
6034	2683	714	ESGRRRLKRRRSPCPGTAGGPGETNPGPGACPRGPREEAAAAM
1			EIAPQEAPPVPGADGDIEEAPAEAGSPSPASPPADGRLKAAAKR
1			VTFPSDEDIVSGAVEPKDPWRHAQNVTVDEVIGAYKQACQKLNC
			RQIPKLLRQLQEFTDLGHRLDCLDLKGEKLDYKTCEALEEVFKR
1	1		LQFKVVDLEQTNLDEDGASALFDMIEYYESATHLNISFNKHIGT
i			RGWQAAAHMMRKTSCLQYL\DARNTPLLDHSAPFVARALRIRSS
1			LAVLHLENASLSGRPLMLLATALKMNMNLRELYL\ADNKLNGLQ
ì	İ		DSAQLGNLLKFNCSLQILDLRNNHVLDSGLAYICEGLKEQRKGL
1			VTL\VLWNNQLTHTGMAFLGMTLPHTQSLETLNLGHNPIGNEGV RHLKNGLISNRSVLRLGLASTKLTCEGAVAVAEFIAESPRLLRL
ľ			DLRENEIKTGGLMALSLALKVNHSLLRLDLDREPKKEAVKSFIE
			TOKALLAEIQNGCKRNLVLAREREEKEQPPQLSASMPETTATEP
			QPDDEPAAGVQNGAPSPAPSPDSDSDSDSDGEEEEEEEGERDET
i			PSGAIDTRDTGSSEPQPPPEPPRSGPPLPNGLKPEFALALPPEP
			PPGPEVKGGSCGLEHELSCSKNEKELEELLLEASOESGOETI.
6035	19	404	SVTYLGIILHKNTGALPADPVQLISQTPTPSTKOOLLSFLGMVG
			YFYLWIPGFAILTKPLCKLTKENLADAIDPKSFSHSSFRSLKTA
6036	1745		LENASTLALPDSSQPF\SLHTAEVQGCVVEILTQGLGPLPV
6036	1/45	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN
! !			SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW
1	i		VLRAALDSGAFQSVWVSTDHDEIBNVAKQFGAQVHRRSSEVSKD
1 1			SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR EEGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD
			WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV
]]			DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS
(' I	į		GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK
1 1			LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK
1 1	1	ı	RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL
6037	2026		MEKGLINFMPKNRNLAVNIGEKK
""	2936	1919	WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA
1 1	ļ		GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR
			SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG
	1		DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL
	ľ		DSPTSITPPPILSADDLLGSPTLPDGTNNPP\AFSSQELASLFA
{	j		PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS
1		į	SSSSHSGSDSPTLDNSRRLPIFSRLSISDD
6038	1450	426	SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH
	ŀ		YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS
			SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG
			NSSCRETETEEBKAKRLL\YCSLCKVAVNSASQLEAHVSGTKHK
1			TMLEARNGSGTI KAFPRAGVKGKGPVNKGNTGLQNKTFHCEICD
1			VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKLQKTAHPL
!		I	GVKLVFSKEPSKPLAPRILPNPLAAAAAAAAVAVSSPFSLRTAP
6039	4073	1000	AATLFOTSALPPALLRPAPGPIRTAHTPVLFAPY
	40/3	1000	LDEYEARLTLANLDDFEEDNEDDDENRVNQEEKAAKITELINKL
ļ			NFLDEAEKDLATVNSNPFDDPDAAELNPFGDPDSEEPITETASP
		1	RKTEDSFYNNSYNPFKEVQTPQYLNPFDEPEAFVTIKDSPPQST
	1	1	KXKNIRPVDMSKYLYADSSKTEEEELDESNPFYEPKSTPPPNNL VNPVQELETERRVKRKAPAPPVLSPKTGVLNENTVSAGKDLSTS

	, , , , , , , , , , , , , , , , , , , 	l n 33 -b 34 ond	They are and a second company of second company
SEQ	Predicted	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	
-	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	amino acid	sequence	Codon, /=possible nucleotide deletion,
Į.	sequence	(⁻	\=possible nucleotide insertion)
	20420		PKPSPIPSPVLGRKPNASQSLLVWCKEVTKNYRGVKI1'NFTTSW
1	<u> </u>	l	RNGLSFCAILHHFRPDLIDYKSLNPQDIKENNKKAYDGFASIGI
1	ł	i	SRLLEPSDMVLLAIPDKLTVMTYLYQIRAHFSGQELNVVQIEEN
1	ł	1	SSKSTYKVGNYETDTNSSVDQEKFYAELSDLKREPELQQPISGA
ì	ļ	i	
1		1	VDFLSQDDSVFVNDSGVGESESEHQTPDDHLSPSTASPYCRRTK
1	į	1	SDTEPQKSQQSSGRTSGSDDPGICSNTDSTQAQVLLGKKRLLKA
1	Į	İ	ETLELSDLYVSDKKKDMSPPFICEETDEQKLQTLDIGSNLEKEK
1		i	LENSRSLECRSDPESPIKKTSLSPTSKLGYSYSRDLDLAKKKHA
ł	ļ		SLRQTESDPDADRTTLNHADHSSKIVQHRLLSRQEELKERARVL
j		1	LEQARRDAALKAGNKHNTNTAAPFCNRQLSDQQDEERRRQLRER
}		1	AROLIAEARSGGKMSELPSYGERAAEKLKERSKASGDENDNIEI
1			DTNEEIPEGFVVGGGDELTNLENDLDTPEQNSKLVDLKLKKLLE
1		1	VOPOVANSPSSAAQKAVTESSEQDMKSGTEDLRTERLQKTTERF
1			RKPVVFSKDSTVRKTQLQSFSQYIENRPEMKRQRSIQEDTKKGN
1	İ		EEKAAITETORKPSEDEVLNKGFKDS\SOYVVGELAALENEQKQ
Į.		1	
1		}	IDTRAALVEKRLRYLMDTGRNTEEEEAMMQEWFMLVNKKNALIR
ì			RMNQLSLLEKEHDLERRYELLNRELRAMLAIEDWQKTEAQKRRE
}]		QLLLDELVALVNKRDALVRDIJDAQEKQAEEEDEHLERTLEQNKG
	1		KMAKKEEKCVLQ
6040	475	1052	PTALMTAPSCAFPVQFRQPSVSGLSQITKSLYISNGVAANNKLM
i	Ī	ł	LSSNQITMVINVSVEVVNTLYEDIQYMQVPVADSPNSRLCDFFD
1	1	J	PIADHIHSVEMKQGR\TLLHCAAGVSRSAALCLAYLMKYHAMSL
1	1	1	LDAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPV
1		1	GMIPDIYEKEVRLMIPL
6041	2	3886	TEKDEKTAHNLENVLIHFWERLSEICVAKISEPEADVESVLGVS
0041	1 -	1	NLLCYLOKPKGSLKSSKKKNGKVRFADEILESNKENEKCVSSEG
1			EKIECWELTTEPSLTHNSSGLLSPLRKKPLEDLVCKLADISINY
Į.	1	ł	VNERKSEQHLRFLSTLLDSFSSSRVFKMLLGDEKQSIVQAKPLE
		l .	IAKLVQKNPAVQFLYQKLIGWLNEDQRKDFGFLVDILYSALRCC
ł	1	ł	
ļ	1		DNDMERKKVLDDLTKVDLKWNSLLKI IEKACPSSDKHALVTPWL
]	i	KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ
j	}	1	HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEAESSDSSVSFIC
1	}		DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAQSKEKTHLPDFLI
Ĭ	1		CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNQVQASSL
i i	1	İ	DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWEK
1	1	i	MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIKTLPSHLCT
j		1	SALLSKMVLIALRKETVLENNELEKIIAELLYSLQWCEELDNPP
1			IFLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW
		1	SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP
1	}	1	FLSKEEKKEFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ
1		1	TKSIDDGELLHGILKIIISWKKEHEDIFLFSCNLSEASPEVLGV
1	1	1	NIEIRFLSLFLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL
1		I	YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK
1	1	}	
Į.		1	EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCETLTY
1		1	ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPLLLFRARP
1			VQIAVYHMLYKLMPELPQYDQDNLKSYGDEEEEPALSPPAALMS
1		1	LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI
1	1	1	LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAB
1	ļ	· ·	TAVEVPNKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTL
1	Ì	•	KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT
1	Ţ	1	STQLFNGMTVKARATTREVMATYTIEDIVIELIIQLPSNYPLGS
1			IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN
1	,		VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY
1		1	KWFTSSNKSTCSLCRETFF
L	 	 	MAELAPASPSDIKASVSNGDTTLLCSRRQSCGMNEVRQVSLTYP
6042	1306	253	
i	}	I	GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHQLFDDTSSAQSRGY
1		1	GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE
1		İ	LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHQDWEV
1			QYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQDRFS
1	1	1	PDLLGLQASSALAWLTLEVLAILLSLYLVTVNTDLTTIDLVAFL
į .	1	1	GYKYVGMIGGVLMGLLFGKIGYYLVLGWCCVAIFVFMIRTLRLK

Г	SEQ	Predicted	[Dec 31 - 5 - 3	•
	ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
.	NO:	nucleotide	ľ	I M-Midifie, C=CVSteine D-Accordic Acid o
- 1		location	location	Graceure Acid, Fephenylalanina C-Clusies
l		corresponding	corresponding	H=HISTIGINE, I=Isoleucine K-Isreine
			to first	L-Leucine, M-Methionine N-Asparagine
- 1		to first	amino acid	Performe, Q=Glutamine, R=Arginine
		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- 1		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1		amino acid	sequence	Codon, /=possible nucleotide deletion,
L		sequence		\=possible nucleotide insertion)
L		1		ILADAAAEGVPVRGARNQLRMYLTMAVAAAQPMLMYWLTFHLVR
	6043	403	599	LCLEEEBCATOUR DE DOCUMENTATION DE LOCALITATION
]		•	1	LCLFFFFPCATPVLPLPSLISAL/CLSHLSVSSWFCPCQPPLPC
	6044	793	412	PLPPLQNKTAKGSLSTEQSERG
- 1			412	KLEMWNFTLISKVKISREVTMIASKFGIGQQVRHSLLGYLGVVV
- 1		1	1	DIDPVISLSEPSPDELAVNDELRAAPWYHVVMEDDNGLDVUTVI
⊢	6045	155		AEAQLSSELQDEHP\EOPSMDELAOTTRKOLOAPPLPM
- 1		133	2299	SPLPQVAAMNYLRRRLSDSNFMANLPNGYMTDLORPOPPDDDDDC
- 1				AHSPGATPGPGTATAERSSGVAPAASPAAPSPGSGGGGFFSGI
				SNAVKQTTAAAAATFSEQVGGGSGGAGRGGAASRVI.VIDEDUT
- [1	ŀ	DWAKYFKGKKIHGEIDIKVEQAEFSDLNLVAHANGGFSVDMEVL
- 1		ļ		RNGVKVVRSLKPDFVLIRQHAFSMARNGDYRSLVIGLQYAGIPS
		ļ		VNSLHSVYNFCDKPWVFAQMVRLHKKLGTEEFPLIDQTFYPNHK
		i i		EMLSS\TTYPVVVKMGHGTLWGWGKVKVDNQHDFQDIASVVALT
- 1				KTYATAEPFIDAKYDVRVQKIGQNYKAYMRTSVSGNWKTNTGSA
- 1		1		MLEQIAMSDRYKLWVDTCSEIFGGLDICAVEALHGKDGRDHIIE
		j		VVGSSVPI.TGDHODPDVOLTUDI JEDUTAVEALHGKDGRDHITE
1				VVGSSMPLIGDHQDEDKQLIVELVVNKMAQALPRQRQRDASPGR
				GSHGQTPSPGALPLGRQTSQQPAGPPAQQRPPPQGGPPQPGPP
- 1				QRQGPPLQQRPPPQGQQHLSGLGPPAGSPLPQRLPSPTSAPQQP
		i		ASQAAPPTQGQGRQSRPVAGGPGAPPAARPPASPSPQRQAGPPQ
- 1				ATROTSVSGPAPPKASGAPPGGQQRQGPPQKPPGPAGPTRQASQ
- [AGPVPRTGPPTTQQPRPSGPGPAGRPKPQLAQKPSQDVPPPATA
- 1				AAGGPPHPQLNKSQSLTNAFNLPEPAPPRPSLSQDEVKAETIRS
	6046	212	1075	LRKSFASLFSD
ı			1075	EGLTGPCERVPFLLGRGPPHGATRAGHRRAVRWAGPESLPPLPR
-				SLIMDSPRAGTHQGPLDAETEVGADRCTSTAYOFOPPOVEOUCK
				QAPUS PGLPAMGGPGPGPCEDPAGAGGAGGAGGGFDI.ITTUTUCON
- 1	- 1	1		FIVALKARRGADLSSLRALLGOALPHO\ AOT.GOT.GVT.ADCEDGT
-	ı	i i		WVPIPEEEELQRAWQDAAACPRGLOLOCRGAGGPDVI.VOVIVA.OU
1	i	1		SISAQGPEDLGFRQGDTVDVI.CEVDQAWI.EGUCDGPICTEDVGB
-	6047			VVPAGPRMSGAPGRLPRSOOGDOP
	004/	49	1405	PVLVTSLRMREADTLRPPOLMEVSADITSTVPFNUTCELLATION
	1	ļ		KGGKVVIFQREPESKNAPHSOGEVDVVSTFOSUPDPEDVI VST D
1	į	•		LEGALNALKWLPQQNAAHSLLSTNDKTIKT.WKTTFFDDVDDFCV37
	- [į.	ı	LKDBEGKLKDLSTVTSLQVPVLKPMDLMVEVSPRRIFANGHTYH
i				INSISVNSDCETYMSADDLRINLWHLAITDRSFTP\NIVDIKPA
-	- 1	1		NMEDLTEVITASEFHPHHCNLFVYSSSKGSLRLCDMRAAALCDK
1		į.		HSKLFEEPEDPSNRSFFSEIIS\SVSDVKFSHSDRYMLTR\DYL
1.	1	•		TVKVWDL\NMEARPIETYQVHDYLRSKLCSLYENDCIFDKFECA
1.	- 1			WNGSDSVIMTGA\YNNFFRMFDRNTKRDVTL\EASRESSKPRAV
1	ļ	i	1	LKPRRVCVGGKRRRDDISVDSLDFTKKILHTAWHPAENIIAIAA
			1	TNNLYIFQDKVNSDMH
1	048	1	3194	GIRTPKFCDQDTCDT PMPNODCO
	!			GIRTPKFCDSPTSDLEMRNGRGRGKRMRPNSNTPVNETATASDS KGTSNSSKTPAGANSKGPRGGSSSKARRPNSNTPVNETATASDS
1	1			KGTSNSSKTRAGANSKGRRGSONSSEHRPPASSTSEDVKASPSS
1	i			ANKRKNKPLSDMELNSSSEDSKGSKRVRTNSMGSATGPLPGTKV
1	J			EPTVLDRNCPSPVLIDCPHPNCNKKYKHINGLKYHQAHAHTDDD
1				SKPEADGDSEYGEEPILHADLGSCNG\ASVSQK\GSLSPARSAT
1	- 1	i	ĭ	PKVRLVEPHSPSPSSKFSTKGLCKKKLSGEGDTDLGALSNDGSD
1	1	İ	ł	DGPSVMDETSNDAFDSLERKCMEKEKCKKPSST.KPFVTDevet v
	- 1	1	i	SARPI/APLAIPPOOIYTFOTATFTAASPGSSSGI.TATUROAMD
!	ļ	ļ		NSPQLKPIQPKPTVMGEPFTVNPALTPAKDKKKKDKKKKESERB
1	- 1		i i	LESPLIPGKVCRAEEGKSPFRESSGNGMKMRGI.I.NGSCDDUOGD
i	ŀ	•	1	LASIKAEADKIYSFTDNAPSPSIGGSSRIENTTPTODITDILTDI
l				TONGARASSVKTNSPAYSDISDAGEDGEGKUDSVKSKDAROLIZZ
1	1		į ·	EGAKKTDFPFQPQSKDSPYYOGFESVVSPSVAOSSDGALNDSSO
1	- 1		1.	AGVESQALKTKRDEEPESIEGKVKNDICEEKKPELSSSSQQPSV
l	1		1	IQQRPNMYMQSLYYNQYAYVPPYGYSDQSYHTHLLSTNTAYRQQ
1	- 1	ł	1 -	YEEQQKRQSLEQQQRGVDKKAEMGLKEREAALKEEWKQKPSIPP
l	1		1.	TLTKAPSLTDLVKSGPGVAKERGLKEKEAALKEEWKQKPSIPP
	- 1	}	1 ;	TLTKAPSLTDLVKSGPGKAKEPGADPAKSVI IPKLDDSSKLPGQ
		į	1:	APEGLKVKLSDASHLSKEASEAKTGAECGRQAEMDPILWYRQBA
			<u> </u>	EPRMWTYVYPAKYSDIKSEDERWKEERDRKLKEERSRSKDSVPK

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
}	location	corresponding	H=Histidine, I=1801eucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
j	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence	\=possible nucleotide insertion)
	sequence	<u> </u>	EDGKESTSSDCKLPTSEESRLGSKEPRPSVHVPVSSPLTQHQSY
			EDGRES ISSUCREPT DEES RESTRICT VOOL STUTTE
		j	IPYMHGYSYSQSYDPNHPSYRSMPAVMMQNYPGSYLPSSYSFSP
{			YGSKVSGGEDADKARASPSVTCKSSSESKALDILQQHASHYKSK
ſ		i	SPTISDKTSQERDRGGCGVVGGGGSCSSVGGASGGERSVDRPRT
•		1	SPSQRLMSTHHHHHHLGYSLLPAQYNLPYAAGLSSTAIVASQQG
i		1	STPSLYPPPRR
		1089	AMTGVFDRRVPSIRSGDFQAPFQTSAAMHHPSQESPTLPESSAT
6049	215	1089	DSDYYSPTGGAPHGYCSPTSASYG\KALNPYQYQYHGVNGSAGS
į		l .	YPAKAYADYSYASSYHQYGGAYNRVPSATNQPEKEVTEPEVRMV
		1	YPAKAYADYSYASSINQYGGAINKYPSAINQPBABYIBPBYKHY
	Į	1	NGKPKKVRKPRTIYSSFQLAALQRRFQKTQYLALPERAELAASL
ļ		1	GLTQTQVKIWFQNKRSKIKKIMKNGEMPPEHSPSSSDPMACNSP
		1	QSPAVWEPQGSSRSLSHHPHAHPPTSNQSPASSYLENSASWYTS
, l	l		AASSINSHLPPPGSLQHPLALASGTLY
		1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL
6050	566	1/10	PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD
1			RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW
	ì		DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY
,	}	1	DCGGQDTFMENYFTSQRDN1FKKVEVLITIVFDVESREDERDINI
į l	1		YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDLR
	1	1	RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN
	1	i	FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
l		1	FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI
ļ		1	PSAATLINIRNARKHFEKLERVDGPKQCLLMR
l	<u> </u>		KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL
6051	566	1718	PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD
1]	1	PNTAMKKKVLLMGKSGSGKTSMKSTTFANTTAKDTKKLGATTED
	l	i .	RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW
1		1	DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY
1	1	1	YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDLR
1	}	1	RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN
	1	· F	FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
]		1	FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI
1	1	1	PSAATLINIRNARKHFEKLERVDGPKQCLLMR
	.l		KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL
6052	566	1718	PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD
l	}	l	PNTANKARVIDINGRASISSIKSTIPANTIAKSTIKSTITALITAKSTIKSTITALITAKSTIKSTITALITAKSTIKSTITALITAKSTIKSTIKSTIKSTITALITAKSTIKSTIKSTIKSTIKSTIKSTIKSTIKSTIKSTIKSTI
ł	1		RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW
1			DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY
ì	1		YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDLR
1		1	RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNLRN
1		}	FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ
		}	FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI
1			PSAATLINIRNARKHFEKLERVDGPKQCLLMR
	 		KGTEMNKSRWQSRRRHGRRSHQQNPWFRLRDSEDRSDSRAAQPA
6053	201	1704	HDSGHGDDESPSTSSGTAGTSSVPELPGFYFDPEKKRYFRLLPG
1			HDSGHGDDESPSTSSG1AG158VPEUPGF1FDFEAARIFRDDPG
ł		İ	HNNCNPLTKESIRQKEMESKRLRLLQEEDRRKKIARMGFNASSM
j		j	LRKSQLGFLNVTNYCHLAHELRLSCMERKKVQIRSMDPSALASD
1	} ,	1	RENLILADINSDRLFTVNDVTVGGSKYGIINLQSLKTPTLKVFM
i	1		HENT.YFTNRKY\NSVCWASLNHLDSHILLCLMGLAETPGCATLL
1		1	PASLFVNSHPAGIDRPG\MLCSFRIPGANSCAWSLNIQANNCFS
1	1		TGLSRRVLLTNVVTGHRQSFGTNSDVLAQQFALMAPLLFNGCRS
1	1	1	GEIFAIDLRCGNQGKGWKATRLFHDSAVTSVRILQDEQYLMASD
1	1		GETTATIDENCEMONE CANDALISM TO AUTHORISM THEMSE
i	1	1	MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEEGILVAVG
l	i	1	QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG
1	1	1	APGLLMAVGQDLYCYSYS
6054	+	1054	P?IARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH
1 5054	1	1	KQSSSQQRRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY
Į.	1	Ì	VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV
		1	DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH
l	1	1	DMILETDATAMKETT SUMMIES PROTOGLEVS ACTS AND A DCH
1	\		
	1	1	GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK
			LVEVARRCRDEATAACRAGAPFSVIGNTISHITHQNGFQVCPHF
			GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPE FKVLEDAWTVVSLD/TSKVSAQFEHTVLITSRGAQILTKLPHEA

r			
SE		Predicted end	Amino agid
II	beginning	nucleotide	
NO	: nucleotide		
1	location	location	
ŀ		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	Leleucine M-Mathiani, Kabysine,
i	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ĺ	amino acid	residue of	^ ~ ~ ~ \ \ - \ - \ - \ - \ - \ - \ - \ -
	residue of		D-Servic, Telhreonine W_U-1:
- 1	amino acid	amino acid	m=iryptophan, Y=Turosing v_m=h-
[sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	1	\-noccible nucleotide deletion,
605	5 421	2364	(-Possible nucleotide insertion)
i i		2364	PPIFLLSFLAWWLYGOSDRTETDISOSACDDDCTT OCCUPATION
i	i	1	GCANCSRFCRDCSPPACQCHTHVFPGNALNGVQPPELSRTLALI
i		İ	SSREPPRKKKKSOTETCKEDERTORE
1	j	ľ	SSREPPRKKKKSQTETGKERERTSFLTQGGKRFELQHGLAGICM
		[1 TODGI VOACAVWDHVIMANREI ARKACDUTUUT DA CATUDOS
	1	i e	I WONT DOES WE PASEVRL WONTED EVER CONTOUT DOMON
ľ	1	ľ	CLCLGRPLQNRDQMRANVINEIMSTERHYIKHLKDICEGYLKQC
1	•	1	RKRRDMESDEOLEVITEDINGSTERMITAHLADICEGYLKOC
ł		i	RKRRDMFSDEQLKVIFGNIEDIYRFQMGFVRDLEKQYNNDDPHL
Į.		1	1 DETGECE DEHODGEWIYSEYCNNHI, DACMEL CVI MVD CDISCISS
	ſ	1	THERED SOME DISCUSSION OF THE PROPERTY OF THE
1	1	i	SDYRYVAAALAVMRNVTQQINERKRRLENIDKIAQWQASVLDWE
i	1	1	GED_LDRSSELTYTCEMANTYON\ VCENTOCTHANDAGASVLDWE
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ļ	1		LADDIARDIDI I KOKIDMDKYEVVDI EDGEDDDENTI CMININ DIGI
i	ŀ		I WAS I DO LITTLE FAKKLISEKIRWI, RAFPEFPKMUADDDVIADDVIADDVIADDVIADDVIADDVIADDVIADD
- 1	i		I MATCHANNI VKKVPKOKGVNGADQVDDQVDDDADDADATATATATATATATATATATATATATATATA
		Ī	\DGIAQSQVFEFTEPKRSQSPFWQNFSRLTPFKK
6056	43	3358	SCCOCOUNTERED CONTRACTOR KK
	1		SGGRGPVRVRSEQLSPSAEQVSQISQISLGRRPLSSLPPPPSRA
	1	'	1 ANDEDIAGITIMEVAEVESPINDSCVTMTEDDOMODDOM
į.	1		1 Imaines AGARKAGLAKVI PPKEWKDDOCVDDIDATE I I I I I I I I I I I I I I I I I I I
ł	1 1		MVTGQSGLFTQYNIQKKAMTVKEFRQLANSGKYCTPRYLDYEDL
	1 1		ERKYMKMI TENADITYCH TAKER KQLIMASGKYCTPRYLDYEDL
- I	į į		ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDVVE
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1	1		1 TALE PERGRADERLAOGFFDSSSOCCON PLOTICIANT TOWARD TO THE
ľ	1 1		LKKYGIPFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNFAT
1			VRWIDYGKVAKI.CTCPKDMUKTONDTTITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
			VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQGKD
1	1 1		1
ł	1 1		MADDE VOLKVEREVENEDSVTDDI.KUSEVSER ALIVE DATES 1
	1 1		OUDDOORSKIIQVEONLSDHTKT,SCNGCT,GTCIPTEGTVPPDTV
	1		YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPESCS
ł	1 1		SVAESNGVIJTEGEFEDVECHOVOV TRANSPERSWPKSPESCS
ł	i i	i	SVABSNGVLTEGEESDVESHGNGLEPGEIPAVPSGERNSFKVPS
- 1	1	1	THEODIKI SKSWKHPLSKPPADSDMTI WYCCZ DODOW STORE STORE
1	1 1	i	ACC ACC TOWARD THE MOLK DOLL A PURE WAY WAS DESCRIBED.
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ļ	1 1	ļ	EICDGWLCARCKRNAWTAEGGT COM DOGGLEVEN HASCYGIPSH
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		1	THE TOTAL CONVIDENCE OF THE PROPERTY OF THE PR
1	1		MFDDGSFSRDTFPEDIVSRDCLKLGPPAEGEVVQVKWPDGKLYG
1	1 1		AKYFGSNIAHMYOVEEEDGGOTAMIGDERAEGEVVQVKWPDGKLYG
1	1 1	F	AKYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF
	1	[VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCNIF LSGTY
6057	1		20011
I	1	000	FVARLKEQEGEGGLGPRKEKGRARGRERRKMQLTRCCFVFLVQ GSLYLVLCGODDCDDCCCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTC
1	1	1	TO THE TOUCH OF THE PROPERTY O
I		1:	RPMANSTILIGITA PPGEAWGII GODDIN DINIONALISPKS
1	1	I 1	RPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFG
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6058	 		LVQKVCPDYNYHSDTPYYPSG
1 0038	1	986	HPI.PSASIGI.DEVELCIVAT CITE
[:	į (HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRARVGSP
		١,	JODANO I PESTREPGVALYLVEPRMGRSRRARI TOT A DOKUMEN
į į	į i	1 1	DACSSEMINVMEETSAERAVSWORDDMAAADDCCHDDA
l I	j	j -	SHIP LESIGAGOPVPVECRHRI.EVACDQKCDI.CDAKMDAVA CO.
1	[) <u>1</u>	PTPLTHHNTGLSEALETLAEA CONCORDED PANMYAYACQR
	Į	17	PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAL
	1	ļ -	OF VII DO VLOGUPHFGEHSSRVVORT.T.ERGVCEEVERINGS.
	†	, 41	TEACONG VAIADEWYREGI, PTI, DDI, PEODOVI TOOOVE CO.
6059			REAGPWASLNCTLDPSASTP
2233	2	3650 0	ODFESLADITOURNURCHCECOROR
- 1	I		QDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT
I	j	1 4	HIGHGCDLGLGEEGGTGI.PVDCOFCDKCPIDI.CVI VDVDO
- 1	1	1 3	DALL FROTI CSRLFKHKRSRDDUTKI.UTCDVVVUOUDODD 7 70
- 1	I	,	OPPORTUDE I RESERVATION DE LA COMPONITATION DE
		E	HLAKSEKRAKKDDEMCDYCEDWIGGESSISSLQSHMQAHKKNK
			HLAKSEKEAKKDDFMCDYCEDTFSQTEELEKHVLTRHPQLSEK

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	/n nine C-Cysteine, D-Aspartic Acid, E=
ID	beginning	nucleotide	Cluramic Acid. Faphenvlalanine, G=Glycine,
NO:	nucleotide	location corresponding	u_uictidine I=Isoleucine, K=Lysine,
1	location		Intercine M=Methionine, N=Asparagine,
Į	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
ļ	to first	amino acid	S=Serine, T=Threonine, V=Valine,
j	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	residue of	amino acid	Codon, /=possible nucleotide deletion,
1	amino acid	sequence	Codon, /=possible nucleotide delector,
	sequence	<u> </u>	\=possible nucleotide insertion)
	50424		ADLQCIHCPEVFVDENTLLAHIHQAHANQKHXCPMCPE\QFSSV
	i	1	\EGVYCHLDSHRQPDSSNHSVSPDPVLGSVASMSSATPDSSASV
	Į	1	ERGSTPDSTLKPLRGQKKMRDDGQGWTKVVYSCPYCSKRDFNSL
		ì	AVIETHIKTIHADKPOOSHTCOICLDSMPTLYNLNEHVRKLHKN
ļ	4	1	UNANDIMORGNISAFHCNYCPEMFADINSLOEHIRVSHCGPNANP
	1		COCKNAPECNOCSMGFI.TESSI.TEHIO\O\AHCSVGSAKLESPV
	1	į	UODTOGEMEUVSCOVCTNSPIFGSILKLTKHIKENHKNIPLAHS
	1	Į.	KKSKAEQSPVSSDVEVSSPKRQRLSASANSISNGEYPCNQCDLK
	1	1	FSNFESFQTHLKLHLELLLRKQACPQCKEDFDSQESLLQHLTVH
	ì	ì	YMTTSTHYVCESCDKQFSSVDD\LQKH\LLDMPHPLCCTHCT\L
]	i	YMTTSTHYVCESCDKQFSSVDD\LQKH\LDDHFHI DCCTACT (2
		· L	CQEVFDS\KVSI\QVHLAVKHSNEKKMYRCTACNWDFRKEADLQ
		1	VHVKHSHLGNPAKAHKCIFCGETFSTEVELQCHITTHSKKYNCK
	1		FCSKAFHAIILLEKHLREKHCVFDAATENGTANGVPPMATKKAE
	}		DADIOGMILKNDEADNSHEASEDDVDASEPMYGCDICGAAYIME
	1		THE COMPAND THE PROPERTY OF THE SECOND STREET OF TH
	1		NCI PRUI OTHROPAKHYMCPICGERFPSLLTLTEHKVTHSKSLD
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	\	1	OF ELVINGTEHMORT AGSSAASSPINGOGLOKLYKCALCLKEEK
		1	GVODI VVI DUNGI DVGI CAGCMARSANGOVGGLAPPEPADRPCA
}		1	CI DCDECCVKEESAEDLESHMOVDHRDLTPETSGPRKGTQTSPV
ì	I	1	PREVENUE TROUBLE TO THVANHMIEEGINHECKLENQM
ì	1	İ	FDSPAKLLCHLIEHSFEGMGGTFKCPVCFTVFVQANKLQQHIFA
l	ł	ì	VHGQEDKIYDCSQCPQKFFFQTELQNHTMSQHAQ
1	t	1	VHGQEDKIYDCSQCFQKFFFQTBBQMTTLPLGENLPLLDRGFR SYEIVGKNKLEVNHSQLKALCKCSLPSRLLPLGENLPLLDRGFR
6060	2145	202	SYEIVGKNKLEVNHSQLKALCKCSDFSKLDAMLAVLLSLAPSASS KEPRSRGSRERDNMLHLHHSCLCFRSWLPAMLAVLLSLAPSASS
1	1	1	KEPRSRGSRERDNMLHLHHSCLCFRSWDFAMILY DISASRPNILLLMADDLGIGDIGCYGNNTMRTPNIDRLAEDGVK
1			DISASRPNILLLMADDLG1GD1GC1GNATMATTATDICTION OWTGAS
		1	LTQHISAASLCTPSRAAFLTGRYPVRSGMVSSIGYRVLQWTGAS
,	1	į.	GGLPTNETTFAKILEEKGYATGLIGKWHLGLNCESASDHCHHPL
	1	1	HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV
}			ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA
ì		1	DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPPLLFV
1	1		SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV
ì	}	l l	EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW
Ì	1	ł	PCCTDVDCTEDWDCVI.PAGRVIGEPTSLMDVFPTVVRLAGSEVP
1	1	1	ODDUTEGODI J.P. J. J. GTAOHSDHEFLMHYCERFLHAARWHQRDR
1		1	COMPLETE TO THE PROPERTY OF TH
1	ł	· ·	LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ
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1			MANTINEEVELLESEQGSPN
6061	110	1330	THIND DARKED I I NAVINGE PPEDSLSVDHFOTOTE PVDLSINA
Į.	1		- PROPERTY COUNTY OF CASSESSES SELASSES VIIIS
1	1		VSSASSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLC
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1	1		SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG
1			HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA
1		i i	RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN
1	į	ì	PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY
ł	1	1	KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDI
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1	1	i	METERCONCEDETIEVHDEKNGYTGIYEVGLQKCF 1KTQ1KV11
		1	PROPORTE TO THE TOTTE FROSVI WVPAEKPIENKUFLKNSK.
1			LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDPI
1			LEICDNVTWW\INFIL\ISGIFARQLEELI EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELI
1			INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYY
1			INDYTENGLEFOPMIDERGYCCTICRROURICRCCCTICARCO
l		1	YPYCYQGGRVICRVIMPCNWWVARMLGRV
6063	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGHVFGILAH
""	·		THE PARCY DEVENDED BY THE TOP VIOLENTE TOP V
	1	1	MULTIPOCNOTORTI RVIDEKNOYTGIYFVGLQKCFIKIQIKVI
1	1	1	THE
1)	ì	LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDF
6063	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSL LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGE

SEQ	Predicted	Drodience	
ID	beginning	Predicted end nucleotide	
NO:	nucleotide	location	
	location		
1	corresponding	corresponding	I TOTAL VELOCITIES ISISOTETICING V T!
1	to first	to first	Julieucille, Memernionine Management
1	amino acid	amino acid	I * Tr tottic, Oscillicamine p-z
ļ	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Sto
	amino acid	sequence	Codon (=possible ====================================
<u> </u>	sequence	_	Codon, /=possible nucleotide deletion,
1			\=possible nucleotide insertion)
1			EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEEI INDYTENGIEFDEN DEEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
Ł			1
6064	913		I TOGGKATCKATMBCMMMADMICDM
1 1		311	NLPQSLPRPTEHSPPYSLEKMTDLVALGOVALGOVALGOVALGOVALGOVALGOVALGOVALG
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1 1			LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYIKAV
6065			SSG\KRKEGIIHTLIVDNREIPEIAS
0003	1153	641	MSVRVARVAWVPGTCACVPDCACGER
]			MSVRVARVAMVRGLGASYRRGASSFPVPPPGAQGVAELLRDAT
1 1	ľ		AEEEAPWAATERRMPGQCSVLLFPGQGSQVVGMGRGLLNYPRV
			1 SELECTION OF THE PROPERTY OF
6066	68	3470	THE PROPERTY OF THE PROPERTY O
	1	-170	VALAMPATRAPHRYGHTEGHTEVCEDDSGSETURGGOS
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' !	- 1		1 TANDEN A A LUCIDE LA VICTORIA DE ANTANA
j			I ARTON CONTRACTOR AND MID MINE AND CONCOUNT AND
1			T TO THE HOUSE COUNTY IN THE TOTAL TO THE TOTAL TO THE TOTAL THE TOTAL T
[f		1 ~~
f	1		ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGLLENG
1			CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNAVEII
	1		SFSKGI INDDEDDEDI MMA SGDEDON SNAGDFLNDNAVEII
			SFSKGIINDDEDDEDLMMASGRPRORSHILEDDENSVDISMLKT
J	1		GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPRQKPFQS
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	}		OTTOR V VOIMBRIEDINK I V V HDCTC DDCDCCC CTTCT
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1		1	TO THE TOTAL PROPERTY OF THE TOTAL PROPERTY
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1	1	i	THE PROPERTY OF THE PROPERTY O
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i	}		KPEIHKPGONSESKSTNESDYCZYSOSYSOSYSOSYSOSYSOSYSOSYSOSYSOSYSOSYSO
1	1	į	KPEIHKPGONSFSKSTNSSDVSAKSGAVTFSSOGRVNPFKVSAS SKEPAMSMNSABSTYLL DYMONOGRAFIE
1		1	SKEPAMSMNSARSTNILDNMGKSSKKSTALSRTTNNEKSPIIKP
1	į		THE ACADAMOTECKINS OF MANDE INCOME.
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1		1	- DOTCHER LUCKISELLVRKWRVKChI CAMOONOT WITHOUT
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J		J i	GSKMADLANEEKPAIAPPVFVFQKDKGQKSPAEQKNLSDSGEEP
}			TO THE TANGLORE SAUKHALIKUDADA CACACMANANA
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- 1	ſ	1 4	THE THE ADADASSING VEGONMS ROLL S DOWN MENCODS THE
1		1 • '	THE COLOSSY CATPERES LARSADAVIKATA DECLE TO THE COLOS
1	J	l G	EEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG
l	1	T	LQSRLSDAGPRGSLP\LILNTYLTTONG
ſ	Ĭ	l n	LQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM
ł	1	,	TO SOUTH TO ASSEND THE OWN AND THE REPORT OF THE PROPERTY OF T
		T	PAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS
069	583		· · · · · · · · · · · · · · · · · · ·
	1	1 -	TRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK
1	1		
	Ì	1 20	HARVTVKYDRRELQRRLDVEKWIDGRLEELYRGMEADMPDEIN DELLELESEEERSRKIQGLLKSCGKPVEDFIQELLAKLQGLHR

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
ł	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	residue of	amino acid	Codon, /=possible nucleotide deletion,
Ì	amino acid	sequence	\=possible nucleotide insertion)
Ì	sequence		Q\PGLRQPSPSP\DGQPSAPFQGPGARTASPLTLLALFPGPPER
		1	RPALLCVLSCI
1			IRVTVDGEFLHYIFPLQFLDSPEW/RFTETHRGRHF\QVTLTAE
6070	478	858	TDCRYVSWRRKKLYLLFAQHRYISRLFSVLIGSDIADKLYALND
Ī		,	RVYIGKRYHYDIRLPNFYQMSTPEIRRSPLTQHFQNSRRYW
1			HEARTKGNMALARP\VRLFSLVTRLLLAPRRGLTVRSPDEPLPV
6071	2	1654	VRI PVALQRQLEQRQSRRRNLPRPVLVRPGPLLVSARRPELNQP
1			ARLTLGRWERAPLASQGWKSRRARRDHFSIERAQQEAPAVRKLS
Į	į		ARLTEGRWERAPDASQGWKSRRARRDHFSI BRAQQBAFA KRUB
	1		SKGSFADLGAWKPRVLHALQE\AAPEVVQ\PTTVQSSTIPSLLR
1	1		GRHVVCAAETGSGKTLSYLLPLLQRLLG\HPSLDSLPIPAPRGL
1	1		VLVPSRELAQQVRAVAQPLGRSLGLLVRDLRGGHGMRRIRLQLS
İ	1		ROPSADVLVATPGALWKALKSRLISLEQLSFLVLDEADTLLDES
	1	J	FLELVDYILEKSHIAEGPADLEDPFNPKAQLVLVGATFPEGVGQ
	1	1	LLNKVASPDAVTTITSSKLHCIMPHVKQTFLRLKGADKVAELVH
ł	1	}	ILKHRDRAERTGPSGTVLVFCNSSSTVNWLGYILDDHKIQHLRL
1			QGQMPALMRVGIFQSFQKSSRDILLCTDIASRGLDSTGVELVVN
İ	1.	į.	YDFPPTLQDYIHRAGRVGRVGSEVPGTVISFVTHPWDVSLVQKI
ì			ELAARRRSLPGLASSVKEPLPQAT
6072	1	742	KMERTEMMPTINSQLEFKSKPFPLVSSSRWLVKRGELTAYVEDT
			VLFSRRTSKQQVYFFLFNDVLIITKKKSEESYNVNDYSLRDQLL
			VESCONEELNSSPGKNSSTMLYSRQSSASHLFTLTVLSNHANEK
	l .		VEMLLGAETQSERARWITALGHSSGKPPADRTSLTQVEIVRSFT
1	1	Ì	AKQPDELSLQVADVVLI\YQRVSDGWYEGER\LRDGERGWFPME
1	1		CAKEITCQATIDKNVERMGRLLGLETNV
6073	620	860	PCRRGLARPLSRRPG/SILVHCAVGVSRSATLVLAYLMLYHHLT
}	ł	1	LVEAIKKVKDHRGIIPNKGFLRQLLALDRRLRQGLEA
6074	168	1110	PGARCMATELQCPDSMPCHNQQVNSASTPSPEQLRPGDLILDHA
1	l .	1	GGNRASRAKVILLTGYAHSSLPAELDSGACGGSSLNSEGNSGSG
Ì	1	i	DSSSYDAPAGNSFLEDCELSRQIGAQLKLLPMNDQIRELQTIIR
1	i		DKTASRGDFMFSADRLIRLVVEEGLNQLPYKECMVTTPTGYKYE GVKFEKGNCGVSIMRSGEAMEQGLRDCCRSIRIGKILIQSDEET
1	İ		QRAKVYYAKFPPDIYRRKVLLMYPILQTG\NTVIEAVKVLIEHG
Į.	1		QRAKVYYAKFPPDIYRRKVLLWIFILQIG (NIVILAVKVBILIG VQPSVIILLSLFSTPHGAKSIIQEFPEITILITEVHPVAPTHFG
1	İ		1
			QKYFGTD PPTCQPQEVEHH\YGYVPILGNKTLPSRCHQCVIVSSSSHLLGT
6075	320	1091	PPTCQPQEVEHH\TGYVPILGNKILPSKCHQCVIVSSSSIEESI KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV
1			LRRPQEFVNRTFETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFP
1			LRRPQEFVNRTFETVF1FWGPPSKMQKPQGSDVKV1QAGDVTF NMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIA
1			NMEAYAVSPGRMRQFDDLFRGETGKDREKSHSMLSTGWFTHVTA VELCDHVHVYGMVPPNYCSQRPRLQRMPYHYYEPKGPDECVTYI
1	1		VELCOHVHVYGMVPPNYCSQRPRLQRMPIHITEFROFDSCVIII QNEHSRKGNHRFITEKRVFSSWAQLYGITFSHPSWT
1			QNEHSRKGNHHRFITERRVFSSWAQLIGITFSHFSWI HPSPTEAPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGAEV
6076	1721	107	HPSPTEAPRVQHLTMDCTWRILFLVAAATGIAAQVQUVQSGABV KKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGAFDPED
			KKPGASVKVSCKVSGYTLTELSMHWVKQAFGRODEMMGAF OF BD GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD
1			GETIYAQKFQGRVTMTEDISTDTAXMELSSLKSEDIAVITCATD HGDYAFDIWGQGTMVTVSSAPTKAPDVFPIISGCRHPKDNSPVV
	1 .		HGDYAFDIWGQGTMVTVSSAPTKAPDVFPTISGCKNFRDNSFVV LACLITGYHPTSV\TVTWYMGTQSQA\QRTFPEIQRRDSYYMTS
]		ĺ	LACLITGYHPTSV\TVTWYMGTQSQA\QKIFFELQAADSITMIS SQLSTPLQQWRQGEYKCVVQHTASKSKKEIFRWPESPKAQASSV
	1		SOUSTPLOOMKOGEIKCVVORTASKSKKEIFKMEESEKKONSSV
		}	PTAQPQAEGSLAKATTAPATTRNTGRGGEEKKKEKEKEEQEERE
	1		TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD
	1		AHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWNA
1	1		GTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSLNLLASSDPPE
1			A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\
			RSTTFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL
		1	EVSYVTDHGPMK
6077	3687	1268	LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIQ
			AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPR
			GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP
1			QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN
I	{		EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS
[1	PFSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMQVA
ļ	ļ	1	VCGSLIGWRNVTRLLVFSTDAGFHFAGDGKLGGIVLPNDGQCHL
L			

SEO	Predicted		
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide location	In-mighting, C=CVStelne, D=Nenartic Noid =
- 1	location	corresponding	Glucamic Acid, FePhenylalanine Cacharine
ł	corresponding	to first	n=nistiding, l=Isoleucine Valueine
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l l	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			ENNMYTMSHYYDYPSIAHLVQKLSENNIQTIFAVTEEFQPVYKE
			LKNLIPKSAVGTLSANSSNVIQLIIDAYNSLSSEVILENGKLSE
i	1		GVTISYQSY\CKNGVNGTGENGRKCSNISIGDEVQFEISITSNK
-			CPKKDSDSFKIRPLGFTEEVEVILQYICECECQSEGIPESPKCH
ı			EGNGTFECGACRCNEGRVGRHCECSTDEVNSEDTGCFTARKENO
			FURSASNIGROPSAGQCVCRKRDNINEIYSGKFCECDNFNCDDS
1			NGLICGGNGVCKCRVCECNPNYTGSACDCSLDTSTCEASNGOIC
- [NGRGICECGVCKCTDPKFOGOTCEMCOTCLGVCAEHKECVOCPA
1			FNKGEKKDTCTQECSYFNITKVESRDKLPOPVOPDPVSHCKEKD
i			VDDCWFYFTYSVNGNNEVMVHVVENPECPTGPDTTPTVACUUAC
į			1VLIGLALLLIWKLLMIIHDRREFAKFEKEKMNAKWDTGENDIV
6078	1426	180	KSAVTTVVNPKYEGK
1	1	180	BTEDVMELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILE
ł			GSVKNSLWRPVPFKCPTCRKKTFSYWELIPLOVMVSLVGTVEVV
I	1		NKIKISPKMPVCKGH\LGQPLNIF\CL\TDMQLDL/CGIC\ATR
1			GEHTKHVFCSIEDAYAQERDAFESLFQSFETWRRGDALSRLDTL
I	1		ETSKRKSLQLLTKDSDKVKEFFEKLQHTLDQKKNEILSDFETMK LAVMQAYDPEINKLNTILQEQRMAFNIAEAFKDVSEPIVFLQQM
1			QEFREKIKVIKETPLPPSNLPASPLMKNFDTSQWEDIKLVDVDK
1			LSLPQDTGTFISKIPWSFYKLFLLILLLGLVIVFGPTMFLEWSL
1]		FDDLATWKGCLSNFSSYLTKTADFIEQSVFYWEQVTDGFFIFNE
6070		·	RFKNFTLVVLNNVAEFVCKYKLL
6079	1586	141	ATARDLGCARRIDRVVMESTPSRGLNRVHLOCRNLORELGGLCD
•			GVLDKLYGHPATCLAVFRELPSLAKNWVMRMI.FI.FODI.DOD AVA
1			LWVKKEFSKAQEESTGLLSGLRIWHTOLLPGGLOGLTLWDIEDO
})		NERTALLEGGERAWSDDTSOLGPDKHARDVPSI.DKVAFFDWFIAM
1			HFMVGSPSAAVSQDLAQLLSOAGLMKSTEPGEPPCTTSAGEOFT
	1		LLDTPAQLWYFMLQYLOTAOSRGMDLVETLSELEOLSPETT CVD
ı	1		ISVEGMSUSLLNFLQHLREFGLVFORKRKSRRVVDT/DALAINT
1	1		SSGVSGAGGTVHQPGFIV\VETNYRLYAYTESELQIALIALFSE
1			MLYPFP\NMVV\ARVTR\ESVQQAIASGITAQQIIHFLRTRAHP
1			VMLKQTPVLPPTITDQIRLWELERDRLRFTEGVLYNQFLSQVDF
			ELL\LAHAPKLGVLVFB/NTPAKRLMVVTPAGHSDVKRFWKRQK
6080	1	1199	
]			IETIDHVGEFAMAAQAAGVSRQRAATQGLGSNQNALKYLGQDFK TLRQQCLDSGVLFKDPEFPACPSALGYKDLGPGSPQTQGIIWKR
Į [PTELCPSPQFIVGGATRTDICQGGLGDCWLLAAIASLTLNEELL
į 1	1		YRVVPRDQDFQENYAGIFHFQPLCPPSP\FWQYGEWVEVVIDDR
ļ			LPTKNGQLLFLHSEOGNEFWSALLEKAYAKINGCVEALACCOM.
1	Ì]	EGFEDFTGGISEFYDLKKPPANLYOITRKALCAGSLLGCGIDUR
1			SAAEAEAITSQKLVKSHAYSVTGVEEVNFOCHDEKT.TDT.DNDWG
			EVENSGANSDDAPEWNHIDPRRKEELDKKVEDGEFWMSLSDEVD
i -			QFSRLEICNLSPDSLSSEEVHKWNLVLFNGHWTRGSTAGGCONV
6081	3		PGSS
	,	865	EMLPLLLPLPLLWA/GALAQDARFRLEMPESVTVQEGLCIFVHC
1	j	ļ	SVFYLEYGWKDSTPAYGHWFREGVSVDOETPVATNNSTOKYOVE
1		1	TOGREFILLGDPSRNNCSLSIRDARRRDNGSYFFWUADGREFFEC
1	1	į	KYSPLSVYVTALTHRPDILIPEFLKSGHPSNI.TCSVPhricecom
ł	į		PPIFSWMSAAPTSLGPRTLHSSVLTI I PRPODHGTMI I COMPAND
_	,	1	GAGVTTERTIQLSVSWKSGTVEEVVVLAVGVVAVKTLLLCLCLT
6082	283	1288	ILSFHKKAVRAVEVSENVYAVMG
			EARSPOPTQTRTAPGLAAPGLAQPAALRLLLSRPPSAAMDGDGD
		1	PESVGQPEEASPEEQPEEASAEEERPEDQQEEEAAAAA\Y\LDE
		1	LPEPLLA/LRVLAALPRHE\LVQACR\LVCLRWKELVDGAPLWL
1		1.	LKCOOEGLVPEGGVEEERDHWQQFYFLSKRRRNLLRNPCGEEDL
1	}	<u> </u>	EGWCDVEHGGDGWRVEELPGDSGVEFTHDESVKKYFASSFEWCR
1		1.	KAQVIDLQAEGYWEELLDTTQPAIVVKDWYSGRSDAGCLYELTV
	1	į:	KLLSEHENVLAEFSSGQVAVPQDSDGGGWMEISHTFTDYGPGVR
6083	1865	309	FVRFEHGGQDSVYWKGWFGARVTNSSVWVEP KQWCAERRGLGMSLADELLADLEEAAEEEEGGSYGEEEEEPAIE
			TOOL TO THE THE THE THE THE THE THE THE THE THE

CEA	Dwodi = 50-3	Predicted end	I Amino soid compart
SEQ	Predicted	1	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	1		
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			DVQEETQLDLSGDSVKTIAKLWDSKMFAEIMMKIEEYISKQAKA
1		1	SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR
		ļ	FPELESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM
1	1	1	VVSVTASTTQGQQLSEEELERLEEACDMALELNASKHRIYEYVE
1	1	1	SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG
I		1	
1		1	AQRKTLSGFSSTSVLPHTGY1YHSDIVQSLPP1PPPFSVAP\DL
	Į.	i	RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
Į	ļ	1	QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ
	1		ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA
ſ		1	RISKTLQRTLQKQSVVYGGKSTIRDRSSGTASSVAFTPLQGLEI
		Ì	VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
6084	1865	309	
1 0003	1005	303	KQWCAERRGLGMSLADELLADLEEAAEEEEGGSYGEEEEEPATE
}	1	!	DVQEETQLDLSGDSVKTIAKLWDSKMFAEIMMKIEEYISKQAKA
1	Į	1	SEVMGPVEAAPEYRVIVDANNLTVEIENELNIIHKFIRDKYSKR
1	Ī	1	FPELESLVPNALDYIRTVKELGNSLDKCKNNENLQQILTNATIM
1	ł	1	VVSVTASTTQGQQLSEEELERLEEACDMALELNASKHRIYEYVE
1		1	SRMSFIAPNLSIIIGASTAAKIMGVAGGLTNLSKMPACNIMLLG
1		Į.	AQRKTLSGFSSTSVLPHTGYIYHSDIVQSLPPIPPPFSVAP\DL
i	1	1	RRKAARLVAAKCTLAARVDSFHESTEGKVGYELKDEIERKFDKW
1	Į.	i	QEPPPVKQVKPLPAPLDGQRKKRGGRRYRKMKERLGLTEIR\KQ
1		1	
	Į.	1	ANRMSFGEIEEDAYQEDLGFSLGHLGKSGSGRVRQTQVNEATKA
ļ		1	RISKTLQRTLQKQSVVYGGKSTIRDRSSGTASSVAFTPLQGLEI
	<u> </u>	1	VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
6085	2	1456	SGPRSFQGNRAVGRISLGGKRNPEVTLLPGVSSERVRRWRRARV
		1	GVARVKPGNPWKPSPATQVPR/VPAQVYLPGRGPPLREGEELVM
}	1	1	DEEAYVLYHRAQTGAPCLSFDIVRDHLGDNRTELPLTLYLCAGT
İ		i	QAESAQSNRLMMLRMHNLHGTKPPPSEGSDEEEEEEDEEDEEER
1		Ì	KPQLELAMVPHYGGINRVRVSWLGEEPVAGVWSEKGOVEVFALR
		Ī	1
i			RLLQVVEEPQALAAFLRDEQAQMKPIFSFAGHMGEGFALDWSPR
1		1	VTGRLLTGDCQKNIHLWTPTDGGSWHVDQRPFVGHTRSVEDLQW
1		1	SPTENTVFASCSADASIRIWDIRAAPSKACMLTTATAHDGDVNV
1		ł	ISWSRREPFLLSGGDDGALKIWDLRQFKSGSPVATFKQHVAPVT
Į.	1		SVEWHPQDSGVFAASGADHQITQWDLG/IVERDPEAGDVEADPG
1		1	LADLPQQLLFVHQGETELKELHWHPQCPGLLVSTALSGFTIFRT
1	1		ISV
6086	2419	1357	GAATQHGGAMNLLPCNPHGNGLLYAGFNQDHGCFACGMENGFRV
1 3000		1 1337	·
j		1	YNTDPLKEKEKQEFLEGGVGHVEMLFRCNYLALVGGGKKPKYPP
1		i	NKVMIWDDLKKKTVIEIEFSTEVKAVKLRR\DKIVVVLDSMIKV
1	I		FTFTHNP\HQLHVFE\TCYNPKGLCVLCPNSNNSLLAFPGTHTG
Į.			HVQLVDLASTEKPPVDIPAHEGVLSCIALNLQGTRIATASEKGT
1	!		LIRIFDTSSGHLIQELRRGSQAANIYCINFNQDASLICVSSDHG
i	1	1	TVHIFAAEDPKRNKQSSLASASFLPKYFSSKWSFSKFQVPSGSP
ŀ	l	1	CICAFGTEPNAVIAICADGSYYKFLFNPKGECIRDVYAQFLEMT
İ	[DDKL
6087	175	1077	
000/	476	1877	QNSQRTGLPITIFSRSFPLLTGSDLCENMPCTCTWRNWRQWIRP
ļ	1	l	LVAVIYLVSIVVAVPLCVWELQKLEVGIHTKAWFIAGIFLLLTI
ĺ	1	1	PISLWVILQHLVHYTQPELQKPIIRILWMVPIYSLDSWIALKYP
1	1		GIAIYVDTCRECYEAYVIYNFMGFLTNYLTNRYPNLVLILEAKD
1	1		QQKHFPPLCCCPPWAMGEVLLFRCKLGVLQYTVVRPFTTIVALI
1 .	1	ļ	CELLGIYDEGNFSFSNAWTYLVIINNMSQLFAMYCLLLFYKVLK
1	1		EELSPIQPVGKFLCVKLVVFVSFWQAVVIALLVKVGVISEKHTW
1	1	1	EWOTVEAVATGLODFIICIEMFLAAIA\HHYTFSYKPYVOEARE
1	1		1 - 1
1	1		GSCFDSFLAMWDVSDIRDDISEQVRHVGRTVRGHPRKKLFPEDQ
1]		DQNEHTSLLSSSSQDAISIASSMPPSPMGHYQGFGHTVTPQTTP
L]_		TTAKISDEILSDTIGEKKEPSDKSVDS
6088	1684	689	GASGLVRLLOOGHRCLLAPVAPKLVPPVRGVKKGFRAAFRFQKE
1 .			LERORLLRCPPPPVRRSEKPNWDYHAEIQAFGHRLQENFSLDLL
l	1		-
1	1		KTAFVNSCYIKSEEAKRQQLGIEKEAVLLNLKSNQELSEQGTSF
			SQTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVARNLAVE
1			QLTLSEEFPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI
	<u></u>		TQMTGKELFEMWKIINPMGLLVEELKKRNVSAPESRLTRQSG\A

SEO	Predicted	T Dec. 22	
ID	beginning	Predicted end	
NO:	nucleotide	nuclectide	[A=Alanine, C=CVsteine, D=Aspartic Acid m
]	location	location	Glutamic Acid, FePhenylalanine G-Glycine
1	corresponding	corresponding to first	H=Histidine, I=Isoleucine K=Iscine
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ł	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
	7	 	\=possible nucleotide insertion)
			PTALPLYFVGLYCDKKLIAEGPGETVLVAEEEAARVALRKLYGF
6089	3	3054	TENRRPWNYSKPKETLRAEKSITAS
	1	3034	TRLGIPGSTISSRPRLCALAAEGHFLGHSWTGSRAGAHTGAPAW
			PSRRLRDLPAGGMWRLRRAAVACEVCQSLVKHSSGIKGSLPLQK
1	1		LHLVSRSIYHSHHPTLKLQRPQLRTSFQQFSSLTNLPLRKLKFS
	1		PIKYGYQPRRNFWPARLATRLLKLRYLILGSAVGGGYTAKKTFD
i			QWKDMIPDLSEYKWIVPDIVWEIDEYIDFEKIRKALPSSEDLVK
ì		İ	LAPDFDKIVESLSLLKDFFTSGSPEETAFRATDRGSESDKHFRK
1		l	VSDKEKIDQLQEELLHTQLKYQRILERLEKENKELRKLVLQKDD
ļ		Į	KGIPFIESLRKSLIDMYSEVLDVLSDYDASYNTQDHLPRVVVVG
1		İ	DQSAGKTSVLEMIAQARIFPRGSGEMMTRSPVKVTLSEGPHHVA
i	1		LFKDSSREFDLTKEEDLAALRHEIELRMRKNVKEGCTVSPETIS
İ	i	·	LNVKGPGLQRMVLVDLPGVINTVTSGMAPDTKETIFSISKAYMQ
		[DPNAIILCIQDGSVDAERSIVTDLVSQMDPHGRRTIFVLTKVDL
1	i		AEKNVASPSRIQQIIEGKLFPMKALGYFAVVTGKGNSSESIEAI
ł	i		REYEEEFFQNSKLLKTSMLKAFQVTTRNLSLAVSDCFWKMVRES
			VEQQADSFKATRFNLETEWKNNYPRLRELDRNELFEKAKNEILD
	•		EVISLSQVTPKHWEEILQQSLWERVSTHVIENIYLPAAQIMNSG
j			TFNTTVDIKLKQWTDKQLPNKAVEVAWETLQEEFSRFMTEPKGK
1			EHDDIFDKLKEAVKEESIKRHKWNDFAEDSLRVIQHNALEDRSI SDKQQWDAAIYFMEEALQARLKDTENAIENMVGPD\WKKRWLYW
			KNRTQEQCVHNETKNELEKMLKCNEEHPAYLASDEITTVRKNLE
i			SRGVEVDPSLIKDTWHQVYRRHFLKTALNHCNLCRRGFYYYQRH
			FVDSELECNDVVLFWRIQRMLAITANTLRQQLTNTEVRRLEKNV
	i		KEVLEDFABDGEKKIKLLTGKRVQLAEDLKKVREIQEKLDAFIE
			ALHOEK
6090	194	1560	PVFVPAPGAVLEQAS/ASPPLATQTVVPLQHCKIPELPVQASIL
1 1			FELQLFFCQLIALFVHYINIYKTVWWYPPSHPPSHTSLNFHLID
			FNLLMVTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTRFTV
1 1			LTATGWSLCRSLIHLFRTYSFLNLL/FPLLSVWDVHSVPAAELR
1	i		P\RKTSLFNHMASMGPREAVSGLAKSRDYLLTLR\RRGSSTQDS
1 1	•		CMARTPCP/PHACCLSPSLIRSEVEFLKMDFNWRMKEVLVSSML
	1		SAYYVAFVPVWFVKNTHYYDKRWSCELFLLVSISTSVILMQHLL
1			PASYCDLLHKAAAHLGCWQKVDPALCSNVLQHPWTEECMWPQGV
1	i		LVKHSKNVYKAVGHYNVAIPSDVSHFRFHFFFSKPLRILNILLL
1 1	1		LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL
			VLGKAYSYSASPQRDLDHRFS
6091	3279	412	SSRTREMEEKEILRROIRLLOGLIDDYKTLHGNAPADGTPAAGG
l 1	1		WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG
!!	1		PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK
[[1		VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGQ
l j			LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE
			PRRTVSESVIAVKASFPSSALPPRTGVALGRKIGSHSVASCADO
	1		LLGDRRVDAGHTDQPVPSGSVGGPARPASGPROAREASI.VVTCP
j	ĺ	i	TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN
İ			KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS
			SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE
			TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLD
ĺ			RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKRA
1	1	}	SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLDSWDA
1			RREGESEVENRERPVASGGGKAOPGSPWWRSKGYRCTGGVT.V
1			KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASPAVO
}	į		RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV
1	1		AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN
1	j	ļ	CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG
1	1	ł	ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG
1			PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS
	Ì	į	SSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLOS
6092			SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL
0032	143	3190	AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYO
- 1			EVFKPENISLRNKLRELCVKLMFLHPVDYGRKAEELLWRKVYYE

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	/ Danie C-Cycleine D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	p=proline, Q=Glucamine, K-Algumine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		504-511-6	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
	sequence	ļ	THE TWINTY PUTTED COLLECTION OF THE VACION TO THE TOTAL TOTA
	İ	}	OF BY OCCUPATHYTOPI.IGCKKPVSASGKEMDWAQMACHROLY!
		ì	1 - COL CONCOURT ACUDITELLARREVYOALSVAPOLGMPFNQUILD
	ì	1	L SOURCEMAYOVI. POTOSEVSFEGAYGNLKRLYDKAARMING
	<u> </u>	1	LKKCETRKLSPGKKRCKDIKRLLVNFMYLQSLLQPKSSSVDSEL
	ì	1	TSLCQSVLEDFNLCLFYLPSSPNLSLASEDEEEYESGYAFLPDL
	l	j	TSLCQSVLEDFNLCLF IDPSSFRIDE TO THE TENT OF
	S .	ł	LIFOMVIICLMCVHSLERAGSKQISAATAFILEEDDEEPPPVT
	}	ì	RLQAELEEGENPVPAFQSDGTDEPESKEPVEKEEEPDPEPPPVT
	1	}	PQVGEGRKSRKFSRLSCLRRRRHPPKVGDDSDLSEGFESDSSHD
		ł	SARASEGSDSGSDKSLEGGGTAFDAETDSEMNSQESRSDLEDME
	i	i	EEEGTRSPTLEPPRGRSEAPDSLNGPLGPSEASIASNLQAMSTQ
	1	1	MEGENT A DEFENT LI OPTENPHTSASHRECVIGOVDRESE
ļ.	}	Ì	DE GERGERGERGERGERGERSCHERSIOEKLOVLMANGLUPAVAVI
į .	1		TOWN DOWNED TIVE A CONSIGNATION TO THE PARTY OF THE PARTY
ļ	1	1	T CONTROL LEGGEL DDI.PSSIJLPEDMALRNLPPLKAARKENE (
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İ	1	1	VSIAQSEQESLLQQAQAQFRMAQEEARRNRLMRDMAQLRLQLEV
ļ	}	}	VSIAQSEQESHIQQAQQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQAQA
}	1	1	SQLEGSLQQPKAQSAMSPILVPDIQAZION VIIPRTVIDGLDLLKKEHPGARDGIRYLEAEFKKGNRYIRCQKE
i i	1	l	VIIPRTVIDGLDLLKKEHPGARDGIRIDGALT LAOGAGEEDPSG
ì	l l	l	VIIPRIVIDGIBBERKER STATE VILLAGE SEED SEED SEED SEED SEED SEED SEED SE
}	1	ľ	MVTIITGLPLDNPSLLSGPMQAALQAAAHASVDIKNVLDFYKQW
Ì	[KEIG
	76	1002	ACGRRAMLALRVART/SRWGAL\RGAVWAPGTRPSKRRACWALL
6093	/*		DRINGGI CCLAEDWDI.PDAAI.GLRLPGIGORNHCSGAGRAAPR \
1	1	\	DARCACAAAFADGGOWGPASTPSLYENPWTIPNMLSMIRIGHAP
Į.	ì	,	THE CALL TERRENTAL GUFAL AGLTDLLDGFIARNWANQRSALGS
j	\	· {	TI DDI ADVII.TCII.VVCI.TVADLIPVPLTYMIISRDVMDIAAVI
1		.	A TO THOSE DEPO TO A CURNIC VATARLE PTEISKUNTAVULLUVA
1	i	}	ASLAAPVFNYADSIYLQILWCFTAFTTAASAYSYYHYGRKTVQV
1	\	1	
1	ł	J	IKD PFLRCLRGDQKAKMSERKVLNKYYPPDFDPSKIPKLKLPKDRQY
6094	23	1010	PFLRCLRGDQRAMMSERRYDMKTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
}	1	l l	VVRLMAPFNMRCKTCGEIIIRGKKTNAKKHIVQAEKIJEEEEK
1	1	}	FYIKCTRCLAEITFKTDPENTDYTMEHGATRNFQAEKLLEEEEK
1	ł.	· }	RVQKEREDEELNNPMKVLENRTKDSKLEMEVLENLQELKDLNQR
}	1	\	QAHVDFEAMLRQHRLSBEERRRQQQEEDEQETAALLEEARKRRL
l		i	
}		1	GSLGSRPPLSRLVVVKKAKADPDCSNGQPQA/APHPRSPAEQES
1	1	j	CODYMDDAWDIT.PEPTGCIPGO
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		}	STMDDAVAGDFALINKLDIQCDLKTLSDDIKESLESEGKNSKKE EPQELLQSQDFVGEKLGSGEPSHS

TRADOCS:1416257.1(%CSH011.DOC)

SEQ	Predicted	Predicted end	•
ID	beginning	nucleotide	
NO:	nucleotide	location	I I''
	location	corresponding	""" ACIO, F=PNenvlalanina C-Classica
- 1	corresponding	to first	""" "" UTTO LITTLE . ISISO PICING V_T
ł	to first	amino acid	Deneucine, Mamethionine Nationalist
	amino acid	residue of	f=f=O+4Me, U=G1Dtamine
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence		COUCH, /=DOSSIDIE NUCleotide deletion
			\=possible nucleotide insertion)
			VKVHTVPKPGKGADLSKPPCRKAKEIRKERKRLKLMQQNPAGEL
ļ	1		EGFQAQGHPPSLFPPKAKSNQPKSLEDLIFESLPENASHKLEVR
	1		VVRSSPPSSQFKATLLESYQVYKRYQMVIHKNPPDTPTESQFTR
	1		FLCSSPLEAETPPNGPDCGYGSFHQQYWLDGKIIAVGVIDILPN
1	1		CVSSVYLYYDPDYSFLSLGVYSALREIAFTRQLHEKTSQLSYYY
ľ	į	· ·	MGFYIHSCPKMKYKGQYRPSDLLCPETYVWVPIEQCLPSLENSK
			YCRFNQDPEAVDEDRSTEPDRLQVFHKRAIMPYGVYKKQQKDPS EEAAVLQYASLVGQKCSERMLLFRN
6096	2277	575	ORVRAALI.SSAMEDSEAL CERTIFICATION
1	1		QRVRAALLSSAMEDSEALGFEHMGLDPRLLQAVTDLGWSRPTLI OBKAIPLALFGKULLARARTSCOVEN
1			QEKAIPLALEGKOLLARARTGSGKTAAYAIPMLQLLLHRKATGP VVEQAVRGLVLVPTKELARQAQSMIQQLATYCARDVRVANVSAA
1	}		EDSVSQRAVLMEKPDVVVGTPSRILSHLQQDSLKLRDSLELLVV
1			DEADLLFSFGFEEELKSLLCHLPRIYQAFLMSATFNEDVQALKE
1			TAXAMENIALIDESOLPGPOOT,OOFOINICEPEEDVER 1 * 125
1			1 EDDIRGROUDE VNTLERSYRLRIFIEDEST DECOME NORT DE DON
1			1 CHAILS OF NOGRIDOVIATDAEVIGADVKCKDDCDCDKCDVACADA
j ,			LAG VARGIDEHHVSAVLNEDI.DDTDEAVTUDACDTADARDCT.
			DIF VERIEURILGKIEELLSGENRGPII.I.DVORDMEETEGERS
i !			CADAMASVIAOAIREARLKEIKERII.HCDVI.VTVDDDVDDV
			J HINTIDDE MILEAV V KPHLGHVPDVT V V DDAT DCT V DDUVV V CD CC-
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		192	APGIMSGGKKKSSFOITSVTTDVFGPGSDGACDDDTDGDDTGGS
	1		TRUPINGEPSPUPGGRGTPRNGSPPDCADGGDEPINGET DEGE GOD
1	1		1 TICKGRWICVUVIERDLEPHSFGGLLEGTPGASGGACGROT DODG
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1.			TO THE TANGES GARTPPLISTREADING TO THE TOTAL TOT
1	ı		RPSSPALYFTHDASLVHKSPDPFGAVAAQKFSLAHSMLAISGHL
1	ľ		DSDDDSGSGSLVGIDNKIEQAMDLVKSHLMFAVREEVEVLKEQI
1 1	Į.		RELAERNAALEQENGLLRALA\SPEQLGSAGPPRGVPR\LGPPA
1 1	į.		PNGPFVLSLPSLTIVPLGLPGLASAAWPPLPMPALIVPVFPGVG VQALSNGPWSPGPLPHLLIIPSLDGGGGGFRTGRQQGAPFGEET
1-600-1			QPPPSLPGTPQQ
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ſ	i	ľ	VF IDAKE QEVENULTIGVEFGARMVN I DCKOTKI OTWOWN CORON
1	1	1.	RSI IRSI IRGARGALLVYDITRRETENHI TENI EDADOUGGODO
1	[VINDIGNASDLESKRDVKREEGEAPAPR\UCI,TEMETCA VIND
	j	1	VELATINIAKEIYRKIOOGLEDVHNEANGIKIGDOOGIGTOOTICE
6101	1		SASQRASRDIGSNSGCC
		1 '	FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR
		1 1	INTO PUSCAVQQYAWGKMGSNSEVAPI.I.AGGDDI.AGTABBURNE
			AELWMGTHPRGDAKILDNRISQKTLSQWIAENQDSLGSKVKDTF

		W	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	••••	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}		-	L=Leucine, M=Methionine, N=Asparagine,
	corresponding to first	to first amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of		Codon, /=possible nucleotide deletion,
[amino acid	acquence	\=possible nucleotide insertion)
	sequence		NGNLPFLFKVLSVETPLSIQAHPNKELAEKLHLQAPQHYPDANH
ł			
	Į		KPEMAIALTPFQGLCGFRPVEEIVTFLKKVPEFQFLIGDEAATH
1	Į	ł	LKQTMSHDSQAVASSLQSCFSHLMKSEKKVVVEQLNLLVKRISQ
1	Į	į	QAAAGNNMEDIFGELLLQLHQQYPGDIGCFAIYFLNLLTLKPGE
1]		AMFLEANVPHAYLKGDCVECMACSDNTVRAGLTPKFIDVPTLCE
l .]		MLSYTPSSSKDRLFLPTRSQEDPYLSIYDPPVPDFTIMKA\EVP
1]		G\SVTEYKDLALDSASILLMVQGTVIASTPTTQTPIPLQRGGVL
ļ			FIGANESVSLKLTEPKDLLIFRACCLL
6102	70	2415	QTPQATLAANGAEDSRGGEMLPAGEIGASPAAPCCSESGDERKN
}	j	1	LEEKSDINVTVLIGSKQVSEGTDNGDLPSYVSAFIEKEVGNDLK
į.		1	SLKKLDKLIEQRTVSKMQLEEQVLTISSEIPKRIRSALKNAEES
1	1	}	KQFLNQFLEQETHLFSAINSHLLTAQPWMDDLGTMISQIEEIER
1	1	ļ	HLAYLKWISQIEBLSDNIQQYLMTNNVPEAASTLVSMAELDIKL
1	1	1	QESSCTHLLGFMRATVKFWHKILKDKLTSDFEEILAQLHWPFIA
l	1		PPQSQTVGLSRPASAPEIYSYLETLFCQLLKLQTSHELLTEPK\
	1]	HSQKNTLFLPPLLSS/WPIQVMLTPLQKRFRYHFRGNRQTNVLS
1			KPEWYLAQVLMWIGNHTEFLDEKIQPILDKVGSLVNARLEFSRG
1	}		LMMLVLEKLATDIPCLLYDDNLFCHLVDEVLLFERELHSVHGYP
1			GTFASCMHILSEETCFQRWLTVERKFALQKMDSMLSSEAAWVSQ
1			YKDITDVDEMKVPDCAETFMTLLLVITDRYKNLPTASRKLQFLE
	1	}	LQKDLVDDFRIRLTQVMKEETRASLGFRYCAILNAVNYISTVLA
1		į.	DWADNVFFLQLQQAALEVFAENNTLSKLQLGQLASMESSVFDDM
1			INLLERLKHDMLTRQVDHVFREVKDAAKLYKKERWLSLPSQSEQ
İ	ļ	1	AVMSLSSSACPLLLTLRDHLLQLEQQLCFSLEKIFWQMLVEKLD
1			VYIYQEIILANHFNEGGAAQLQFDMTRNLFPLFSHYCKRPENYF
L		<u> </u>	KHIKEACIVLNLNVGSALTAGKDVLPVQLQGSFPAT
6103	207	2523	ESNSTMTTYLEFIQQNEERDGVRFSWNVWPSSRLEATRMVVPVA
1		•	ALFTPLKERPDLPPIQYEPVLCSRTTCRAVLNPLCQVDYRAKLW
1	1	1	ACNFCYQRNQFPPSYAGISELNQPAELLPQFSSIEYVVLRGPQM
l l	}	Ì	PLIFLYVVDTCMEDEDLQALKESMQMSLSLLPPTALVGLITFGR
1	1	1	MVQVHELGCEGISKSYVFRGTKDLSAKQLQEMLGLSKVPVTQAT
1	i		RGPQVQQPPPSNRFLQPVQKIDMNLTDLLGELQRDPWPVPQGKR
ı		1	PLRSSGVALSIAVGLLECTFPNTGARIMMFIGGPATQGPGMVVG
t	1		DELKTPIRSWHDIDKDNAKYVKKGTKHFEALANRAATTGHVIDI
1	1		YACALDQTGLLEMKCCPNLTGGYMVMGDSFNTSLFKQTFQRVFT
1	1	1	KDMHGQFKMGFGGTLEIKTPR\EIKISGAIGPCVSLNSKGPCVS
1	1	1	ENEIGTGGTCQWKICGLSPTTTLAIYFEVVNQHNAPIPQGG\RG
1			A\IQFVTQY\QHSSGQRRIRVTTIARN\WADAQTQIQNIAASFD
1	1	1	QEAAAILMARLAIYRAETEEGPDVLRWLDRQLIRLCQKFGEYHK
1	1		DDPSSFRFSETFSLYPQFMFHLRRSSFLQVFNNSPDESSYYRHH
1		1	FMRQDLTQSLIMIQPILYAYSFSGPPEPVLLDSSSILADRILLM
			DTFFQILIYHGETIAQWRKSGYQDMPEYENFRHLLQAPVDDAQE
	1		ILHSRFPMPRYIDTEHGGSQARFLLSKVNPSQTHNNMYAWGQES
L			GAPILTDDVSLQVFMDHLKKLAVSSAA
6104	124	732	KVSEYIILSKDKILFHALAMLVLVVSPWSAARGVLRNYWERLLR
1			KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL
l l			LDSIFWMAAPKNRRTIEVNRCRRRNPQKLIKVKNNIDVCPECGH
Į.		1	LKQKHVLCAYCYEKVCKETAEIRRQIGKQEGGPFKAPTIETVVL
			YTGETPSEQDQGKRIIERDRKRPSWFTQN
6105	3	989	PLHGACTSLVLQRFCHRRPRPCAPARPEDMRRPAAVPLLLLLCF
			GSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHF
ļ			CGGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAM
1	,		YARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPD
1			PSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDT\PR
1			CNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSAGPLV
1	1		CLVGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK
L	I	. L	

SEQ	Predicted	18-37-5-3	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid E-
	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
i	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
	1 4		\=possible nucleotide insertion)
6106	3	1302	LQVQPSEVGRPEVTPPGPGAP
		1302	GRPPTAPHTGRPPTANRGDPRLDLKRGCARLLTSIESRGRPAAS
			AGLRRDRCALRRWPLRRAPLARATRRRAGSPRRCAPRPRACPQG
	i		WSRARHQPGGLCLLLLLLCQFMEDRSAQAGNCWLRQAKNGRCQV
1	}		LYKTELSKEECCSTGRLSTSWTEEDVNDNTLFKWMIFNGGAPNC
	.		IPCKETCENVDCGPGKKCRMNKKNKPRCVCAPDCSNITWKGPVC
1			GLDGKTYRNECALLKARCKEQPELEVQYQGRCKKTCRDVFCPGS
1	i .		STCV\VDQTNNAYCVTCNRICPEPASSEQYLCGNDGVTYS\SAC
1			HLRKATCLLGRSIGLAYEGKCIKAKSCEDIQCTGGKKCLWDFKV
!	1		GRGRCSLCDELCPDSKSDEPVCASDNATYASECAMKEAACSSGV
6107	623	168	LLEVKHSGSCNSISEDTEEEEEDEDQDYSPPISSILEW
[SRCSSPRPEPGRGRGK/LSPSEHRKWVEVFKACDEDHKGYLSRE DFKTAVVMLFGYKPSKIEVDSVMSSINPNTSGILLEGFLNIVRK
1	1		KKEAORYRNEVRHIFTAFDTYYRGFLTLEDFKKAFROVAPKLPE
L	1		RTVLEVFREV\DRDS\DGHVSF
6108	3	1348	GGSLRFSPPRVPSCSRVFCPVPPGGCGLPSPMSASRPQSPTTPW
1	1		CLPRRYMKHKRDDGPEKQEDEAVDVTPVMTCVFVVMCCSMLVLL
1			YYFYDLLVYVVIGIFCLASATGLYSCLAPCVRLP\SASAGESA
1	ļļ		LLAPTIPNNSLPYFHKRPQARMLLLALFCVAVSVVWGVFRNEDQ
1	i 1		WAWVLQDALGIAFCLYMLKTIRLPTFKACTLLLLVLFLYDIFFV
}			FITPFLTKSGSSIMVEVATGPSDSATREKLPMVLKVPRLNSSPL
!			ALCDRPFSLLGFGDILVPGLLVAYCHRFDIQVQSSRVYFVACTI
	1		AYGVGLLVTFVALALMQRGQPALLYLVPCTLVTSCAVALWPPEL
	1		GVFWTGSGFAKVLPPSPWAPAPADGPOPPKDSATPLSPODDSFF
]		PATSPWPAEQSPKSRTSEEMGAGAPMREPGSPAESEGRDQAQPS
6109			PVTQPGASA
0105	1	1381	CRSRAGAASGGAILEGTKLRRQRVDTNKPLDPLVPSALRAAMLY
<u> </u>			LEDYLEMIEQLPMDLRDRFTEMREMDLOVONAMDOLEORYSEFF
]	į	•	MNAKKNKPEWREEQMASIKKDYYKALEDADEKVOLANOTYDLYD
			RHLRKLDQELAKFKMELEADNAGITEILERRSLELDTPSQPVNN
			HHAHSHTPVEKRKYNPTSHHTTTDHIPEKKFKSEALLSTLTSDA
	j		SKENTLGCRNNNSTASSNNAYNVNSSQPLGSYNIGSLSSGTGAG
			GI\TMAAAQAVQATAQMKEGRRTSSLKASYEAFKNNDFQLGKEF
	1		SMARETVGYSSSSALMTTLTQNASSSAADSRSGRKSKNNNKSSS
1	}		QQSSSSSSSSSSSSSSSSSSTVVQEISQQTTVVPESDSNSQVDWT
	•		YDPNBPRYCICNQVSYGEMVGCDTQDCPIEWFHYGCVGLTEAPK GKWYCPQCT\AAMKRRGSRHK
6110	77	2464	ACPSAATMSDQDHSMDEMTAVVKIEKGVGGNNGGNGGGAFSQ
}	1		ARSSSTGSSSSTGGGGQESQPSPLALLATCSRIESPNENSNNS
}	Ť	İ	QGPSQSGGTGELDLTATQLSQGANGWQIISSSGATPTSKEQSG
}		İ	SSTNGSNGSESSKNRTVSGGQYVVAAAPNLQNQQVLTGLPGVMP
ļ		l	NIQYQVIPQFQTVDGQQLQFAXTGAQVQQDGSGQIQIIPGANQQ
i		1	IITNRGSGGNIIAAMPNLLQQAVPLQGLANNVLSGQTQYVTNVP
ļ	ļ	ļ	VALINGNITLLPVNSVSAATLTPSSQAVTISSSGSQESGSQPVTS
İ		j	GTTISSASLVSSQASSSSFFTNANSYSTTTTTSNMGIMNFTTSG
1		j	SSGTNSQGQTPQRVSGLQGSDALNIQQNQTSGGSLQAGQQKEGE
ļ	[1	Q\NQQTQAAPKSI:SRPQLVQGG\OALO\AFOAAPI.SGOTETTOX
!			ISQETLQNLQLQAVPNSGPIIIRTPTVGPNGQVSWQTLQLQNLQ
			VQNPQAQTITLAPMQGVSLGQTSSSNTTLTPIASAASIPAGTVT
1	ľ	• 1	VNAAQLSSMPGLQTINLSALGTSGIQVHPIOGLPLAIANAPCDH
		1	GAQLGLHGAGGDGIHDDTAGGEEGENSPDAOPOAGRRTRREACT
		ł	CPYCKDSEGRGSGDPGKKKQHICHIQGCGKVYGKTSHLRAHLRU
1	1	Í	HTGERPFMCTWSYCGKRFTRSDELQRHKRTHTGEKKFACPECPK
- 1			RFMRSDHLSKHIKTHQNKKGGPGVALSVGTLPLDSGAGSEGSGT
Ì	i i	1.	ATPSALITTNMVAMEAICPEGIARLANSGINVKEGGQFCSPINT
			SANGF

			, , , , , , , , , , , , , , , , , , ,
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	Sequence	\=possible nucleotide insertion)
6111	1637	797	RVDPRVRGAMAPWGKRLAGVRGVLLDISGVLYDSGAGGGTAIAG
9111	163/	, ,,,	SVEAVARLKRSRLKVRFCTNESQKSRAELVGQLQRLGFDISEQE
!	1		
ļ	i	l .	VTAPAPAACQILKERGLRPYLLIHDGV\ASEFDQIDTS/STPNC
Į.	i		VVIADAGESFSYQNMNNAFQVLMELEKPVLISLGKGRYYKETSG
1	1	į.	LMLDVGPYMKALEYACGIKAEVGGKPSPEFFKSALQAIGVEAHQ
i	}	İ	AVMIGDDIVGDVGGAQRCGMRALQVRTGKFRPSDEHHPEVKADG
i	ļ	1	YVDNLAEAVDLLLQHADK
6112	77	196	MSSHKSFKSKRFLAKKQKPNRPILQWIWLKTGNKIRHNWK
6113	1779	567	WEGRSWAACGVNLOGAWGERSGVRASEAESPGKRADVSWWSRQL
1	1	1	ETMVDHLANTEINSQRIAAVESCFGASGQPLALPGRVLLGEGVL
	i		TKECRKKAKPRIFFLFNDILVYGSIVLNKRKYRSQHIIPLEEVT
	1		LELLPETLQAKNRWMIKTAKKSFVVSAASATERQEWISHIEECV
			RRQLRATGRPA\STEHAAPWIPDKATDICMRCTQTRFSALTRRH
l		3	HCRKCRVVVCAECSRQRFLLPRLSPKPVRVCSLCYRELAAQQRK
1			EEAEEQGAGVPRAASHLARPICGRPVEMTMTPTRTRRAAGTATG
Į.		· .	1 7
[1	1	PAAWSSTPRGWPGLPSTADPRPAEHLSPSQLHCPGPQEGSSRSC
1	1	1	PGLRDPIPWWQVQRWGVALSGLPVPFCWTLCPYGFTAGNAFPFR
		L	KPQNTHRSW
6114	818	246	PTSRPRPSPGSPAMSWSACVSAAPSSSWPASSSWPCGPRRCCTR
ŀ		ļ	RRRCSPRCGLAAGSMCSCSPSWRCTPVPACWPSPPP\PAEQVQC
1			GHLPPHADRRALRLPVAAPARGPGPGHPAGPAGPRPARTPPASP
į.	Ì		HGPGRPTVPAPPCPLLAATEPTPSRPHQRWTREDRMLGRGSQVT
1)	1	GRPQWFLRGLVLFSL
6115	324	71	DVCGRVCAHPHLYTHIHMHICAHAC\IHTHAQLC/ITASHALAH
1	1	1	SHLYTCMVMLTASHTPSHTHPHTAVHKEHRADVLRGTLTPLR
6116	595	1430	TGVMPPGRWHAA/ISSSGPVFEGARA\LQTVKKBEEDESYTPVQ
		1	AARPOTLNRPGQELFRQLFRQLRYHESSGPLETLSRLRELCRWW
1		1	LRPDVLSKAQILELLVLEQFLSILPGELRVWVQLHNPESGEE\L
Ì	ł	i	WPCWRSCRGTLMGHPGGTRALP\EPRCALDGYRS\LRSAQIWSL
}		1	ASPLESSALGDHLEPPYEIEARDFLAGQSDTPAAQMPALFPRE
ļ	l .	1	GCPGDQVTPTRSLTAQLQETMTFKDVEVTFSQDEWGWLDSAQRN
1		1	1 1
			LYRDVMLENYRNMASLGK
6117	1433	222	VGVPSPAPPCSWEVGPGGGWTPGILKEGQGGRRTPLLLLATRTR
1			GLISLFPPAAMHPAAFPLPVVVAAVLWGAAPTRGLIRATSDHNA
1	1		SMDFADLPALFGATLSQEGLQGFLVEAHPDNACSPIAPPPPAPV
1			NGSVFIALLRRFDCNFDLKVLNAQKAGYGAAVVHNVNSNELLNM
.l	1		VWNSEBIQQQIWIPSVFIGERSSEYLRALFVYEKGARVLLVPDN
1			TFPLGYYLIPFTGIVGLLVLAMGAVMIARCIQHRKRLQRNRLTK
1			\EQLKQI\PTHDYQKGDQYDVCAICLDEYEDGDKLRVLPCAHAY
1	ļ	1	HSRCVDPWLTQTRKTCPICKQPVHRGPGDEDQEEETQGQEEGDR
i			GEPROHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL
1			SPPSSPVILV
6118	1044	247	STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK
5210	1011	~~*/	KEKEKETOKEKIGEKGREEKVKRKEVEQKIKQEKQEKQERRKGK
j	j	ļ	EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK
1	1	i	
l		1	NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE
1			DSQMEFLBIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP
1			ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA
<u>L</u>		L	II
6119	1217	462	DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL
l	1	1	LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR
i .		ļ	QELLAKALETLLLNGVLTLVLEEDGTAVDSRDFFQLLEDDTCLM
1			VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR
1			DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ
1			GLGHMLLGISSTLRHAVEGAEOWOOKGRLHSY
1	i	1	

Set Deginning nucleotide and nucleotide location of nucleotide location and nucleotide location and nucleotide location corresponding to first amino acid maino acid maino acid maino acid maino acid maino acid maino acid maino acid maino acid maino acid maino acid maino acid sequence sequenc	SEQ	Predicted	Predicted end	
No: location corresponding to first amino acid residue of amino acid residue of amino acid sequence se				Tamano della sequient containing signal pentia-
corresponding to first amino acid amino acid residue of anino acid anino acid anino acid sequence sequ	NO:			M=AldRine, C=CVSteine, D=Aspartic Acid p
to first amino acid residue of amino acid residue of amino acid sequence 6120 785 179 179 179 179 179 179 179 17	- 1			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first anino acid residue of residue of residue of anino acid anino acid sequence 6120 785 179 179 LERGOGGILSERIUGGGGCISTORIA NEADYLANGERIUGGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEGEG	- 1	corresponding		L-Leugine, M-Mathieric, K-Lysine,
amino acid residue of amino acid sequence sequen	1			Paproline Occlubation NaAsparagine,
### ### ### ### ### ### ### ### ### ##	Į			S=Serine T-Throning W.W-line,
Sequence 179 179 179 179 179 179 178 179 178 179 179	1		amino acid	W=Tryptophan V=Tyrosine V=tylenous
179 LEPROGGGLESERRLUSSACLELJVARANGELEGEKKEFVERVR VRYVAFRYRFYPRAVCLRIMSCREZUMSGREGOGUTARAKSER SESRACIOF POEGWERLEIKEGERBUMSGREGOGUTARAKSER SESRACIOF POEGWERLEIKEGERBUMSGREGOGUTARAKSER SESRACIOF POEGWERLEIKEGERBUMSGREGOGUTARAKSER LIELAGNARADHKKTRITPHHOLAITANDEELNELIGKVEFTATAN (VLENTOAULEKTESSOCHESELAVEVERSCERVEDELIGKVEFTATAN FORGARAYTEHROELIFREDELIFFSDELAYTYVCKSGEGNEPLEVEFTATAN ROMGERAVTEHROELIFREDELIFFSDELAYTYVCKSGEGVEDECLIGKE KIMMCSGCRVAKYCSAKCOKKAMPDHKRECKCLKSCERPYDDS VRILGRUVFELHDGAPSEERKLIFFDELAYTYVCKSGEGVEDLOCHCLIGKE KIMMCSGCRVAKYCSAKCOKKAMPDHKRECKCLKSCERPYDDS VRILGRUVFELHDGAPSEERKLIFFDELAYTYVCKSGEGVEDLOCHCLIGKE KIMMCSGCRVAKYCSAKCOKKAMPDHKRECKCLKSCERPYDDS VRILGRUVFELHDGAPSEERKLIFFDELAYTYVCKSGEGVEDLOCHCLIGKE KIMMCSGCRVAKYCSAKCOKKAMPDHKRECKCLKSCERPYDDS VRILGRUVFELHDGAPSEERKLIFFSDENGSTUFTUNGENERGER GUTUMTFOHREETODASOLPPARDLIFERAFAKVICHSFTI CNAB MOEGVEVGLVYSTSILLIMISCDHOCHCI ISSNEERL DIDINTYCLKVLDCANDACINGLIEBEADFYGTETMEPYR FPPE SETIVEGOVORWCGSLOLHOROPPOANSKILERAUTSTERVTSTERMEPYR FPPE SIJEBLILLILLE/AMRRCHGSILRERSOREIRRVSLIALIRSHT LOFSVENINSYKKECSFVP ARREMADGGAASODESSAAAAAADRINDSETSTERBEGGO NOTGYTLITPAOOOLILLOONAQAQALLAAAGIBHOVOLAGGTU LUHPTTNILOPA (VEITSOPAGITSAQAGALTSAQAAGAISTOLAGRA) GGCTGGTLITPAOOOLILLOONAQAQALLAAAGIBHOVOLAGGTU LUHPTTNILOPA (VEITSOPAGTITAGAGAISTAQAGAETHAGAGA) GGCTGGTLITPAOOOLILLOONAQAQALLAAAGILAAVALAAGA GGCTGGTLITPAOOOLILLOONAQAQALLAAAGILAAVALAAGA GGCTGGTTITPAOOLILLOONAQAQALLAAAGAINACHCAGA LLGSOPRITTITSOCOLILOONAQAAAGALAAAAGAINTOACHCAGA LLGSOPRITTITSPESSIPLISTAANTALTISAA THISPESIPLINOOCHTS PSPTTTFREPALINISFMMCCIKPILLEKKINDAERILSSDSISS PSALNSGIGGISRRKKRTISTEA NIRVELERINOOCHTSCHITTSPAATTILS VTGTSDTTSNINTATVISTAPPASSAVTSBSLSSPSSASATSEA SSASETSTTOTTSTENSSIPLISTAAGATAGALLEKRETULFACHTOTTSAATTILOONACHTITSPAATTISAA VTGTSDTTSNINTATVISTAPPASSAVTSBSLSSPSSAGAALLEINPGTLS SABASTABAGARASAATTTASAAGA VTGTSDTTSNINTATVISTAPPASSAVTSBSLSSPSSAGAAGALLEINPGTLS SABASTSHITTSTERGOSIPLTSVASAGAAGAATTTASAGA CALAPALMSMISTLATACAAGASSATTTASAGA CALAPALMSMISTLATACAAGASSATTTASAGA CALAPALMSMISTLATACAAGASSATTTASAGA CALAPALMSMISTL			sequence	Codon, /=possible nucleotide delete
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SSKARLIGP FVGENRALLEKGNYAERVGGAGAPVILEVILTAGE GLVLPNIGAVLEKTESGKDEGANDP FVRAGARGNERKERT IPRHILDLAIR TRENKLIGHT VITAGE GLVLPNIGAVLEKKTESGKDEGANDP FVRAGARGNER PVREPLELAGSSELKERSGGMEPLKVEKFATAN RONGLRAWTPLR TEGELLERSDPLATTVCKSSRGVVCDRCLLIGKE KLMRCSGCGVAWKVCSAKCKAMPDHKEVCKJASCVLORCHLIGKE KLMRCSGCGVAWKVCSAKCKAMPDHKAVAVICNSTITONAE MOEVGUGLYPS ISLLINHSCDPROST VFROHLLLRAWDLEVGE ELTICYLDHAMTSEER KROKLORDOYFEDC VFRCOTODKADML TODEGVMKEVGBSLKKIEELKAHWKWEGVLAMGOALISSNSERL PDINIYQLKVLOCADDAGINGLINGLEAD THREW THERE SHPVKSGVGVMKVSKLOLHGGMFPOAMKNLELAAD IMRVTHGREH SLIEDLILLLEL/AMRRGHGISIRERSGREIR TRYSTHABP PET FPE SHPVKSGVGVMKVSKLOLHGGMFPOAMKNLELAAD IMRVTHGREH SLIEDLILLLEL/AMRRGHGSILRERSGREIR TRYSTHABP PET FPE SHPVKSGVGVMKVSKLOLHGGMFPOAMKNLELAAD IMRVTHGREH SLIEDLILLLE/AMRRGHGSILRERSGREIR TRYSTHABP PET FPE SHPVKSGVGVMKVSKLOLHGGMFPOAMKNLELAAD IMRVTHGREH LOFVSCVNLSYMKFCSVPV PREKKADGAASGDESSAAAAAAADSHRAND SETSKESMESGGO NGCTOTNGTTILTPAQCOLLLOQAQANOLALAAVGCHSAGQGHSA GAATISASAATPHOTOPINSTOLLOQAQANOLALAAVGCHSAGQGHSA GAATISASAATPHOTOPINSTOLLOQAQANOLALAAVGCHSAGQGHSA GAATISASAATPHOTOPINSTOLLOQAQANOLALAAVGCHSAGQGHSA GAATISASAATPHOTOPINSTOLLOQAQANOLALAAVGCHSAGGGHSA GAATISASAATPHOTOPINSTOLLOQAQANOLALAAVGCHSAGGGHSA GAATISASAATPHOTOPINSTOLLOQAQANOLALAAVGCHSAGGGHSA GAATISASAATPHOTOPINSTOLLOQAQANOLALAAVGCHSAGGGHSA GAATISASAATPHOTOPINSTOLLOQAQANOLALAAVGCHSAGGGHSA LEEP \SDLEELIQOPAKTFKORBILKIGFT\QCDAGLAVKLIVOND FSPTTIFFFFFALMISTOTHAKKLEFTLEKHINDASTISSISSISSISSISSISSISSISSISSISSISSISSIS	[l .	}	VRYVAFRYRTPRAVCLRLWSCRREVIMSGRGKOGGKVDAYAVGD
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REMINCASQCEVARYCSARCORKAMPDHERSEKCHSCRERYPPDS VRILGROVFKIMDGAPSESEKIYSPTDLESNINKITERKEGIR QUAMTFQHFMEREIQDASQLPPAFDLFEAFAXVICNSFTICNAR MQEVAUGUFPSISLIANISCDMCSIVPDHILLEAVEDIFUCE ELTICYLDMLMTSEERRKQLRDQYCFECQ\CFRCQTQDKDADML TODEQVMEVQESLKIETEKAMRWGVLAMCQAIISSNSSRJ BIPVREQUOVMKVQKLQLRQGSFDQAKTRINKIPPRIFFEG SIPVREQUOVMKVGKLQLRQGSFDQAKTRIVELLAALIRSHT COPYSCYNLZYMKPGSVV RFRKRDDGGAASQDESSAAAAAADSRMNNPSETSKFSMESCDG MYGTQTINGLDFOKQPVFVGGAISTAQAQAFLGHLHQVGLAGTSL GGQITGILTLTPAQOGLLLQAAQAQLLAAAVQOHSASQQHSAA GGAISASAATPMTQHSSGPGIAQAQALLAAAVQOHSASQQHSAA GGQITGILTLTPAQOGLLLQAAQAQALLAAAVQOHSASQQHSAA GGQITGILTLTPAQOGLLLQAAQAQALLAAAVQOHSASQQHSAA GGQITGILTLTPAQOGLLLQAAQAQALLAAAVQOHSASQQHSAA LLQSQPRIVLTSGPGATTTCITAATPUTQQSQSTVAAIFOTQMAI GGQITGILTLTPAQOGLLLQAAQALLAAAVQHSASQQHSAA LLQSQPRIVLTSGPGATTTCITAATPUTQQSQSTVAAIFOTQMSQAA LLQSQPRIVLTTSGPATTTCITAATPUTQQSQSTVAAIFOTQMSQAA LLQSQPRIVLTTSGPATTTCITAATPUTQQSQSTVAAIFOTQMSQAA LLQSQPRIVLTTSGPATTTCITAATPUTQQSQSTYRKIPTDTPS LEEP\SDLEELBGFARTFKQRTKKRTSIGA\MYALLAAVQHSSSSSSSSSSSSSSTSTTTTTSTSTESFTGTTSGWCKKKRTNPSSGGTSSSSP FAALMSGGIBGLSRRKKRTSIGA\MYALLAKSFLEN\QKFTS TKAIFPSPAILASTSPLATTSVSTSAATTLTVSSVLPSGGTSSSST EEITMIADQLAMBEKGVIKVMFGGRRQKKKRTNPSGGTSSSSTSSA SASETSTTQTTSTTSSPLSTSTAGTTLTVSSVLPSGAAASTSEA AAQLPANASIAAMAAAQGLAPSIAMPSOFAAGGALLSINFGTLS GAISPALMMSTLATIQLAASGGSLPTSLATGKAQ PNIVTAPLPINFONLSLITSNPVSLVSAAAASAGNSAPVASLHA TSTSAESIONSIFTVASASGAASTTTLTVSSVLPARAGGA PNIVTAPLPINFONLSLITSNPVSLVSAAAASAGNSAPVASLHA HLAFRWFGTDMQMINFTTGSFQUTSACCPYLGTHSESFGTILHL HLQPLEKKRQVVFPPADJCKVTSLILIRNNITVIIMIGVEGFG ARELLKVGGRLDGAGGSLRFKVPBSTLMDCRRQLKOKGVISTT KNNKVSNIGPLPTTVSLSKINGTNCTLOPHHLL PLCADVV PQBSWESSFRRITUTFVSLSLALLIRNNITVIIMIGVEGFG ARELLKVGGRLDGAGGSLRFKVPBSTLMDCRRQLKKKKCVYSK HKSGIQTCMFPKETDIKTSKONGNSPDVJCHQFCSDLPHT PRATTQRANGSSSGGNOSPDVISTSNNCHKNITTYPHLEHLL PLADVV PQBSWESSFRRITUTFVSLSLALLIKRNITVIPSNPSSEC MKSGIQTCMFPKETDIKTSKONGNSPDVJCHQPCSDLPHT PRATTQRANGSSSGGNSSTSSSGGNKSSTSSSGGNKKSGGNSTSSSGGNKKM SLRYASGINVANGKNITTSRVARQAVSRPPGGDLKKVOTK PASSEKKIHKTSRDAMPFECKQOIPFPGKQDIFFSELIS SDINVSWGIPSRVCKADAGAASSTSSSDGR	- [ľ	RGNGLRAVTPLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKE
WILLGROYFKIMGAPSSESKIYSFYDLESNINKLTEDKENGIR QLVMTFQHFMEEIQDASQLPPAPALPARAVIONSTICINAE MQEVGVGLYPSISLLNISCDENGSIVFNOPHILLRAVRDIEVGE ELTICYLDMLMTSEERRKQLRQVGCD-CPRCQTDGRADML TGDEQVMKEVQESLKKIEELKAHKKMEQULANCOLISSNISERL PDINITYQLKVLDCAMDACINIGLIERLFYGTTMEPYETIFPE SHPVEGVQVMKEVQESLKKIEELKAHKKMEQULANCOLISSNISERL PDINITYQLKVLDCAMDACINIGLIERLFYGTTMEPYETIFPE SHPVEGVQVMKEVQESLKKIEELKAHKKMEQULANCOLISSNISERL PDINITYQLKVLDCAMDACINIGLIERLFYGTTMEPYETIFPE SHPVEGVQVMKEVQESLKKIEELKAHKKMEQULANCOLISSNISERL SILEDLLILLE/AMREQUESTAAAAAAAARADSRMNNFSETSKESMESGDS SHPVEGVQVMKEVQEVP SHPVEGVQVMKEVQEVP SHPVEGVALAAAAAAAAAASRMNNFSETSKESMESGDE QAAAQSILNVQSKSNEESGDSQDPSQDSVQAAIFQTUMHAL GOQITGEILTTPAQOCILLQOAQAAQAAFLGHLHQVQLAGGTSL QAAAQSILNVQSKSNEESGDSQDPSQDSVQAAIFQTUMHAL GOQITGEILTTPAQOCILLQOAQAAQAAIAVQCHASGQMSAA GATISASSAATPMTQIPLSQPIQIAQDLQQLQQQCQONLALQGFV LUHPITTMLQPA\GFIISTDTDQGQGLAQAINLQQFV LUHPITTMLQPA\GFIISTDTDQGGQLAQAILQOTLAQAAQAILQGFV LUHPITTMLQPA\GFIISTDTDQGGGATAAAAAAASRAINAVQHASGQMSAA GATISASSAATPMTQIPLSQPIQIAQAACALSKINLQSKTEKRIDTPS LEEBY\SDLEELEGFARTKQRTKLGF\GQAAAAAAAASANSANAVAILYSMD FSPTTIFRFBALNLSFKMCKLKFLIEARVAQCHASGGTSSSSSSSASTTTIFRFBALNLSFKMCKLKFLIEARVAQCHASGATSSSSISS PSALMSFGIIGGLSGRKKRTSTIEAR\GQATSLEARVAYNLS VTGTSDTTSNNTATVISTAPPASSAATSPELSPPSARASTSEA SASASTTTTTSTSSPJGTSQUWYTASCLQTA/AQLLPFKC AAQLPANASIAAMAAAAGLAFSLMTSSPLSPPSARASTSEA AAQLPANASIAAMAAAAGLAFSLMTSSLAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA				KLMRCSQCRVAKYCSAKCOKKAWPDHKRECKCLKSCKPRVPPDS
QUAMTIQUEMREZIQUASQLIPRAFILIRADPRISTURARYDIEVUSE ELTICYLDMIMTSERRKQLRDQYCFECD\CFRCCTODKDADML TOBCOWKEVQBSIKITEBIKAMEQVIAMCAIISSNSERI PDINTYQLKVLDCAMDACINLGLLERALFYGTRYMEPYRIFPE SHPVRSVQVMKUGLUGHCOMPROWLIRLAFDIHRVTHGEH SLIEDLILLLE/AMRRCHQSILRERSGREIRRVSLURALLRSHI- LCFVSCVVLISYMKYCSVPV RFRKMADGGAASQDESSAAAAAAABDSKMNPSETSKFSMESGDG MYGTQTINGLDPQKQPVPVGGAISTAQAQAFIGHLHQVQLAGTSL QAAAQSLWVQSKSMESEGSQQQPSQOPSVQAAATQTOTUMLA GGQITGLITTPACOCULLCOQAQAQAOLLAAAVQCHSASQQNSAA AGAISSAATPMTQIPLSQPTIQLQQQLQQANLLQTPCULLVHPTTNLQPA\GFIISQTPQQQQLLQA\QNLLTQLPROSQAN LUSSQPRI\TUTSQPAPTPCTIATQTDQQSCTRKIDTPS LEEP\SDLEBLEQPARTFKQRRIKLGFT\QQAAALMVKLYGND FSPTITFFFFALNISFFMCKLKGLEKWLDKAMDAENLSSDSSLSS PSALNSGGIBGLSGRRKKRTSIEA\NIRVALEKSPLEN\QXPTS EEITMIADQLMMEKGVIRVWFCNRRQKEKRINPPSSGG\TSSSP JKAIFPSPTSLVATTFSLVTSSAATTIVSVPLVPLTSAAVTNLS VYGTSDTTSANTATVISTAPPASSAVTSSELBSPSASASTSEA SSASETSTTQTTSTFISSPLGTSQVWTASGLQTAAQLLPKK AQLPANASLAAMAAAGINPSIMAPSQPAAGGALLSINPGTLS GALSPALMSNSTLATIQALASGGSTUMTASGUQTAAQLLPKK AQLPANASLAAMAAAAGINPSIMAPSQPAAGGALLSINPGTLS GALSPALMSNSTLATIQALASGGSTUTSLADAGGALLSINPGTLS GALSPALMSNSTLATIQALASGGSTLEPLISADATGNILVTANAGGA PNIVTAPLPELNPONLSLITSSPVSUSAAAASAGNSAVASLHA TSTSAESIONSLETVASASGAASTTTASKAQ HLLHRWGGTDMOMINFTGEFQLTEACPYLGFHSEESREGILHI HLCHRWGGTDMOMINFTGEFQLTEACPYLGFHSEESREGILHI HLCHRWGGTDMOMINFTGEFQLTEACPYLGFHSEESREGILHI HLCHRWGGTDMOMINFTGEFQLTEACPYLGFHSEESREGILHI HLCHRWGGTDMOMINFTGEFQLTEACPYLGFHSEESREGILHI PLCADVVFQOFSMEESFWELTVFVSLSLLGVDLSKKHKCSVYTYSK KNKYUNGLGPLDTTADSKSQNOMGPMUTSPHYVENGLTDLTGPS DKGRGKNCLPVNTPQSRQNAARSSPATYGHSOKKHKCSVYTYSK HKSTGTAAASSTSTTTEERKOTSPLGSAAKBGICTHDWTDLTHHLL PLCADVVFQOFSMEESFWELTVFFVSLSLLGVTAVPLDHHLK PRINTARASSTSTTTEERKOTSPLGSAAKBGICTHDWTDLTHHHL SLEYAASGTIVTPDPTSSWVIRDLSLUTARADLEFRFTLINTVPLHHLL PLCADVVFQOFSMEESFWELTVFFVSLSLLGVTAKAGLGKLEGMI QNLNMSKSRTCRKNKRGVAPVSRPPEGSDLKLVCSDFERSELS SDINVSNCIQGSTREVCKADAEIAASSLFTARKCLQEKKEGMI QNLNMSKSRTCRKNKRGVAPVSRPPEGSDLKLVCSDFERSELS SDINVSNCIQGSTREVCKADAEIAASSLFAARGRAGCTYQKERK NOOPCYLIGESSAPVKNSTIDMSATCSGQFSSAYCCEBLINDYNAPP	- 1	1		VRLLGRVVFKLMDGAPSESEKLYSFYDLESNINKI.TEDKKEGI.P
MQEVGUGLYPSISLLNISCOPNCSIVINGPHILLRAYRDIEVGE ETITCYLDMIANTSEERRKQLRAYCPCD\CFRCOTQDKDAML TODEQVWKEVQESILKITELKAHWKWEQYLAMCQAIISSNSERL PPINITYQLKVLDCAMACINGLERAFYCTETRWBYRIFPFO SHPVRGVQWMKVGKLOLHGGMPPQAMKNLRLAFDIMRVTHGREH LCFVSCVALSYWKPCSVFV RFRKMADGGARGQUESSAAAAAADSRMNPSETSKFSMESGDG NTCTQTMCLDFWCGASTAQAQAFIGHLHQVOLAGTSL QAAAQSLAVVGSKSNESSGDSQPSGPSQOPSQDSVQAATPOTOLMIA GGQITGITLTPAGCOLLLQQAQAQAQLLAAAQAGAGHLHQVOLAGTSL LUHPTTMLQPA\QPTISOPTOCOLLQQAQAQAGLAAAQAGAGAGAGAGAGAGAGAGAGAGAGA		1		QLVMTFQHFMREEIODASOLPPAFDLFEAFAKUTCMSETTCMAE
TODGOVMEVOGESIKK IEBLAKHEVOLAMOATISINSERIA PDINTYQLKVILOCAMDACTNIGLLERALFYGTRYMBEYRI FFOG SHPVERVOVMKUGLOLHOGMPGVAKURLAFDINRVTHGREH SLIEDLILLLE/AMRROHOSILRERSQRETRRVSLLNALIRSHT LCFVSCVALSVWKCSVFV RFRKMADGAASQDESSAAAAAADSRMNNPSETSKFSMESGDG MYGTGTMALDFOKQPVPVGGAISTAQAQAFIGHHQVOLLAGTSL QAAAQSLNVQSKRENESGSQQOFSQPSVQAAIPOTOLMLA GGQITGITLTPAQOGLLLQAQAQAQALLAAAVQOHSASQQMSA AQASANVQSKRENESGSQQOFSQPSVQAAIPOTOLMLA GGQITGITLTPAQOGLLLQAQAQAQALLAAAVQOHSASQOMSA LCGSPRI\THISQAPTFYCTIAATPIQTLPQSQSTFKRIDTPS LEEP\SDLEBLEGFAKTFKQRRIKLGFT\QGDAGLAMVKLYKND FSPTTIFRFBALMLSFKNNCKLKFLLEKWINDAENLSSDSSLSS PSALMSGGIGLSFRKKRTSTSERT\QGDAGLAMVKLYKND FSPTTIFRFBALMLSFKNNCKLKFLLEKWINDAENLSSDSSLSS PSALMSGGIGLSFRKKRTSTSERT\TVSVPLEKFLENOVAPTS EEITMIADQLMMEKGVIRWYGNRQKEKRINPSSGGTTSSF IKAIFPSPSTSLVATTPSLVTSSAAITUSVPLVEKFLENOVAPTS EEITMIADQLMMEKGVIRWYGNRQKEKRINPSSGGTTSSF IKAIFPSPSTSLVATTPSLVTSSAAITUSVPLVELTSAAVTNLS VTGTSDTTSNNTATVISTAPPASSAVTSPSLSPSPSASASTSSA SASETSTTOTTSTFJSSFLGTSQVUTVISAAAASGANSAVVASHA TSTSAESIONSLTTVASASGASTTTTASKAQ PNIVTAPLETHPONISLLTSNPUSAAAASGANSAVASHA TSTSAESIONSLFTVASASGASTTTTASKAQ HLLHMWRGTDMQMINTTGGEPUGAPTGFTHSESFRGILHL HLLHWWRGTDMQMINTTGGEPUGAPTGFTHSESFRGILHL HLLHWWRGTDMQMINTTGGEPUGAPTGFTHSESFRGILHL HLLHWWRGTDMQMINTTGGEPUGAPTGFTHSESFRGILHL KNPKVENIGPLFITVSSKINGNYQVFFFTMNVLDHHLL PLADVVPOPSWEESFPRILTYFFYSLIGUTLIAFONLOPSLDPHT SRDISIVFTPDFTSSWVIRDLSLVTAADLEFFFTLNVTLPHHLL PLADVVPOPSWEESFPRILTYFFYSLIGUTLIAFONLOPSLDPHT SRDISIVFTPDFTSSWVIRDLSLUTAADLEFFTLNVTLPHHLL PRINSPQYHQPDLPFITSSKNIRGNYQVFFVSLOCKHKCSVYYSK HXTSTAAASSTSTTEEKOTSPIGSSLPAKKEDLICTDAMRENNI SLEYAAGSINVNLQKNILTIPNLINKERNILLKUTIVFSNPSSEGS MKEGIQTCMFFFETDIKTSINTAEFKERELCPLITSKLEDERILK PRINSPQYHQDDLPFISKNINGNYQQVPVRDECENLKKUPIK PRINSPQYHQDDLPFISKNINGNYQQVPVRDECENLKKUPIK PRINSPQYHQDDLPFISKNINGNYQQVPVRDECENLKKUPIKE SDINNSRCITORTRECKQDIFFYNKUTGEREGRIL QNINMSKSRTCRKKKKGVAPVSRPPBGSDIKKUCSDFFESELS SDINNSRCIORSTRECVCAADALSDAAQREGDICTVBEK KCVDKFCSDSSDCGSSSGSVASRGSSGSSSTSSSDGDKKM VDAOHFLPAGDUSQNDFFSEAPIGHTPPVUCUTSSLNCTLE NOVPCVIQESAPVNNSIDNSATCGOGSSAYCPLEINDYNAPP				MQEVGVGLYPSISLLNHSCDPNCSIVFNGPHILLRAVPDIEVGE
TODECOWNEYOESLIKKIEELKAHWKNEOVLAMCOAIISSNSERL PPINITYCIKVLICAMDACINICLERAFYGYETRWBYYEIFPPE SHPVKGVQWWKVGKLOLHOGMFPQAMKKLRLAFDIMEVTHEGEH SLIEDLILLE/AMRCHQSILERESQREIRRVSLLNALLRSHT LCFVSCVALSYWKFCSVFV PERKARDGGAASQDESSAAAAAABRAMNPSETSKFSMESGDG NTCTQTNGLDPCKCPVPVGGAISTAQAQAFLGHLHOVOLAGTSL QAAAQSLWVGSKSNESSGDSQPSGPSGOSVQAATPOTOLMLA GGQITGLITPAGCOLLLQOQAQAOLLAAAVQOHASGQMESA GATISASAATPMTQIPLSGPIQIAQDLQOLQOLQONLMLQOFV LVHPTTNLQPA\GPITTAATPIQTLQSGSTRKIDTPS LLGSQPRI\TLTSGPATPTCITAATPIQTLQPSGSATKKINDPS LEPY\SDLEELGPATTFKGRIKLGFT\QGDAGLAMVKLIGND FSPTTIFFPRALNLSFKNKCKLKPLLEKWINDAENLSSDSILSS PSALNSPGIBGLSGRRKKRTSIEA\NIRVALEKSFLEN\QUPTS EEITMIADQLAMBKGVIKWWCNEKKRINPPSSGG\TSSSF IKAIPPSPTSLVATTSLVTSSAATTLTVSPVLPLTSAAVTNLS VTGTSDTTSNNTATVISTAPPASSATTLTVSPVLPLTSAAVTNLS SASAETSTTQTTSTPLSSFLGTSQVMVTASGLOTA\AQLLPPKC AAQLPAANSLAMAAAAAGAINSIAWSPSLBSBSPSAGASTEAS SSASETSTTQTTSTPLSSFLGTSQVMVTASGLOTA\AQLLPPKC GALSPALMENSTLATIQALAGGSLPTSLDATGNLVFANAGGA PNIVTAPLFLNPQNLSLLTSNPUSAAAASAGNSAPVASGLHA TSTSABSIQNSTTAASAGAASTTTTAKRAQ 6123 3 2944 HLLPRWFGTDMQMINFTTGFFQLIEACPYLGHSESERFGILHL KNKVUSNIGPLDITVSSLKINGTVASAAASAGNSAPVASGLHA TSTSABSIQNSLFTVSSLKINGTVASAAASAGNSAPVASGLHA TSTSABSIQNSLFTVSSLKINGTVASAAASAGNSAPVASGLHA TSTSABSIQNSLFTVSSLKINGTVASAAASAGNSAPVASGLHA TSTSABSIQNSLFTVSSKNITAFSFQLIEACPYLGHSESERFGILHL PLCADVVPGPSWEESFFWLTVFFVSISLLGVILLAFQQAQYILM EFKKTQQNONASSSQQMNGPMDVISPHSYKSNCKNFIDTYGSF DKGRGKNCLPVMTPQSKVTTSSLKINGTVAGVFSELOKHKKSVYTYSK KNKVUSNIGPLDITVSSLKINGTVAGAREPTLINTTVFSNPSSECS MKGGIGTCMFPKETDITKTSSLTAFFRELPCLITKTKLPENDSSECS MKGGIGTCMFPKETDITKTSSLTAFFRELPCLITKTKLPENDSSECS MKGGIGTCMFPKETDITKTSSLTAFFRELPCLITKTKLPENDSSECS MKGGIGTCMFPKETDITKTSSLTAFFRELPCLITKTKLEEMLINKLTUTGEREGNL QNLNMSKSRTCRKKKKRGVAPVSRPPBQSDLKLVCSDFRSELS SDINVNSKGIGTSTRSVAKRNGNOQQVPVUNDEHCEBLKKVDTK PSSEKKIHTSTEEDMFSSKQLIFTFYBLOTHERCEDLIKVDTRK VDAGHFLBAGBSVSQNDFFSBAPISINLSHINCHPTPVCUTTSSLNCTLE NOVPCUIGESAPVINSFIDMATCRGQFSSAYCPLELNDYNAPP	İ	1		ELTICYLDMLMTSEERRKOLRDOYCFECD\CFRCOTODKDADMI
SHIPMSVOWKKGKLOLHQGMFPQAMMIRLARDINNYTHGERH 5.11ELILLLE/AMRRQGSILBERSQREIRRVSLLNALLRSHT 1.CFVSCVNLSYMKFCSVV APRKMADGGASAQDESSAAAAAAADERMNNFSETSKPSMESGDG ATGTOTNGLDFOKQFVEVGGAISTAQAQAFLGHLHQVOLAGTSL QAAAQSLBVQSKSNESSGSQQSSQSOQSVQAAIPOTOLMLAA GGCTIGHLTHAOQOLLLQQAQAQAGLLAAAVQQHSASQQNSAA GGTISASAATPMTQIFLSQFIOLAQDLQLQQCQCMINLQQFV LVHPTTNLQPA\QFIISOTPQQGGLLQA\QMLLTQLFQSQAN LLQSQPRI\TLTSQPATPTCTIAATPIQTLPQSQSTFRKIDTPS LEEP\SDLEELEQFAKTFKQRRIKLGFT\QGDAGLAMVKLYGND LLGSQPRI\TLTSQPATPTCTIAATPIQTLPQSQSTFRKIDTPS LEEP\SDLEELEQFAKTFKQRRIKLGFT\QGDAGLAMVKLYGND FSPTTIFFFRALMSFKNMCKKFLLEKWINDAEMLSSSSLSS PSALMSPGIEGLSRRRKRTSIEA\MIRVALEKSFLEN\QNFTS HAIFPSFTSLVATTPSLVTSSAATTLTVSPVLPLTSAAVTNLS VTGTSDTTSNNTATVISTAPPASSAVTSPSLSPSPSASASTSEA AQQLPARASLAAMAAAAGLNPSLMPSSCAPAGGALLSINPGTLS SSASETSTTQTTSTFLSSVIGTSQWVTASGLQTA\AQQLPFKC AQQLPARASLAAMAAAAGLNPSLMPSSQPAGGALLSINPGTLS GALSPALMSNSTLATIQALAGGSLFFVORDAAAASAGNSAPVASLHA TSTSAESIONSLFTVADSGGAASTTTTASKAQ FILHRWFGTDMQMINFTTGFFQLTEACFYLGTHSEESRFGILHL HLQPLEMKRGVVYFTEADVGKVTSLILIRNNLTVIDMIGUEGFG ARELLKVGGKLPGAGGSLFFYDGAGGGVLFYDCHOPSLDPBT SRDISIVFTDPTSSWVIABLSLATAADLERFTHUVTLPHHLL PLCADVVPGPSMESSWRLTVFFVSLSLLGVILIAFQQAQYILM EPMKTRQRQNASSSQONGPMDVISPFXKNNCMFLDTYGPS DKGRGINCLPVNTPQSRIQNAKRSPATYGHSOKKHKCSVYYSK HKTSTAAASSTSTTTEKGTSPLGSSLFAAKEDLCTDAMRENWI SLRYASGINVINGVANLTLFKHLINKERNTLKRTIVPSNDSSBCS MKSGIOTCHPPKSTDIKTSENTAEFKERELCPLKTSKKDPENLL PRNSSQYHQPDLPEISRKNNCNNQQVVEMEVDHCENLKKVDTK PRSSEKKIHTTSRDDMFSEKQIFFVEGGEDFIRKKQEKKEGNL QNLNMSKSTCRKRKGVAPVSRPPEQDSLKLVCSDFRSSLS SDINWSWCIQESTREVCKADAFLASSIPAQREAGGYYQKPEK KCVDKFCSDSSBCGSSGSVARRGSWGSWSTSSSDGDKKPM VAQHLPAGBSVSONDFPSEAPISINLISHINICNPTVSSLQQY ASPSCPSIPAGFTGVEEKGLIFFSGLLEWPTPVVVSISLNCTLE NOVPCVIQESAPVINSFIDWSOSTMYTPV\NAPAS\WENDA	ļ			TGDEQVWKEVQESLKKIEELKAHWKWEOVI.AMCOATTSSNSERI
6122 2 2324 RPRKMADGGAASQDESAAAAAAABDSRMNNPSETSKPSMESCDC NTGTOTNGLIDPKOKPPVPUGAISTAQAQAFLGHLHQVQLAGTSIL QAAAQSLNVQSKSNEESGDSQQPSQOPSVQAAIPGTOMLA GGQITGLTLTPAQCOCILLQQAQAAQLLAAAVQQHSASQQHSAQAFLGHLHQVQLAGTSIL LGEQPRI\UTLSQAATGTIAAPTQTILSQTDSQSGANAAAAAAAAAVQQHSASQQHSAQAFLGHLHQVQLAGTSIL LUSQPRI\UTLSQAATGTIAAPTQTILSQTDSQSGANAAAAAAAAVQQHSASQQHSAQAFLGHLHQVQLAGTSIL LUSQPRI\UTLSQAATGTIAAPTQTILTQSQSTPKRIDTPS LEEP\SQLEELBQFAKTFKQRRIKLGFT\QGDAGLAWVKLYGND LLQSQPRI\UTLSQAATGTIAAPTQTILTQSQSTPKRIDTPS LEEP\SQLEELBQFAKTFKQRRIKLGFT\QGDAGLAWVKLYGND FSPPTIFFRFBAINLSFKWIKLKPLLEKWINDAAHVSLSSSISS FSALMSPGIEGLSRRKKRTSIEA\NIRVALEKSFLEN\QKPTS EEITMIADQLAMEKSVIRVWFCNRRQKEKHINPPSSGG\TSSSF FSALMSPGIEGLSRRKKRTSIEA\NIRVALEKSFLEN\QKPTS LKAIFPSFTSIXVATTPSLVTSSAATTILTSVPLVLTSAAAVTNLS VTGTSDTTSNNTATVISTAPPASSAVTSPSLSPSPSASASTSEA SASETSTTOTTSTFLSSFISTQOMVTASGLQTA\AQALLPFKC AAQLPANASLAAMAAAAAGLNSSIMAPSOPAAGGALLSINPGTLS GALSPALMSNSTLAATQALASGGSLPITSIDATGNIVFANAGGA AAQLPANASLAAMAAAAAAGLNSSIMAPSOPAAGGALLSINPGTLS GALSPALMSNSTLAATQALASGGSLPITSIDATGNIVFANAGGA AAQLPANASLAAMAAAAAAGLNSSIMAPSOPAAGGALLSINPGTLS GALSPALMSNSTLAATQALASGGSLPITSLDATGNIVFANAGGA AAQLPANASLAAMAAAAAGLNSSIMAPSOPAAGGALLSINPGTLS GALSPALMSNSTLAATQALASGGSLPITSLDATGNIVFANAGGA AAQLPANASLAAMAAAAAGLNSSIMAPSOPAAGGALLSINPGTLS GALSPALMSNSTLAATQALASGGSLPITSLDATGNIVFANAGGA AAQLPANASLAAMAAAAAGLNSSIMAPSOPAAGGALLSINPGTLS GALSPALMSNSTLATQALASGGSLPITSLDATGNIVFANAGGA AAQLPANASLAAMAAAAAGLNSSIMAPSOPAAGGALLSINPGTLS GALSPALMSNSTLATQALASGGSSTAAAKAGTATAAAGGA AAQLPANASLAAMAAAAAGLNSSIMAPSOPAAGGALLSINPGTLS GALSPALMSNSTLATQALASGGSSTAAAAAAGAACAATAAAGGAAAAAAAAAAAAAAA	I			PDINIYQLKVLDCAMDACINLGLLEEALFYGTRTMEPYRIFFPG
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NTGTQTNGLDFQKQPVPVGGAISTAQAQAFLGHLHQVQLAGTSL QAAQSLAVQSKSNESGBSQQSGPSQPSQPSQAAIPOTOLMLA GGQITGILITPAQQGLLLQQAQAQALLAAAVQGKSASQQHSQA GATISASAATPMTQIPLSQPIQIAQDLQQLQQCLQAVALTQGFV LVHPTTNLQPA\QFIISOTPGQGGLLQA\QNLLTQLPGSQAN LLQSQPRI\TLTSQPATPTLATPIQTLPGSQSTPKRIDTPS LEEP\SDLEELEQFAKTFKQRRIKLGFT\QGDAGLAWKLYGND FSPTIFFFBEALNLSFKMKLKPLLEKWINDAENLSSDSSLSS FSALMSPGIEGLSRRKKRTSIEA\NIRVALEKSFLEN\QKPTS EEITMIADQLAMEKSVIKVWFCNRRQKEKRINPFSSGG\TSSSP SALMSPGIEGLSRRKKRTSIEA\NIRVALEKSFLEN\QKPTS EEITMIADQLAMEKSVIKVWFCNRRQKEKRINPFSSGG\TSSSF SASETSTTOTTSTFLSSPLTSQVMVTASGLQTA\AQLLPFKG AQLPANASIAAMAAAGLNPSLMAPSQFAAGGALLELNPGTLS GALSPALMSNSTLATIQALASGGSLPITSLDATGNLVFANAGGA AQLPANASIAAMAAAGLNPSLMAPSQFAAGGALLELNPGTLS GALSPALMSNSTLATIQALASGGSLPITSLDATGNLVFANAGGA AQLPANASIAAMAAAGLNPSLMAPSQFAAGGALLELNFGTLS GALSPALMSNSTLATIQALASGGSLPITSLDATGNLVFANAGGA AQLPANASILAMNASICATICALASGGSLPITSLDATGNLVFANAGGA AQLPANASILAMNASAGNSASATTTASKAQ PNIVTALFIRPQNISLITSPQVSLVSAAASAGNSAPVASLHA TSTAGESIONSLFTVASASGAASTTTTASKAQ HLLHRWFGTDMQMINFTGEFQUTEACPYLGTHSEESFFGILHL LQPLEMKRVGVVFTPADYCKVTSLILIRNLTVIDMIGVEGFG ARELLKVGGRLPGAGGSLRFKVPESTLMDCRQQLFSCPLDCHQPSLDPNT KNPKVENIGPLPITVSSLKUNCQQGVFEVLDCHQPSLDPNT SRDISIVFTPDPTSSWVIRDLSLUTLAADLEFRFTLNVTLPHHLL PLCADVVPGPSWEESFWRLTVFFVSLSLGVILIAFQQAQYILM FPKNSTQQAASSSQQNMPPMVISPHSCKCKMFLDTYGPS DKGRGKNCLPVNTPQSRIQNAARSPATYGHSCKKHKCSVYYSK HKTSTAAASSTSTTEEKQTSPJGSLPAAKEDICTDAMREMWI SLRYASGINVNLQKNLTLFKNLINKEENTLKXTIVPSNBSSRCS MKEGIQTCMFPKSTDLKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNGRQQVPVXRPUDHCENLKVVDTK PSSEKKIHTTSREDMFSEKQDIPFVEQEDFYRKKLQERKGNNL QNLNWSKSRTCRKNKKRGVAPVSRPPGSDLKLVCDFERSELS SINVRSWCIQESTRSVCAABAELASSLPAAGRAEGFYORFEK KCVDKPCSDSSSGCSSSSSVRARGSWGSWSTSSSDGDKKPM VDAQHFLPAGDSVQNDFPSERJINLSNILINICNPMTGNSLQQV VDAQHFLPAGDSVQNDFPSERJINLSNILINICNPMTGNSLQQV VDAQHFLPAGDSVQNDFPSERJINLSNILINICNPMTGNSLQQV VDAQHFLPAGDSVQNDFPSERJINLSNILINICNPMTGNSLQQV VDAQHFLPAGDSVQNDFPSERJINLSNILINICNPMTGNSLQQV AEPSCFSLPAGPTGVEEWGLYSPGDLWPTPVCVTSSLNCTLE MGVPCVIQESAPVHNSFIDWSATCEGGPSSAYCPLELNDYNAP	6122	2	2324	REPKMADGGAAGODEGGAAAAAA
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TRAIPPSPTSLVATTPSLVTSSAATTLTUSPVLPLTSAAVTNLS VTGTSDTTSNTATVISTAPPASSAVTSPSLSPSPSASATSTES SSASETSTTQTTSTPLSSPLGTSQVMVTASGLQTA/AQLLPPKG AAQLPANASLAMAAAAGLNPSLMAPSQFAAGGALLSLNPGTLS GALSPALMSNSTLATIQALASGGSLPITSLDATGNLVFANAGGA PNIVTAPLPFLNPQNISLLTSNPVSLVSAAAASAGNSAPVASLHA TSTSAESIQNSLFTVASASGAASTTTTASKAQ 6123 3 2944 HLLHRWFGIDMOMINFTTGEFQUIEACPYLGTHSEESRFGILHL HLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFG ARELLKVGGRLPGAGGSLRFKVPESTLMDCRRQLKDSKQILSIT KNFKVENIGPLPITVSSLKINGYNCQGYGFEVLDCHQFSLDPNT SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHHLL PLCADVVPGPSWEESFWRLTVFFVSLSLLGVILIAFQQAQYILM EFMKTRQRQNASSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS DKGRGKNCLFVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK HKTSTAAASSTTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKFTIVFSNPSSECS MKEGIQTCMFPKETDIKTSRNTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK PSSEKKIHHTSREDMFSEKQDIPFVEQEDFTRKKLQEKREGNL QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS SDINVRSWCIQESTREVCKADAEIASSLPAAQREAGGYYQKPEK KCVDKFCSDSSDCGSSSGSVRASRGSWGSWSTSSDGDKKPM VDAQHFLPAGDSVSQNDFFSEAPISLNLSHNICNPMTONSLPQY AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE NGVPCVIQESAPVNNSFIDWSATCEGQFSSAYCPLBLIDYNAPP EENMNYANGFPCPADVOTDFIDHNSOSTWNTPPD NNDAS\WEND	1	j		EEITMIADQLNMEKGVIRVWFCNRROKEKRINPPSSCG\TSSSB
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HLLHRWFGTDMQMINFTTGEFQLTEACPYLGTHSEESRFGILHL HLQPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFG ARELLKVGGRLPGAGGSLRFKVPESTLMDCRRQLKDSKQILSIT KNFKVENIGPLPITVSSLKINGYNCQGYGFEVLDCHQFSLDPNT SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHHLL PLCADVVPGPSWEESFWRLTVFFVSLSLLGVILIAFQQAQYILM EFMKTRQRQNASSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLMKEENTLKYNTIVFSNPSSECS MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK PSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEKREGNL QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK KCVDKFCSDSSDCGSSSGSVRASRGSWSSTSSSDGDKKPM VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPQY AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTTSSLNCTLE NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLEINDYNAFP EENMNYANGFPCPADVOTDFIDHNSOSTWNTPP\NMPAS\WGNA		1		TSTSAESTONSI ETIVA CA GGA AGMITTA AND THE
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DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK HKTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVPSNPSSECS MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK PSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKLQEKREGNL QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSTSSSDGDKKPM VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPQY AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLBLNDYNAFP EENMNYANGFPCPADVOTDFIDNSOSTWNTPP\NMPAS\WGNA	1		l	PLCADVVPGPSWEESFWRLTVFFVSLSLLGVTLTAFOOAOVTIM
DKGRGKNCLPVMTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSMPSSECS MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK PSSEKKIHKTSREDMFSEKQDIPFVEQEDPTRKKLDEKREGNL QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPQY AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLBLNDYNAFP EENMNYANGFPCPADVOTDFIDNSOSTWNTPPNMPAS\WGNA		i i		EFMKTRQRQNASSSSOONNGPMDVISPHSVKSNCKNFIDTVGDC
HKTSTAAASSTSTTTEEKQTSPLGSSLPAAKEDICTDAMRENWI SLRYASGINVALQKNLTLPKNLLNKEENTLKTTIVFSNPSSECS MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK PSSEKKIHKTSREDMFSEKQDIPFVEQEDPTRKKKLQEKREGNL QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPQY AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLBLNDYNAFP EENMNYANGFPCPADVOTDFIDNSOSTWNTPPNMPASNEGNA	1			DKGRGKNCLPVNTPQSRIONAAKRSPATYGHSOKKHKCSVVVCV
SLRYASGINVNLOKNLTLPKNLLNKEENTLKNTIVFSNPSSECS MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK PSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKLQEKREGNL QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPQY AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLBLNDYNAPP EENMNYANGFPCPADVOTDFIDNSCSTWNTPP\NMPAS\WGNA]	1		HKTSTAAASSTSTTTEEKOTSPLGSSLPAAKEDICTDAMPENDIT
MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK PSSEKKIHKTSREDMFSEKQDIPFVEQEDPTRKKKLQEKREGNL QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPQY AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLBLNDYNAFP EENMNYANGFPCPADVOTDFIDINSOSTWNTPP\NMPAS\WGNA	1 1			SLRYASGINVNLQKNLTLPKNLLNKEENTLKNTIVFSNPSSPCC
PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK PSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEKREGNL QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPQY AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLBLNDYNAFP EENMNYANGFPCPADVOTDFIDMSOSTWNTPP\NMPAS\WGNA]			MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLDENHI
PSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEKREGNL QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPQY AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLBLNDYNAPP EENMNYANGFPCPADVOTDFIDMSOSTWNTPP\NMPAS\WGNA	1 1		Ī	PRNSPQYHQPDLPEISRKNNGNNOOVPVKNEVDHCENLYKDDE
QNLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK KCVDKFCSDSSDCGSSSGSVRASRGSWGSWSSTSSDGDKKPM VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPQY AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLBLNDYNAFP EENMNYANGFPCPADVOTDFIDMSOSTWNTPP\NMPAS\WGNA		!	ļ	PSSEKKIHKTSREDMFSEKODIPFVEGEDPIRKKKLOFKBRONT.
SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPQY AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLBLNDYNAFP EENMNYANGFPCPADVOTDFIDINSOSTWNTPP\NMPAS\WGNA	1 !		į	QMLNWSKSRTCRKNKKRGVAPVSRPPEOSDLKI.VCSDFEPSELS
KCVDKFCSDSSSCGVRASRGSWGSWSSTSSSDGDKKPM VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPQY AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLBLNDYNAFP EENMNYANGFPCPADVOTDFIDINSCSTWNTPP\NMPAS\WGNA] [Į.	SDINVRSWCIQESTREVCKADAEIASSLPAAOREAEGYYOKDEV
VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPQY AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLBLNDYNAPP EENMNYANGFPCPADVOTDFIDHNSOSTWNTPP\NMPAS\WGNA	!!		ļ	KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKVDM
AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLBLNDYNAPP EENMNYANGFPCPADVOTDFIDHNSOSTWNTPP\NMPAS\WGNA]		ļ	VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLDOV
NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLBLNDYNAFP EENMNYANGFPCPADVOTDFIDHNSOSTWNTPP\NMPAS\WGNA		1		AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSI.NCTLF
QFPSSSRPYLKSTPKACLPMSGLFGPI\WAP\OSDVYENCCPIN			- 1	NGVPCVIQESAPVHNSFIDWSATCEGOFSSAYCPI.RI.NDVNARD
QFPSSSRPYLKSTPKACLPMSGLFGPI\WAP\OSDVYENCCPTN		1	1	EENMNYANGFPCPADVOTDFIDHNSOSTWNTPP\NMPAS\wgwa
	<u> </u>			QFPSSSRPYLKSTPKACLPMSGLFGPI\WAP\QSDVYENCCPIN

050	Danadi at - 3	I Dun 44 ar - 3 3	
SEQ	Predicted	Predicted end nucleotide	Amino acid segment containing signal peptide
ID NO:	beginning nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	
ĺ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	sequence	\=possible nucleotide insertion)
<u> </u>	Sequence		PTTEHSD/THMENOA\VVCKEYYPGF\NPFRAYMNLDIWTTT\A
1			NRNANFPLSRDSSYCGNV
6124	1573	236	SDEALRLAGERGMGRVQLFEISLSHGRVVYSPGEPLAGTVRVRL
0==1	1	1	GAPLPFRAIRVTCIGSCGVSNKANDTAWVVEEGYFNSSLSLADK
		Ì	GSLPAGEHSFPFOFLLPATAPTSFEGPFGKIVHOVRAAIHTPRF
1		•	SKDHKCSLVFYILSPLNLNSIPDIEOPNVASATKKFSYKLVKTG
i			SVVLTASTDLRGYVVGQALQLHADVENOSGKDTSPVVASLLQKV
ļ]		SYKAKRWIHDVRTIAEVEGAGVKAWRRAQWHEQILVPALPQSAL
i	ì		PGCSLIHIDYYLQVSLKAPEATVTLPVFIGNIAV/NPCPSEPPA
1			RPGAASWGPTPGG\PSAPPQEEAEAEAAAGGPHFLDPVFLSTKS
İ		1	HSQRQPLLATLSSVPGAPEPCPQDGSPASHPLHPPLCISTGATV
1			PYFAEGSGGPVPTTSTLILPPEYSSWGYPYEAPPSYEQSCGGVE
1			PSLTPES
6125	1	904	KTCPKLTCAFTVSVPDSCCRVCRGDGELSWEHSDGDIFRQPANR
			EARHSYHRSHYDPPPSRQAGGLSRFPGARSHRGALMDSQQASGT
ł	l	·	IVQIVINNKHKHGQVCVSNGKTYSHGESWHPNLRAFGIVECVLC
		İ	TCNVTKQECKKIHCPNRYPCKYPQKIDGKCCKVCPG/KKAKEBL
ŀ			PGQSFDNKGYFCGEETMPVYESVFMEDGETTRKIALETERPPQV
1	1		EVHVWTIRKGILQHFHIEKISKRMFEELPHFKLVTRTTLSQWKI
			FTEGENQISQMCSSRVCRTELEDLVKVLYLERSEKGHC
6126	1224	389	RLLSEAPCPRSRRRFQMNPEWGQAFVHVAVAGGLCAVAVFTGIF
İ	ļ		DSVSVQVGYEHYAEAPVAGLPAFLAMPFNSLVNMAYTLLGLSWL
	}	}	HRGGAMGLGPRYLKDVFAAMALLYGPVQWLRLWTQWRRAAVLDQ
ĺ			WLTLPIFAWPVAWCLYLDRGWRP\WLFLSLECVSLASYGLALLH
}		1	PQGFEVALGAHVVPAVGQALRT\HRHYG/SATPSATYLALGVLS
	İ		CLGFVVLKLCDHQLARWRLFQCLTGHFWSKVCDVLQFHFAFLFL THFNTHPRFHPSGGKTR
6127	1335	463	VLPRRCLVFVVNTMDSSREPTLGRLDAAGFWQVWQRFDADEKGY
012,	1333	. 303	IEEKELDAFFLHMLMKLGTDDTVMKANLHKVKQQFMTTQDASKD
]	Ì	ļ	GRIRMKELAGMFLSEDENFLLLFRRENPLDSSVEFMOIWRKYDA
]	1	ì	DSSGFISAAELRNFLRDLFLHHKKAISEAKLEEYTGTMMKIFDR
l			NKDGRLDLNDLARILALQENFLLQFKMDACSTEKRKGDFEKIFA
	1	i	YYDVSKTGALEGP\EVDGFVKDMMELVQPSISGVDLDKFREILL
1			RHCDVNKDGKIQKSELALCLGLKINP
6128	2511	843	TCRMSRRQLERWVWSSQQVQARGRNVRAPRLGKIAMGLEMSSKD
	1	l	SPGSLDGRAWEDAQKPQSAWCGGRKTRVYATSSRRAPPSEGTRR
	1		GGAARPEKTAEEGPPAAPGSLRHSGPLGPHACPTALPEPQVTSA
1			MSSQVVGIEPLYIKAEPASPDSPKGSSETETEPPVALAPG\PAP
			TRCLPGHKEEEDGEGAGPGEQGGGKLVLSSLPKRLCLVCGDVAS
			GYHYGVASCEACKAFFKRTIQGSIEYSCPASNECEITKRRRKAC
1	1	Į	QACRFTKCLRVGMLKEGVRLDRVRGGRQKYKRRPEVDPLPFPGP
			FPAGPLAVAGGPRKTAAPVNALVSHLLVVEPEKLYAMPDPAGPD
			GHLPAVATLCDLFDREIVVTISWAKSIPGFSSLSLSDQMSVLQS
		1	VWMEVLVLGVAQRSLTLQDELAFAEYLVLDEEGARPAGLGELG\
	1	(AALLQLVRRLQALRLEREEYVLLKALALANSDSVHIEDEPRLWS
			SCEKLLHEALLEYEAGRAGPGGGAERRRAGRLLLTLPLLRQTAG
	152		KVLAHFYGVKLEGKVPMHKLFLEMLEAMMD
6129	1764	771	ARFARSAHEGKMPKKKTGARKKAENRREREKQLRASRSTIDLAK
1			HPCNASMECDKCQRRQKNRAFCYFCNSVQKLPICAQCGKTKCMM
			KSSDCVIKHAGVYSTGLAMVGAICDFCEAWVCHGRKCLSTHACA
			CPLTDAEC\VECERGVWDHGGRIFSCSFCHNFLCEDDQFEHQAS
	1		CQVLEAETFKCVSCNRLGQHSCLRCKACFCDDHTRSKVFKQEKG
	ļ		KQPPCPKCGHETQETKDLSMSTRSLKFGRQTGGEEGDGASGYDA
			YWKNLSSDKYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS
6130		E 22	DLFTNLNLGRTYASGYAHYEEQEN
0130	3	577	GRGGTMREYKVVVLGSG\GVGKSALTV\QFVTCTFIEKYDPTIE

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		· · · · · · · · · · · · · · · · · · ·	DFYRKEIEV\DSSPSVAGISWTQQGTEQF\ASMRDLYIKKGQGC
i	1	ł	ILVYSLVNQQSFQ\DIKPMRDQIIRVKVSEKVPVI\LVGN\SVD
1	l	}	LESEREVSSSEGRALAEEWGCPFMETSAKSKTMVDELFAEIVRQ
		1	MNYAAQPDKDDPCCSACNIQ
6131	3	1811	SSPREKTSDSSHRPSRHGFLFLRLVGLSPFSYLCVPPSRPVPGS
·			PRSLSAMRLLPLAPGRLRRGSPRHLPSCSPALLLLVLGGCLGVF
l l		}	GVAAGTRRPNVVLLLTDDQDEVLGGMTPLKKTKALIGEMGMTFS
1			SAYVPSALCCPSRASILTGKYPHNHHVVNNTLEGNCSSKSWQKI
	1	İ	QEPNTFPAILRSMCGYQTFF\AGKYLNEYGAPDAGGLEHVPLGW
1		j	SYWYALEKNSKYYNYTLSINGKARKHGENYSVDYLTDVLANVSL
}			DFLDYKSNFEPFFMMTATP\APHSPWTAAPQYQKAFQNVFAPRN
į	į.	}	KNFNIHGTNKHWLIRQAKTPMTNSSIQFLDNAFRKRWQTLLSVD
ł	i		DLVEKLVKRLEFTGELNNTYIFYTSDNGYHTGOFSLPIDKROLY
			EFDIKVPLLVRGPGIKPNQTSKMLVANIDLGPTILDIAGYDLNK
			TQMDGMSLLPILRGASNLTWRSDVLVEYQGEGRNVTDPTCPSLS
1			PGVSQCFPDCVCEDAYNNTYACVRTMSALWNLQYCEFDDQEVFV
1	1		EVYNLTADPDQITNIAKTIDPELLGKMNYRLMMLQSCSGPTCRT
6132	96	1241	PGVFDPGYRFDPRLMFSNRGSVRTRRFSKHLL
		1241	AAGLLPPGLVPEDPRRTRNLLPFGIQGPFFALSRPLFSCVESGW
1			AWEAMEPEFLYDLLQLPKGVEPPAEEELSKGGKKKYLPPTSRKD
			PKFEELQKPA\VLMEWINATLLPEHIVVRSLEEDMFDGLILHHL FQRLAALKLEAEDIALTATSQKHKLTVVLEAVNRS\CSWRSGRP
			SGA/WESIFNKDLLSTLHLLVALAKRFQPDLSLPTNVQVEVITI
1			ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVFDELFKLAPEKVNA
			VKBAIVNFVNQKLDRLGLSVQNLDTQFADGVILLLLIGQLEGFF
			LHLKEFYLTPNSPAEMLHNVTLALELL/IGRGPAQLPC/LALK/
			TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTPHGAPN
6133	2	4256	FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
			TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAONSDSTK
			KTLVTLIANNNAGNPLVQQGGQPLILTONPAPGLGTMVTOPVI.R
1 1			PVQVMQNANHVTSSPVASQPIFITTOGFPVRNVRPVONAMNOVC
1 1			IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
1 1	j		STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
1 - 1			TATOPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
1	1		VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
1 1	ì		GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
1	ŀ		RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS /THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
ł	ł		GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
1			LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
	i		KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
	ļ		VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
]	ì	[CNKCRVQFLFAKDKIEHKLOHHKTFRKPKOLEGLKPGTKVTTDA
			SRGQPRTVPVSSNDTPPSALOEAAPLTSSMDPLPVFLYPPVOPS
1 1	J		IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
			CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
]		j	SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGOTRDRVHDP
) !]	NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
ĺ	j	İ	STATPPPTPTHPQALALPPLATEGAECLNVDDODEGSPVTOEPE
1 1	1		LASGGGGGGGGKKEQLSVKKLRVVLFALCCNTEOAAEHFRNPO
	1	Í	RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTOREOOLD
f			VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
		ł	VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
		.	DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
1	1		RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
L	<u>_</u>		RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL

	1 = 31 = 31		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l .	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u></u>	sequence		\=possible nucleotide insertion)
	1		DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
·	i		LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
<u> </u>	L	i	FYGFEEADLDLMEI
6134	2	4256	PVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
ł	1		TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
f	[KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
ļ			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
ł	ŀ		IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
			STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
İ	ŀ		TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
			VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
1			GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
i	1		RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
			/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
	ļ		GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
1			LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
	1		KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
}]		VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
			CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
	t		SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
			IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
]	·	CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
1	[SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
i	i		NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
1			STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
1			LASGGGGGGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
ļ		ļ	RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP
į.			VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
i			VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
			DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
l	<u>,</u>		RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
J			RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
			DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
1	1		LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
<u> </u>			FYGFEEADLDLMEI
6135	2	4256	FVHGSMADTDLFMECEEEELEPWQKISDV1EDSVVEDYNSVDKT
i	į i		TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
1			KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
			IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
ļ			STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
			TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
!			VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
<u> </u>			GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
			RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
	ļ		/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
(GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
			LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
			KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
			VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
	l .		CNKCRVOFLFAKDKIEHKLOHHKTFRKPKQLEGLKPGTKVTIRA
			SRGOPRTVPVSSNDTPPSALOEAAPLTSSMDPLPVFLYPPVORS
			IOKRAVRKMSVMGROTCLECSFEIPDFPNHFPTYVHCSLCRYST
1			CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
			,

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible rucleotide insertion)
	 	 	SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
1	1	1	NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
1			STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
1	1	1	LASGGGGGGGGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
ļ	1	l l	RRIRRWLRRFQASQGENLEGKYLSFEABEKLAEWVLTQREQQLP
		ł	VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
Į.			VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
İ			DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
1	Í	{	RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWOKHTACO
1			RSKGMLVMDCHRTHLSEEVLANLSASSTLPAVVPAGCSSKIOPL
1	· ·	1	DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
1			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
l .	•		LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
İ	1		FYGFEEADLDLMEI
6136	1704	539	FGVRMALEGMSKRKRKRSVQEGENPDDGVRGSPPEDYRLGQVAS
1	1		SLFRGEHHSRGGTGRLASLFSSLEPQIQPVYVPVPK\ESALASA
1			DLEEFIHQKQGQKRKNSQPGVKVADRKILDDTEDTVVSQRKKIO
1			INQEEERLKNERTVFVGNLPVTCNKKKLKSFFKEYGQIESVRFR
}			SLIPAEGTLSKKLAAIKRKIHPDQKNINAYVVFKEESAATQALK
1			RNGAQIADGFRIRVDLASETSSRDKRSVFVGNLPYKVEESAIEK
1			HFLDCGSIMAVRIVRDKMTGIGKGFGYVLFENTDSVHLALKLNN
ļ		<u> </u>	SELMGRKLRVMRSVNKEKFKQQNSNPRLKNVSKPKQGLNFTSKT
			AEGHPKSLFIGEKAVLLKTKKKGQKKSGRPKKQRKQK
6137	141	2656	RALRKRRCGPGRRGALGSGPGPQRRPGRVPEERPAPPRERKHPG
1			MWNMLIVAMCLA/LLGLPGKAQELQGHVS/IILAGEQLGDLAKK
			YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKD1EAQ
	1		LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV
l			LEKPFGHDHFSAQQLATELGTFFQEEEMYRVDHYLGKQAVAQIL
1	(§	
	1		PFRDQNRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV
			IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL
			IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL
			IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS
			IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG
			IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL
			IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS
			IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL
			IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPN
			IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM
			IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH
			IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV
			IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATTAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY
6138	4587	974	IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG
6138	4587	934	IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL
6138	4587	934	IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL
6138	4587	934	IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ
6138	4587	934	IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK
6138	4587	934	IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE
6138	4587	934	IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGGERFSLYQTRSLHHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM
6138	4587	934	IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIEATAVRAVRFGQFHLALSGGSSPVALFQQLATAHYGFPN AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPEHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDLNTWVVFMEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL
6138	4587	934	IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPN AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVWVLKEQIE HLHRQWEDLCLRVAIR KQEIEDRLNTWVVPNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI
6138	4587	934	IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVFNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQOD
6138	4587	934	IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQOD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS
6138	4587	934	IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPN AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLKVAIRKQEIEDRLNTWVFNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB
6138	4587	934	IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTFTFAGVLVHIDNL RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL ANDIBATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW AHTHLWLVDERCVPLSDPESNFQGLQAHLLQHVRIPYYNIH\AM PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH TASLFPQSPTGLDGEQLVVLTTSPSQPHRRMSLSLPLINRAKKV AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY DAFLG EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE HLHRQWEDLCLRVAIRKQEIEDRLNTWVVFNEKNKELCAWLVQM ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQOD LQRDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS

	T 800 22 25 22	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	location	to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	to first	residue of	S=Serine, T=Threonine, V=Valine,
ļ	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of		Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
L	sequence		NOREEFEGTRESILVWLTEMDLQLTNVEHFSESDADDKMRQLNG
	T	[FQQEITLNTNKIDQLIVFGEQLIQKSEP\LDAVLIEDELEELHR
	1		YCQEVFGRVSRFHRRLTSCTPGLEDEKEASENETDMEDPREIQT
1			DSWRKRGESEEPSSPQSLCHLVAPGHERSGCETPVSVDS\IPLE
	Į.		WDHTGRRGGPSSSH\EEDEEAQYY\SALSGKSISDGHSWHVPDS
	1	1	PSCPEHHYKQMEGDRNVPPVPPASSTPYKPPYGKLLLPPGTDGG
	\	ł	KEGPRVLNGNPQQEDGGLAGITEQQSGAFDRWEMIQAQEL\HNK
1	ļ		LKIKQNLQQLNSDISAITTWLKKTEAELEMLKMAKPPSDIQEIE
	1	1	LRVKRLQEILKAFDTYKALVVSVNVSSKEFLQTESPESTELQSR
ļ	1	1	LRQLSLLWEAAQGAVDSWRGGLRQSLMQCQDFHQLSQNLLLWLA
1			LRQLSLLWEAAQGAVDSWRGGLKQSLMQCQDFHQLSQNDDDWLA SAKNRRQKAHVTDPKADPRALLECRRELMQLEKELVERQPQVDM
1			LQEISNSLLIKGHGEDCIEAEEKVHVI\EKKLKQLREQVSQDLM
	1		LQEISNSLLIKGHGEDCIEAEEKVHVI\EAKLEQUEEQVSQDDH ALQGTQNPASPLPSFDEVDSGDQPPATSVPAPRAKQFRAVRTTE
,		'	ALQGTQNPASPLPSFDEVDSGDQPPATSVPAPRARQFRAVRITE GEEETESRVPGSTRPQRSFLSRVVRAALPLQLLLLLLLLLACLL
			PSSEEDYSCTQANNF\ARSFYPMLRYTNGPPPT LGDWVWSRTCGVLETPTSVLRRARARGPCPTDSKWALPRLREGE
6139	52	1131	TERRPWEASSWKTL/LAGWIGGAASVIVGHPLDTVKTRLQAGVG
I	1	1	YGNTLSCIRVVYRRESMFGFFKGMSFPLASIAVYNSVVFGVFSN
1			TORFLSQHRCGEPEASPPRTLSDLLLASMVAGVVSVGLGGPVDL
			TQRFLSQHRCGEPEASPPRTLSDLLLASMVAGVVSVGLGGFVDL IKIRLQMQTPPVSGRQPRFEVQGSGSCG\EPAYQGPVHCITTIV
1			RNEGLAGLYRGASAMLLRDVPGYCLYFIPYVFLSEWITPEACTG
	İ		PSPCAVWLAGGMAGAISWGTATPMDVVKSRLQADGVYLNKYKGV
1	1		PSPCAVWLAGGMAGAISWGTATPMDVVKSKLQALGVILMKIKGV LDCISQSYQKEGLKVFFRGITVNAVRGFPMSAAMFLGYELSLQA
ļ	1	1	
ĺ		<u> </u>	IRGDHAVTSP RPELELWRLRSRSWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP
6140	694	136	RPELELWRLRSRSWRPLGVPRRCHRRNWRBPVRAQFISVIVMAP RCQRP/QPPAPEPSSPNAAVPEAIPTPRAAASAALELPLGPAPV
		1	SVAPQAEAEARSTPGPAGSRLGPETFRQRFRQFRYQDAAGPREA
Ì		į.	FRQLREL/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR
		1	ARRIERTDURITG
			ARKIRRIDVRITG AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS
6141	2	984	ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFEIS
1	1	£	PSEILYCTLNTPKIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY
ļ		,	KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI
	1	1	NGENIVGWRHYDVAKKLKELKKEELFTMKLIEPKKAFEIELRSK
	1		AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD
	1	1	VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP
	1		DEFVFDVWGVIGDAKRRGL
		602	EAEGEQVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN
6142	116	502	LIVENVNQENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR
1			FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMBKL
		1	REKQLSHSLRAVSTDPPHHDHHDEFC\LMP
		L	FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q
6143	2802	270	\QLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED
			LLLNEWEASKCNIVCTQPRRISAVSLANRVCDELGCENGPGGRN
		1	SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM
			FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE
	1		KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC
			QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK
1			YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI
1		1	YSSRTQHAILYMNPHKINLDLILELLAILDKSFQFKWIEGAVDI FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF
ļ		1	LPACTORIAN SWALLE COLLEGE AND AND AND AND AND AND AND AND AND AND
			TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS
1	1	}	QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD
	1	1	YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN
1	1		A COMP A DISTAR AND STRUCK MAT AREST A RT DISSISTED TO SERVE A LOCAL
			AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF
			AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL TIYNAYLGWKKARQEGGYRSEITYCRRNFLNRTSLLTLEDVKQE

CEC	Dwo di abad	1 5 37 - 5 3	
SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
ļ. <u> </u>	sequence		\=possible nucleotide insertion)
Ì	1	1	LIKLVKAAGFSSSTTSTSWEGNRASQTLSFQEIALLKAVLVAGL
1	l	ŧ	YDNVGKIIYTKSVDVTEKLACIVETAQGKAQVHPSSVNRDLQTH
	l		GWLLYQEKIRYARVYLRETTLITPFPVLLFGGDIEVQHRERLLS
1	1		IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENDKI
	<u> </u>		LQIITELIKTENN
6144	1289	568	SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPYQN
1	1	i	VSASGGARHGGRGSGGPVICTYGPDLFPLVA\TIGAAFVAKVMS
I	1	Į	VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDSSS
			FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFHDV
ı		l	QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVMTE
L			DKGVDLGQKPNPYFYSCCHH
6145	1109	196	GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGPVL
ļ	1		GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKMEDT
	1		DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYALD
	İ		QGVNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALYPV
1			\VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDPQD
1	1	i	/TKAWLKEHVEPVF\GFP\QFVRF\SWRTAQTI\LEKEAEDVIR
l .	1		EDSASENQEGLRKITSYFLNEGSQARPRSSHRYFLERGLESTTS
			L L
6146	428	781	LKKKGKEKAEAQQVEALPGPSLDQWHRSAGEEEDGPVLTDEQKS
I	İ		R/YPGHEAHDQGG\WDARQSIIRKVVDPETGRTRLIKGDGEVLE
	<u> </u>		EIVTKERHREINKQATRGDCLAFQMRAGLLP
6147	1	2304	GTRQLPPPSPGSGPGDSPEGPEGEAPERRRKAHGMLKLYYGLSE
İ	1		GEAAGRPAGPDPLDPTDLNGAHFDPEVYLDKLRRECPLAQLMDS
	i		ETDMVRQIRALDSDMQTLVYENYNKFISATDTIRKMKNDFRKME
	•		DEMDRLATNMAVITOFSARISATLQDRHERITKLAGVHALLRKL
į.	j ,		QFLFELPSRLTKCVELGAYGQAVRYQGRAQAVLQQYQHLPSFRA
			IQDDCQVITARLAQQLRQRFREGGSGAPEQAECVELLLALGEPA
			EELCEEFLAHARGRLEKELRNLEAELGPSPPAPDVLEFTDHG\S
			SGFVGGLCQVAAAYQELFAAQGPAGAEKLAAFARQLGSRYFALV
1			ERRLAQEQGGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT
j .	ļ		EIVERVARERLGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGP
			GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF
1			CSQGVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLLLS
1			RLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA
			RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAVMKRV
1			VEDTTAIDVQVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG
			GGDMCIWASHGASSVARASVREPQGNKSPRMNTKRAGECLCPRS
			CSFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS
			CILPLPHSTGSINSDHVPTK
6148	3056	353	VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ
			KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT
			SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV
1 1	1		PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT
			SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES
!!!			VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE
[LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ
!!			LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW
1			DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR
, ,			LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS
			ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG
			ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK
į l			THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQQTFVDRLVHLM
[]			KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK
]			IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLRQD
			QLILQIISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E≈
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
{	sequence		\=possible nucleotide insertion)
			PVAEVLDTEGSIONFFRKYAPSENGPNGISAEVMDTYVKSCAGY
Ì		1	CVITYILGVGDRHLDNLLLTKTGKLFHIDFGYILGRDPKPLPPP
		1	MKLNKEMVEGMGGTQSEQYQEFRKQCYTAFLHLRRYSNLILNLF
1	ł	İ	SLMVDANIPDIALEPDKTVKKVQDKFRLDLSDEEAVHYMQSLID
1			ESVHALFAAVVEQIHKFAQYWRK
6149	1	1413	RVDPRVRENGTANP I KNGKTSPASKDQRTGKKTSVQGQVQKGND
}	ļ	_	ESESDFESDPPSPKSSEEEEQDDEEVLQGEQGDFNDDDTEPENL
ì		Ì	GHRPLLMDSEDEEEEEKHSSDSDYEQAKAKYSDMSSVYRDRSGS
	1	1	GPTQDLNTILLTSAQLSSDVAVETPKQEFDVFGAVPFFAVRAQQ
1	1	İ	PQQEKNEKNLPQHRFPAAGLEQEEFDVFTKAPFSKKVNVQECHA
1	1	1	VGPEAHTIPGYPKSVDVFGSTPFQPFLTSTSKSESNEDLFGLVP
1	1	1	FDEITGSQQQKVKQRSLQKLSSRQRRTKQDMSKSNGKRHHGTPT
	1	1	STKKTLKPTYRTPERARRHKKVGRRDSQSSNEFLTISDSKENIS
į	ł	}	VALTDGKDRGNVLOPEESLLDPFGAKPFHSPD\LSWHPP\HQGL
			S\DIRADHNT\VLPGR\PRQNSLHGSFHSADVLKMDDFGAVP/F
	1		LTELVVQSITPHQSQQSQPV\ELDPFGAAPFPSKQ
6150	372	37	MSNIKKYIIDYDWKASIEIEIDHDVMTEEKLHQINNFWSDSEYR
1 0130	}	1	LNKHGSVLNAVLIMLAQHALLIAISSDLNAYGVVCEFDWNDGNG
1		1	OEGWPPMDGSEGIRITDIDTSGIF
6151	1555	521	DSNQQSVSGTAASTLLHSFKATIYYQGTGHVQQFYGVTSPYSQT
61.5.0	1 1333	322	TPPIVQSYAQPSLQYIQGQQIFTAHPQGVVVQPAAAVTTIVAPG
1	1		QPQPLQPSEMVVTNNLLDLPPPSPPKPKTIVLPPNWKTARDPEG
		1	KIYYYHVITRQTQWDPPTWESPGDDASLEHEAEMDLGTPTYDEN
Į.	1	}	PMK\ASKKPKTAEADTSSELAKKSKEVFRKEMSQFIVQCLNPYR
1	1	1	KPDCKVG\RITTTEDFKHLARKLTHGVMNKELKYCKNPE\DLEC
			NENVKHKTKEYIKKYMQKFGAVYKPKEDTEFRVTVGPGWEDGWS
i	ł	1	GKTDSRERKSCGPFCSTPVSTVLLMIHHPGBFNPADVN
6152	1366	648	NRTWSTPSTWMGVALPPLCSTGPWPVTRQITARTTCGAVPAKCP
6152	1366	, ,,,,	PWC/DVHEPRCOPPDCHGHGTCVDGHCQCTGHFWRGPGCDELDC
1		ł	GPSNCSQHGLCTETGCRCDAGWTGSNCSEECPLGWHGPGCQRPC
1	l	1	KCEHHCPCDPKTGNCSVSRVKQCLQPPEATLRAGELSFFTRTAW
	Į.	}	LALTLALAFLLLISTAANLSLLLSRAERNRRLHGDYAYHPLQEM
[NGEPLAAEKEQPGGAHNPFKD
<u> </u>	 	3368	GRVGARSPGRAYALLLLICFNVGSGLHLQVLSTRNENKLLPKH
6153	2	3368	PHLVROKRAWITAPVALLEGEDLSKKNPIAKIHSDLAEERGLKI
1		j	TYKYTGKGITEPPFGIFVFNKDTGELNVTSILDREETPFFLLTG
1	1		YALDARGNIVEKPLELRIKVLDINDNEPVFTQDVFVGSVEELSA
Ţ		l	
1			AHTLVMKINATDADEPNTLNSKISYRIVSLEPAYPPVFYLNKDT
1		İ	GEIYTTSVTLDREEHSSYTLTVEARDGNGEVTDKPVKQAQVQIR
1			ILDVNDNIPVVENKVLEGMVEENQVNVEVTRIKVFDADEIGSDN
1		1	WLANFTFASGNEGGYFHIETDAQTNEGIVTLIKEVDYEEMKNLD
1		İ	FSVIVANKAAFHKSIRSKYKPTPIPIKVKVKNVKEGIHFKSSVI
1			SIYVSESMDRSSKGQIIGNFQAFDEDTGLPAHARYVKLEDRDNW
1]	ISVDSVTSEIKLAKLPDFESRYVQNGTYTVKIVAISEDYPRKTI
1		1	TGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLDGHPN
-			SGPFSFSVIDKPPGMAEKWKIARQESTSVLLQQSEKKLGRSEIQ
1			FLISDNQGFSCPEKQVLTLTVCEVLHGS\GCREAQHDSYVGLGP
1	1	1	AAIALMILAFLLLLVPLLLLMCHCGKGAKGFTPIPGTIEMLHP
1	l	1	WNNEGAPPEDKVVPSFLPVDQGGSLVGRNGVGGMAKEATMKGSS
		1	SASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAI\MTTE
1			TTITARATGASRDVAGAQAAAVALNEEFLKNYFTDKAASYTEED
1	1	}	ENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFLDDLGL
		1	KFKTLAEVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTM
}			VNSENTYSSGSSFPVPKSLQEANAEKVTQEIVTERSVSSRQAQK
			VATPLPDPMASRNVIATETSYVTGSTMPPTTVILGPSQPQSLIV
)]	TERVYAPASTLVDQPYANEGTVVVTERVIQPHGGGSNPLEGTQH
L_	1	Ī	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
]	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
-	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			LQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
į			APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGH
			SNSTITTSSTRVTKHSTVQHSYS
6154	3660	2146	KKKTKMKNTLQKTVNFGAWPKPTISDKSHLLQMVSKLDLTDAKN
			SDTAHIKSIEITSILNGLQASESSAEDSEQEDERGAQDMDNNGK
			EESKIDHLTNNRNDLISKEEQNSSSLLEENKVHADLVISKPVSK
1			SPERLRKDIEVLSEDTDYEEDEVTKKRKDVKKDTTDKSSKPQIK
ı			RGKRRYCNTEECLKTGSPGKKEEKAKNKESLCMENSSNSSSDED
			EEETKAKMTPTKKYNGLEEKRKSLRTTGFYSGFSEVABKRIKLL
			NNSDERLQNSRAKDRKDVWSSIQGQWPKKTLKELFSDSDTEAAA
1			SPPHPAPEEGVAEESLQTVAEEESCSPSVELEKPPPVNVDSKPI
1			EEKTVEVNDRKAEFPSSGSNFSA*IPLPYLHLNRLHQSL*QKGS
1	1		RQQSSVTVSEPLAPNQEEVRSIKSETDSTIEVDSVAGELODLOS
İ			ERE*LASRF*CQCELEQ**SARTRTS*KSLYRSEKSERCSGRRK
6155			FIKKAEKKP*SNSGKQQKEGK
6133	869	121	HLLPELRGKSWITMKYVFYLGVLAGTFFFADSSVQKEDPAPYLV
			YLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRVRDG
1			TEQTINPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPKVQALN
1	•		P\PTTNVRPGTVCLLSGLDWSQENSGRHPDLRQNLEAPVMSDRE
İ	ļ i		CQKTEQGKSHRNSLCVKFVKVFSRIFGEVAVATVICKDKLQGIE
6156	5725	3984	VGHFMGGDVGIYTNVYKYVSWIENTAKDK
	3,23	2204	GTSTVTMATKKHFSIILNLLGMLLKKDNQDTRKLLMTWALEVAV VMKKSETYAPLFCLPSFHKFCKGLLADTLVEDVNICLQACSSLH
			ALSSSLPDDLLQRCVDVCRVQLVHRGTCIRQAFGKLLKSIPLGV
	· .	•	FLSNNNHTEIQEISLALRSHMSKAPSNTFHPQDFSD/VISFILY
İ			GNSHRTGKDKWLERLFYSCQRLDKRDQSTIPRNLLKTDAVLWQW
l			AIWEAAQFTVLSKLRTPLGRAQDTFQTIEGIIRSLAGHTLNPDQ
			DVSQWTTADNDEGHGNNQLRLVLLLQYLENLEKLMYNAYEGCAN
			ALTSPPKVIRTFLYTNRQTCQDWLTRIRLSIMRVGLLAGQPAVT
1 .	[VRHGFDLLTEMKTTSLSQGNELEVSIMMVVEALCELHCPEAIQG
1			IAVWSSSIVGKHLLWINSVAQQAEGRFEKASVEYQEHLCAMTGV
			DCCISSFDKSVLTLASAGCKSASLKHCLNGESRKSVLSKPTDSS
			PEVINYLGNKACECYISTADWAAVQEWQNAIHDLKKSTSSTSLN
j			LKADFNYIKSLSSFESGKFVECTEQLELLPGENINLLAGGSKEK
63.57			IDMKKLLRNM
6157	946	329	MANRGPSYGLSREVQEKIEQKYDADLENKLVDWIILQCAEDIEH
	İ		PPPGRAHFQKWLMDGTVLCK_INSLYPPGQEPIPKISESKMAFK
] .			QMEQISQFLKAAETYGVRTTDIFQTVDLWEGKDMAAVQRTLMAL
1			GSVAVTKDDGCYRGEPSWFHRKAQQNRRGFSEEQLRQGQNVIGL
6158	441	1482	QMGSNKGASQAGMTGYGMPRQIM*DAASCP
		7406	LGSLIVLSLHCKVIFSSQSLERAMKEKAVDLVPILAQNPGLAQN
į	1		PILEGKDHNQNTGVDPIIDHVQDRKTD/SRSKSPHKKRSKSRER
[1		RKSRSRSHSRDKRKDTREKI KEKERVKEKDREKEREKEREKE KERGKNKDRDKBREKDREKDKEKDREREREKEHEKDRDKEKEKE
1 1	1	ı	QDKEKEREKDRSKEIDEKRKKDKKSRTPPRSYNASRRSRSSSRE
	ĺ		RRRRSRSSSRSPRTSKTIKRKSSRSPSPRSRNKKDKKREKERD
	İ		HISERRERESTSMRKSSNDRDGKEKLEKNSTSLKEKEHNKEPD
1 1	ľ		SSVSKEVDDKDAPRTEENKIQHNGNCQLNEENLSTKTEAV
6159	53 .	84	AVIAPLHISLGDRARPYLKNTEKSSTTCSRRRNQSFPPVMSLTH
		••	RLHLCKYWGCAVSNVCRFWEGRPLPLMIVVPYTLPVSLPVGSCV
] [IITGTPILTFVKDPQLEVNFYTGMDEDSDIAFQFRLHFGHPAIM
1 1			NSCVFGIWRYEEKCYYLPFEDGKPFELCIYVRHKEYKVMVNGOR
j 1		•	IYNFAHRFPPASVKMLQVFRDISLTRVLISD*GRCVRITAVQEF
	}		DVSVSCDCTTAYQPG
6160	1626	1790	AGAKFFP*F*KVADAQPTESEKEIYNQVNVVLKDAEGILEDLQS
[YRGAGHEIREAIQHPADEKLQEKAWGAVVPLVGKLKKFYEFSQR
			THE TAXABLE AND THE PROPERTY OF THE PROPERTY O

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
IĐ	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
1			LEAALRGLLGALTSTPYSPTQHLEREQALAKQFAEILHFTLRFD
ł	ľ	Į.	ELKMTNPAIQNDFSYYRRTLSRMRINNVPAEGENEVNNELANRM
1	1		SLFYAEATPMLKTLSDATTKFVSENKNLPIENTTDCLSTMASVC
Î	1	1	RVMLETPEYRSRFTNEETVSFCLRVMVGVIILYDHVHPVGAFAK
ì	1		TSKIDMKGCIKVLKDQPPNSVEGLLNALRYTTKHLNDETTSKQI
ł	1	1	KSMLQ*QLLTLVNKG
6161	455	1569	PVSGSESSLRRAWASILRLMLGPRVAVSILCEDGISH*LLEKH*
0202		l .	KSHVLEPLSSLALEEQCLALSLDWSTGKTGRAGDQPLKIISSDS
1			TGQLHLLMVNETRPRLQKVASWQAHQFEAWIAAFNYWHPEIVYS
ì			GGDDGLLRGWDTRVPGKFLFTSKRHTMGVCSIQSSPHREHILAT
j	j	Ì	GSYDEHILLWDTRNMKQPLADTPVQGGVWRIKWHPFHHHLLLAA
1			CMHSGFKILNCQKAMEERQEATVLTSHTLPDSLVYGADWSWLLF
1			RSLQRAPSWSFPSNLGTKTADLKGASELPTPCHECREDNDGEGH
l		Į.	ARPOSGMKPLTEGMRKNGTWLQATAATTRDCGVNPEEADSAFSL
1	}	1	LATCSFYDHALHLWEWEGN
6162	1	586	RTIHATGRAGASPMHRLIVWRLAEANKQHVRCQKCLEFGHWTYE
0102	1 -	1	CTGKRKYLHRPSRTAELKKALKEKENRLLLQQSIGETNVERKAK
	1	1	KKRSKSVTSSSSSSSSSSSASDSSSESEETSTSSSSEDSDTDESS
ł	1	· I	SSSSSSASSTTSSSSSDSDSDSSSSSKQ*HQHR*QL*R*TTKEE
1	1	ł.	EKEIELLHSYWTDGLKTLM
<u> </u>	1081	785	RIRSTTEGCAVRLHPTQNTGKARIMILLSVSLGRHWAFTYKFFL
6163	1081	/ "	TPVVFVFFFFFFFHRKE*VMQKNPMKSREDEWMEKLNNLHVQRAD
1	i		MNRLIMNYLVTEGFKEAAEKFRMESGIEPSVDLETLDERIKIRE
	1	1	MILKGQIQEAIALINSLHPELLDTNRYLYFHLQQQHLIBLIRQR
1			ETEAALEFAQTQLAEQGEESRECLTEMERTLALLAFDSPEESPF
1	1)	GDLLHTMQRQKVWSEVNQAVLDYENRESTPKLAKLLKLLLWAQN
	1	1	ELDOKKVKYPKMTDLSKGVIEEPK
		406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
6164	90	406	SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
			VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
i			NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
ì			WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
l l	1		YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
.		i	GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
1			RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE
1			
j	•		LMQTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSVSGRHS
1			KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE
1	ł		PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTDIN
ı	'		ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN
J			HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
I	1		PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA
i	1	l	EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
1	1		VOAKLGALELNORDAAAETELRVHPPCQRHCPEPPSAPEENKAT
1			SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
		1	HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN
1	1	Ì	GGERFG
6165	90	405	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGT1LSNVLKKR
			SCISRTAPRILCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
1		1	VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
1	1	1	NPDDDSMGIOIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
1	1		WNKTVGYCOGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
-			YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
l l		1	GYEPPLINVFTMOWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
			RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE
		S	LMOTVYSMAPFPFPOLAELREKYTYNITPFPATVKPTSVSGRHS
I		[KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE
j	1	1	Chronian Paris

SEQ	Predicted	Predicted end	I Projection
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence	<u></u>	\=possible nucleotide insertion)
			PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTDIN
1			ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN
1			HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
			PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA
1			EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
			VQAKLGALELNQRDAAAETELRVHPPCQRHCPEPPSAPEENKAT
-			SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
			HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN GGERFG
6166	2	1206	HKLWRTVAMAGAEWKSLEECLEKHLPLPDLQEVKRVLYGKELRK
i		1200	LDLPREAFEAASREDFELQGYAFEAAEEQLRRPRIVHVGLVQNR
			IPLPANAPVAEQVSALHRRIKAIVEVAAMCGVNIICFQEAWTMP
1]		FAPCTREKLPWTEFAESAEDGPTTRFCQKLAKNHDMVVVSPILE
1	1		RDSEHGDVLWNTAVVISNSGAVLGKTRKNHIPRVGDFNESTYYM
			EGNLGHPVFQTQFGRIAVNICYGRHHPLNWLMYSINGAEIIFNP
Ĭ			SATIGALSESLWPIEARNAAIANHCFTCAINRVGTEHFPNEFTS
			GDGKKAHQDFGYFYGSSYVAAPDSSRTPGLSRSRDGLLVAKLDL
	1		NLCQQVNDVWNFKMTGRYEMYARELAEAVKSNYSPTIVKE*PAS
6167	1220		VPALG
1 010/	1220	1844	YGIVTGPSLCAGDKQPKKQEKNPVLVSPEFVDEALCACEEYLSN
ı			LAHMDIDKDLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTQ
· ·	ļ		VQRCEDILQQLQAVVPQIDMEGDRNIWIVKPGAKSRGRGIMCMD
ľ	1		HLEEMLKLVNGNPVVMKDGKWVVQKYIERPLLIFGTKFDLROWF LVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDK+APLYLTPEGWS
}	[LFLQRYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDMEG
İ	j		DRNIWIVKPGAKSRGRGIMCMDHLBEMLKLVNGNPVVMKDGKWV
			VQKYIERPLLIFGTKFDLRQWFLVTDWNPLTVWFYRDSYIRFST
			QPFSLKNLDK
6168	84	1392	VWPVPSVSAMPPKKQAQAGGSKKAEQKKKEKI1EDKTFGLKNKK
j			GAKQQKFIKAVTHQVKFGQQNPRQVAQSEAEKKLKKDDKKKELQ
]			ELNELFKPVVAAQKISKGADPKSVVCAFFKQGQCTKGDKCKFSH
			DLTLERKCEKRSVYIDARDEELEKDTMDNWDEKKLEEVVNKKHG
1			EABKKKPKTQIVCKHFLEAIENNKYGWFWVCPGGGDICMYRHAL
]			PPGFVLKKKKKKKKEDEISL*DLIERERSALGPNVTKITLESF LAWKKRKRQEKIDKLEQDMERRKADFKAGKALVISGREVFEFRP
1			ELVNDDDEEADDTRYTQGTGGDEVDDSVSVNDIDLSLYIPRDVD
1]		ETGITVASLERFSTYTSDKDENKLSEASGGRAENGERSDLEEDN
			EREGTENGALDAVPVDENLFTGEDLDELEEELNTLDLEE
6169	112	662	APAAAMAERPEDLNLPNAVITRIIKEALPDGVNISKEARSAISR
	ļ		AASVFVLYATSCANNFAMKGKRKTLNASDVLSAMEEMEFORFVT
1 1			PLKEALEAYRREQKGKKEASEQKKKDKDKKTDSEEODKSRDEDN
	ł	į	DEDEBRLEEEEQNEEEEVDN * KGRETVAPWKVPLEMRRATCFCE
63.70			AFPCWAE
6170	62	667	STKVMLPNTGRLAGCTVFITGASRGIGKAIALKAAKDGANIVIA
]	[AKTAQPHPKLLGTIYTAAEEIEAVGGKALPCIVDVRDEQQISAA
1	į		VEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG
1	. [}	TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWFKQHCGRW*VV
6171	382	941	G*GDGLCLICFELNLCMSDVITICT
	302	741	HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST
] [1	MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRRHAN SGGDIFGDSEAAVEDDVI KOVINAL SI SORAVEDDSEAAVEDDVI KOVINAL SI SORAVEDDSEAAVEDDVI KOVINAL SI SORAVEDDSEAAVEDDVI KOVINAL SI SORAVEDDSEAAVEDDVI KOVINAL SI SORAVEDDSEAAVEDDSEAAVEDD
]]	1	SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT
		[NATLRYTKSK
6172	651	54	GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR
1			SAQERKERLRRALEENRLIPTELRREALALQGSLEFDDAGGEGV
		ļ	TSHVDDEYRWAGVEDPKVMITTSRDPSSRLKMFAKELKLVFPGA

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	i	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine.
	location	corresponding	H=H1Stidine, I=ISOIeucine, K=Bysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1		sequence	\=possible nucleotide insertion)
L	sequence		ORMNRGRHEVGALVRACKANGVTDLLVVHEHRGTPVGLIVSHLP
	1	1	FGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRV
ſ	I	1	SDILRYLFPVPKDDSHRVITFANQDDYISFRHHVYKKTDHRNVE
ł	1	1	SDILKILFPVPKDDSHKVIIFANQDDIISFKHMVIKKIDIKKV
	1	l	LTEVGPRFELKLYMIRLGTLEQEATADVEWRWHPYTNTARKRVF
1	1	I	LSTE*AAPRPLGQLL
6173	3	288	SVDHREVQVLSQSMPLTPHQAVLRGERPYMCVECGKCFGRSSHL
02/3	1		LQHQRIHTGEKPYVCSVCGKAFSQSSVLSKHRTIHTGEKPYECN
1			ECGKAFRVSSDLAQHHKIHTGEKPHECLECRKAFTQLSHLIQHQ
ì		i	RIHTGERPYVCPLCGKAFNHSTVLRSHQRVHTGEKPHRCNECGK
ì	l .	1	TFSVKRTLLQHQRIHTGEKPYTCSECGKAFSDRSVLIQHHNVHT
ì	1	1	GEKPYECSECGKTFSHRSTLMNHERIHTEEKPYACYECGKAFVQ
1			HSHLIQHQKVHRKL*PTCVLSVGSALAGVPTSFSISVSTLERSP
1			HSHLIQHQKVHRKL*PTCVLSVGSALAGVPTSFSISVSIDERSP
ł.		1	MCAVYVGRPSARAQSLVNTGQFTQVRSPMSVMSVEKPLE
6174	1060	959	PRPPGKRWMVAGLGNPGLPGTRHSVGMAVLGQLARRLGVAESWT
1		1	RDRHCAADLALAPLGDAQLVLLRPRRLMNANGRSVARAAELFGL
			TAREVYLVHDELDKPLGRLALKLGGSARGHNGVRSCISCLNSNA
ŀ		}	MPRLRVGIGRPAHPEAVQAHVLGCFSPAEQELLPLLLDRATDLI
ł	1	1	LDHIRERSQGPSLGP*H*WFSKKA
			RYFRADPRSRSGQPRAEGLGAFAEGPLRAMAAPVKGNRKQSTEG
6175	2204	334	DALDPPASPKPAGKQNGIQNPISLEDSPEAGGEREEEQEREEEQ
1	ì	i	AFLVSLYKFMKERHTPIERVPHLGFKQINLWKIYKAVEKLGAYE
	1	ì	AFLVSLYKFMKERHTPIERVPHLGFRQINDWKIIRAVERLGAIL
1	1	Ĭ	LVTGRRLWKNVYNELGGSPGSTSGATCTRRHY*RLVLPYVRHLK
	İ	1	GEDDKPLPTSKPRKQYKMAKENRGDDGATERPKKAKEERRMDQM
}	Ì	ĺ	MPGKTKADAADPAPLPSQEPPRNSTEQQGLASGSSVSFVGASGC
1	1	t	PEAYKRLLSSFYCKGTHGIMSPLAKKKLLAQVSKVEALQCQEEG
ì	ł	İ	CPHCAEPOASPAVHLPESPOSPKGLTENSRHRLTPQEGLQAPGG
i	1	}	STREEAOAGPCPAAPIFKGCFYTHPTEVLKPVSQHPRDFFSRLK
1	, i	1	DGVLLGPPGKEGLSVKEPQLVWGGDANRPSAFHKGGSRKGILYP
1	•	}	KPKACWVSPMAKVPAESPTLPPTFPSSPGLGSKRSLEEEGAAHS
į.			GKRLRAVSPFLKEADAKKCGAKPAGSGLVSCLLGPALGPVPPEA
		1	YRGTMLHCPLNFTGTPGPLKGQAALPFSPLVIPAFPAHFLATAG
1	1	l	YRGTMLHCPLNF IGI PGPLKGQAADF SELVIFFI LFER ANDUF
1	Į.	1	PSPMAAGLMHFPPTSFDSALRHRLCPASSAWHAPPVTTYAAPHF
ļ			FHLNTKL
6176	1040	402	PLSALRAMAEVHVIGQIIGASGFSESSLFCKWGIHTGAAWKLLS
1	1	1	GVREGQTQVDTPQIGDMAYWSHPIDLHFATKGLQGWPRLHFQVW
l l	1	1	SODSFGRCOLAGYGFCHVPSSPGTHQLACPTWRPLGSWREQLAR
i i		i	AFVGGGPOLLHGDTIYSGADRYRLHTAAGGTVHLEIGLLLRNFD
1		1	RYGVEC*GTLPPTSPPSTPRTPSDGGGWHSGQEHRL
			VPIESLVGKVHNFPLIAFYCCEKGKRQPHKSLHDRCFGEALDPN
6177	1400	992	CSHCYLDQIKRSDFLGFSGYSPHFVAISTNSEHKMQPSSMQQAL
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1	1	1	VCPI
6178	1027	254	STORGGIKGVARAASLVGRRRAGTGMALLLCLVCLTAALAHGCL
1 52,0	1	1	HCHSNFSKKFSFYRHHVNFKSWWVGDIPVSGALLTDWSDDTMKE
1	1		LHLATPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELR
1	Ī	{	NIFREQVHLIQNAIIESRIDCQHRCGIFQYETISCNNCTDSHVA
1			CFGYNCESSAQWKSAVQGLLNYINNWHKQDTSMRPRSSAFSWPG
1		1	THRAAPAFLVLPALRCLEPPHLANLSLEDAA*CLKQH
1			RGETREMAGNLLSGAGRRLWDWVPLACRSFSLGVPRLIGIRLTL
6179	806	276	RGETREMAGNILLSGAGKKLWDWVPLACKSFSLGVPKDIGIRDIE
1		ļ	PPPKVVDRWNEKRAMFGVYDNIGILGNFEKHPKELIRGPIWLRG
1			WKGNELQRCIRKRKMVGSRMFADDLHNLNKRIRYLYKHFNRHGK
l			FR*KRKLRTSEKAHLSPWRRETVLFPVRKRLCIFSVIKWGFFGI
6300	156	1833	DHHILKAASTTHVCARGNIFAIPNTRCLEC*ATATPSSLECQN*
6180	136	1033	SHLSLCPLPATTSGLTPNSMIPEKERQNIAERLLRVMCADLGAL
ì		1	SVVSGKEFLKLAQTLVDSGARYGAFSVTEILGNFNTLALKHLPR
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TOTOREDGAPVAPEGUVUSRANKRSGAGEGGGGGARGAEE EPPPPLQAVLVADSFDRFFFISKDQPRVLLPLANVALIDYTLE FLTATATOQETFVFCCKKAQIKEHLLKSKWCRPTSLNVVRIITS ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL HFQKTQGLRRFAFPLSLFQGSSDCVEVRYDLLDCHISICSPQVA OLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS NLHNYSAVCADVIRRWYYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEELQQNLWGLKI NMEEESESESEGSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED PFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ OLRKNQQLQRFIQWLKEAEEESSEDD GLRKNQQLQRFIQWLKEAEESSEDD GLRKNQCLQRFIQWLKEAEESSEDD FFLLFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFPSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQS PALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR	6700			VP
EPPPPLQAULVADSFDRRFFPISKDQPRVLLPLANVALIDYTLE FLTATGVQETFVFCCWKAAQIKEHLLKSKMCRPTSLINVVRIITS ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWYYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEEELQQNLWGLKI NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEAEEESSEDD GLKKNQQLQRFIQWLKEAEEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR HKLKGTSFLLGGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNILDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR	0104	. 1	2191	IVTVREEDGAPAVAPPGVVVSRANKRSGAGPGGSGGGGARGAEE
FLTATGVQETFVPCCWKAAQIKEHLLKSKWCRPTSLNVVRIITS ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVAVDSTTMRVL HFQKTQGLRRFAFPLSLFQGSSDCVEVRYDLLDCHISICSPQVA QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGS ILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMMMEEEEELQQNLWGLKI NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHFALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEAEEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISTTEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFPSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR		}		EPPPPLQAVLVADSFDRRFFPISKDOPRVII.PIANVAI.TDVTIE
ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA OLFTDNFDYQTRDDFVRGLLVNEE!LGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGS!LEENVLLGSGTVIGSNCFITMSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMMMEERELQQNLWGLKI NMEEESESESESESGMDSEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEAEEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFPFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	1		i	FLTATGVQETFVFCCWKAAOIKEHLLKSKWCRPTSINAAPITTS
LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA QLFTDNFDYQTRDDFVRGLLVNEE!LGNQIHMYTAKEYGARVS NLHMYSAVCADVIRRWYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGS!LEENVLLGSGTVIGSNCF!TNSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEBELQQNLWGLK! NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLBINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED PFLEHEALGISMAKVLMAFYQLETLAEBTILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEAEEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFPFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	[Ì		ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEFHD
HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHHHVTAKEYGARVS NLHMYSAVCADVIRRWYYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEELQQNLWGLKI NMEEESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED PFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEAEEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFPFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	1 1			LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNPVI.
OLFTONFYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG PEVSLGHGSILEENVLLGSGTVIGSGCHSTHSVIGPGCHIEPGD NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEELQQNLWGLKI NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCONLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEFTILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEAEEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFPFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	1	1		HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDI.LDCHISTCSDOVA
PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD NVVLDQTYLWQGVVVAAGAQIHQSLLCDNAEVKERVTLKPRSVL TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMMMEEEELQQNLWGLKI NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWIKEAEEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGNLLFLIGLSLIIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMLFTUGFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	1	1	ļ	QLFTDNFDYQTRDDFVRGLLVNEEILGNOIHMHVTAKEVGABVC
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TSQVVVGPNITLPEGSVISLHPPDAEDEDDGGFSDDGADQEK DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI NMEEESESESEQSMDSEEPDSRGGSPQMDDIKVFQNEVLGTLQR GKEENISCDNLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEAEEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFILFGTLLYFDSVLLAFGRLLFLTGLSLIIGLRKTFWFPFQR HKLKGTSFLLGGVVIVLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	; [1		PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEDGD
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MDSPLDSSRYCALLPLIKAWSPVFRNYIKRAADHLEALAAIED PFLEHEALGISMAKVLMAFYQLEIIAEBTILSWFSQRDTTDKGQ QLRKNQQLQRFIQWLKEAEEESSEDD 6185 791 44 PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG IFFLLYFDSVLLAFGNLLPLIGLSLIIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWEEK	1		ľ	GAEENISCONLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ
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IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV+KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWBEK			44	PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG
HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWBEK	[[IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFRFOR
GFLGNVCN1PFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWBEK			I	HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFDVAF
REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR GCQEAEMQTPRRLGWGWYHTLTLYLWBEK		}	1	GFLGNVCNIPFLGALFRRLOGTSSMV*KTEMSSLNLDHWLKCAK
GCQEAEMQTPRRLGWGWYHTLTLYLWEEK				REEWEPPPQSPALTHSPTYPGPPOVOKERNGAEOLTSNPOVDSP
VYGIDSSNTNTHGAEERNRKLKKHWKLCHAOSRIDVNCI AL MA	6186	569		GCQEAEMQTPRRLGWGWYHTLTLYLWEEK
THE PROPERTY OF THE PROPERTY O			238	VYGIDSSNTNTHGAEERNRKLKKHWKLCHAQSRLDVNGLALKMA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			KERKVKNKVKNKADTEEVFNNSPTNQEKMPTSAILPDFSGSVIS
1			NIRNQMETLHSQPHQEENLCFENSFSLINLLPINAVE?TSSQQI
ļ			PNRETSEANKERRKMTSKSSESNIYSPLTSFITADSELHDIIKD
			LEDCLMVGLHTCGDLAPNTLRIFTSNSEIKGVCSVGCCYHLLSE
1			EFENQHKERTQEKWGFPMCHYLKEERWCCGRNARMSACLALERV
			AAGQGLPTESLFYRAVLQDIIKDCYGITKCDRHVGKIYSKCSSF
			LDYVRRSLKKLGLDESKLPEKIIMNYYEKYKPRMNELEAFNMLK
1	Í		VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLFDPVKSPRCYA
	•		VIALKKQQ*FPLKQIIRCISL*DSAGCAEEVSVGDGGPALRDAP
	1	<u> </u>	PSGSRVGSRYD
6187	1701	771	DAWGPETRLARILNPDSFIEPRPGRLPELEATRPHMEPKASCPA
ł	1		AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDIPGLEVAVVTT
1			ERAKHFYSPQDIPVTLYSDADEWEMWKSRSDPVLHIDLRRWADL LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSKPLLFCPAMNT
Ì	•	İ	AMWEHPITAOOVDOLKAFGYVEIPCVAKKLVCGDEGLGAMAEVG
1			TIVDKVKEVLFQHSGFQQS*PGISVMGVPLYSEWVQAKSVKMDV
į		ì	GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPGLSFFQPGEAA
1			A
6188	238	1534	KGFVNAGPLMAELOVSPOWKAPEMSQICLSCGHPSA*GPRWASW
]		1	NIGVFICIRCAGIHRNLGVHISRVKSVNLDOWTOEOIOCMOEMG
1]	j	NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYEKKKYMDRSLD
			INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVKMPQKKEDPQLP
1	İ		RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTLEKDLDLLASV
}	}	l	PSPSSSGSRKVVGSMPTAGSAGSVPENLNLFPEPGSKSEEIGKK
1			QLSKDSILSLYGSQTPQMPTQAMFMAPAQMAYPTAYPSFPGVTP
1	i		PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGYMGGMQASMMG
]			VPNGMMTTQQAGYMAGMAAMPQTVYGVQPAQQLQWNLTQMTQQM
L			AGMNFYGANGMMNYGQSMSGGNBQAANQTLSPQMWK
6189	1297	793	LGEPLGDLCELIPGDVQQLQMGEVHPGTGAQGSAAQSVAGEVQL
l	1		TQLSHARQRPSCQGSQLIALDLQHMDISRQPRWQHVQPVARQVQ
			RAQQAQLAEGVAVHLWAGDAVVAEVELLQEVGGGKVFAANACDL
1	1		VVQDHEGAHAARQATGHALQRVIVQVRRVQPLEAL*RVPSGLPR
ļ		,	RVRAFMILHNQITGIGREDFATTYFLEELNLSYNRITSPQVHRD
1			AFRKLRLLRSLDLSGNRLHMLPPGLPRNVHVLKVKRNELAALAR GALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQ
1		ļ	LTEIPEGLPESLEYLYLQNNKISAVPANAFDSTPNLKGIFLRFN
]		KLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKE
1			EEEEDEVEEEETR
6190	66	1309	ILVGNVSFLLSFAEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQ
			GLHCETCKEGFYLNYTSGLCQPCDCSPHGALSIPCNSSGKCQCK
			VGVIGSICDRCQDGYYGFSKNGCLPCQCNNRSASCDALTGACLN
			CQENSKGNHCEECKEGFYQSPDATKECLRCPCSAVTSTGSCSIK
1			SSELEPECDQCKDGYIGPNCNKCENGYYNFDSICRKCQCHGHVY
	1	}	PVKTPKICKPESGECINCLHNTTGFWCENCL*GYVHDLEGNCIK
]		KVILPTPEGSTILVSNASLTTSVPTPVINSTFTPTTLQTIFSVS
			TSENSTSALADVSWTQFNIIILTVIIIVVVLLMGFVGAVYMYRE
1			YQNRKLNAPFWTIELKEDNISFSSYHDSIPNADVSGLLEDDGNE
			VAPNGQLTLTTPIHNYKA
6191	1212	1511	VNLCHGGLLHLSTHHLGIKPSMH*LFFLMLSFPHLTPQQPKCPS
1	}		MIDWIKKIWYIYTMEYYATIKRNEIMFFAGTWMEMEAIILSKLM
			QDYMFSLISGS
6192	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
1			KGGLVSDAYGEDDFSRLGGDEDGYEBEEDENSRQSEDDDSETEK
i			PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
1			RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI
L			QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
		 	AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
		ł	DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
1		ĺ	IVKKAKO
6193	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
1			KGGLVSDAYGEDDFSRLGGDEDGYEZEEDENSRQSEDDDSETEK
			PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
1	<u> </u>		RCSNHLQDKIQKLYBRKIKEGMDMNYIIQRKKEFRNPSIYEKLI
ŀ			QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK
1			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
1	1		DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
			IVKKAKQ
6194	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
1	1		KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK
ł			PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
1			RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI
	}		QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK
			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
1	(DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
6195			IVKKAKQ
0195	736	235	VANGLQSNMPKFYCDYCDTYLTHDSPSVRKTHCSGRKHKENVKD
1			YYQKWMEEQAQSLIDKTTAAFQQGKIPPTPFSAPPPAGAMIPPP
1]		PSLPGPPRPGMMPAPHMGGPPMMPMMGPPPPGMMPVGPAPGMRP
6196	1512	633	PMGGHMPMMPGPPMMRPPARPMMVPTRPGMTRPDR
0230	1312	623	KTGKRRSAAYVRNILDNAEQVISNLEARNLGPRLTPLLQEEDSH
			QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC
			HIVETNWRKENLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL
1	}		FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR
			NHVTRLLQNYKKQPRNSMINKSSFSVEFLPLNYFIEILTDIESS
1			NQALYPFEGHDNVDAEFVEEAALKHTAMLLGL
6197	3	819	ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG
			PIVDVYIPLDFYTRPRGFAYVQFEDVRDAEDALYNLNRKWVCG
1			RQIEIQFAQGDRKTPGQMKSKERHPCSPSDHRRSRSPSQRRTRS
1			RSSSWGRNRRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ
1			SRTPRRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS
			RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS
			YRHKNSW
6198	111	1912	SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE
			RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ
1			REMPPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASOFL
[]			LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW
[]	Į.		GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV
]]	ļ į		SRQPSFTYSEWMEEKIEDDFLDLDPVPETPVFDCVMDIKPEADP
			TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES
j i	ļ		AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY
	ļ		DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG
]]	}		YGGEEKVYIATQGPIVSTVADFWRMVWQEHTPIIVMITNIEEMN
!!	Ī		EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER
Į [1		GLKHYWFTSWPDQKTPDRAPPLLHLVREVEEAAQQEGPHCAPII
] [i	VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG
6199			MIQHCEQYQFVHHVMSLYEKQLSHQSPE
0199	144	1211	MARENGESSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA
ļ l			TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY
1 /	i		ESPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV
, .			
j i	ŀ	1	YYLHRMGIVHRDLKPENLLYYSQDEESKIMISDFGLSKMEGKGD VMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPP

Predicted Predicted end				
No: location corresponding to first amino acid residue of stidien, Isloelucine, K-Lyssine, L-leucine, M-Methionine, M-Asparagine, mino acid residue of amino acid sequence sequence sequence sequence Sectine, T-Threonine, V-Valine, Section, V-Valine, Section, V-Valin	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding to first smin acid mainto acid maint	ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, E-
to first amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid sequence Poproline, Qedittamine, R-Arginine, S-Serine, T-Threonine, V-Valine, S-Serine, T-Threonine, N-Serine, V-Valine, V-Valine, S-Serine, T-Threonine, S-Serine, V-Valine, V-Valine, V-Valine, V-Valine, S-Serine, T-Threonine, S-Serine, V-Val	NO:	nucleotide	location	
to first amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid sequence Poproline, Qedittamine, R-Arginine, S-Serine, T-Threonine, V-Valine, S-Serine, T-Threonine, N-Serine, V-Valine, V-Valine, S-Serine, T-Threonine, S-Serine, V-Valine, V-Valine, V-Valine, V-Valine, S-Serine, T-Threonine, S-Serine, V-Val		location	corresponding	H=Histidine, I≈Isoleucine, K=Lysine,
to first amino acid residue of amino acid residue of amino acid sequence Secrime, Tothreomine, V-Valine, Mattyptophan, Y-Tyrosine, X-Unknown, **.Stop Codon, /-possible nucleotide deletion, Appossible nucleotide insertion Sequence		j -		
amino acid residue of amino acid sequence shado of anino acid sequence sequence sequence control of anino acid sequence sequence control of anino acid sequence control of anino acid sequence control of anino acid sequence control of anino acid sequence control of anino acid sequence control of anino acid sequence control of anino acid sequence control of anino acid sequence control of anino acid sequence control of anino acid sequence control of anino acid sequence control of anino acid sequence control of anino acid sequence control of anino acid sequence control of anino acid sequence control of anino acid sequence control of anino acid sequence control of anino acid sequence control of acid sequence control of anino acid sequence control of acid sequence contr				
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anino acid sequence Codom, /-possible nucleotide insertion			1	
Sequence _possible nucleotide insertion		residue of	amino acid	
FYDENDSKLPEGILKAEVYERDS FYWDDI SDGAKDFIRNIMSKOD NKRYTCKQAARHPHIAGDTAMKHIEWSKAFKAKSKOR AFNATAVYERMRKIHLGSSLDSSNASVSSSISLASQKDCASGTP HAL* 6200 702 96 LDEVPHSLRERWKPHLCCAQDAVRWARLPKLAVFLDYTLMPF WOUTTUPP PHIS SDGTWLDREGQOVELYPSYEVPVLKKLQSLGV QCKCOLPPSONT FPDERRRIVUSKLGVCLTYMPF HAL* 6201 2809 2383 GGTPRVRWERSLEBSDFRA GGTPRVRWERSLEBSDFRA GGPPQTRILIKEPTSNOVVSSPSTSTRTLPVKSLAOREAYRAR RKRILGSASPEERGER FILDRETT LOVKSLAOREAYRAR RKRILGSASPEERGER FILDRETT LOVKSLAOREAYRAR RKRILGSASPEERGER FILDRETT LOVKSLAOREAYRAR RKRILGSASPEERGER FILDRETT LOVKSLAOREAYRAR RKRILGSASPEERGER FILDRETT LOVKSLAOREAYRAR RKRILGSASPEERGER FILDRETT LOVKSLAOREAYRAR RKRILGSASPEERGER FILDRETT LOVKSLAOREAYRAR RKRILGSASPEERGER FILDRETT LOVKSLAOREAYRAR RKRILGSASPEERGER FILDRETT LOVKSLAOREAYRAR RKRILGSASPEERGER FILDRETT LOVKSLAOREAYRAR RKRILGSASPEERGER FILDRETT LOVKSLAOREAYRAR RKRILGSASPEERGER FILDRETT LOVKSLAOREAYRAR RKRILGSASPEERGER FILDRETT LOVKSLAOREAYRAR RKRILGSASPEERGER FILDRETT LOVKSLAOREAYRAR RKRILGSASPEERGER FILDRETT LOVKSLAOREAYRAR RKRILGSASPEERGER FILDRETT LOVKSLAOREAYRAR RKRILKKYLKKYLKKYLKKINAERDELROWLASSOKETYSLAVRYSE BEGSASPANEDD LOVKSLAOREAR RKRICKARARA FILDRETT LOVKSLAOREAR RESCHMERERGER RKRIVTUELEL LOVKSLAOREAR RESCHMERERGER RKRIVTUELEL LOVKSLAOREAR RESCHMERERGER RKRIVTUELEL LOVKSLAOREAR RESCHMERGERGER RKRIVTUEL LOVKSLAOREAR RESCHMERGERGER RKRIVTUEL LOVKSLAOREAR RESCHMERGERGER RKRIVTUEL LOVKSLAOREAR RESCHMERGERGER RESCHMENT LOVKSLAOREAR RESCHMENT LOV		amino acid	sequence	Codon, /=possible nucleotide deletion,
FYDENDSKJEFGILKARYFIDSPYMDIJ SDSAKDFIRNLEKKOP NKRYTCKQARAFIPNIADTALIKKYHIESVSAKJAKGKUKASGTP HAL!* 6200 702 96 LPEVEHSLRPRVKPHLCCAQPAVRVARALPKLAVFLIDTTIMFF WIDTIVIDPPHIKSSDGTVARROGQURLIPFSVEPVLKKILGSLGY PGAASSTSEISGANQLLEIFDJERVFVURSITYESKITHERIL QOKTGIPFSOM FFDERRINIVDVSKLGYCHINGKINLQTLSY OGGETFAKAGTEPLESSLERSPFRA 6201 2803 2383 GOTPEVRSKRINSSLERSPFRA GPPOINTLIKEPTSINGVVSSINSTSRPTLPVKSLAGREAFYRA RKRILGSASPEERGEKRIJLDRFTRISQPEDSKOPNVIROPLGF GPPOINTLIKEPTSINGVVSSINSTSRPTLPVKSLAGREAFYRA RKRILGSASPEERGEKRIJLDRFTRISQPEDSKOPNVIROPLGF DSGSCFRORR 6202 2 426 INADARAVASSLLSSPTRKANDOKORKPKRSTNEFHLDLTHPVS DGIFDSGRFEOFLREKVKVARGKTONLENVVHIRFFKNKITVVSE KQFSKTILKYLIKKYLKKNINLENVALOSKETYSHTYOISQ DSGSCFRORR 6203 419 2550 RCFRFFATRANARSFDDESPEGISGEBAAGAGAAAAFSOHPA LNODCLDAVSKYGEVTINNLEFAKELQRSFMALSQDIQYTIKKTAL RKREJLKKYLKVINNLEPKRKUKUDSVCHTEKTYOISQ DLDSSESSI DLDSSESSI RCFRFFATRANARSFDDESPEGISGEBAAGAGAAAAFSOHPA LNODCLDAVSKYGEVTINNLEFAKELQRSFMALSQDIQYTIKKTAL RREQLMERERABGKRIKTVLELIDVROSKTETHIRGOLLGESDAA SAPAVEDOVPRABEDEPARETTSQSEVESTEIVVRRSLAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		semence	1 -	\=possible nucleotide insertion)
NRRYTCEQAARHPUTAADTALMKRIHESVSAQIRKNFAKSKWRQ APMATAVVRIMEKILLGSSLDSSMASVSSSLSKORCASGFF HAL* 1000 100 100 100 100 100 100			 	EVDENDSKI.FEOII.KAEVEEDSPYWDDISDSAKDFIRNLMEKDP
APMATAVYRHMEKIHLESSIDSSNASVSSISJASQKDCASGTF HALL* 6200 702 96 LPEVENBLERREKVENHLCCAQPAVRWARLPKLAVFDLDYTLMFF WUDTIVDPPPHKSBOTVKDRRGQDVRLYPEVEVLKKLGSLGV PGAAASTSETEGANQLLELFDJERRYVURSLTYGSKTHFERL QOKTG1PFSORT FFDERRINI VUDVSKLGVCHOKGNILQTLS GUGETFAKAOTTPJERSSLEBSPFRA 6201 2803 2383 GOTPEVBREKRESSILESSIDESSPFRA RKRICASASPESEQEKPILDRFTRISQEBSKOPHVIVQDDSLPA GPPDIRILKEDTSNGVVSSBNSTSRTLPVKSLAQREAEVARA RKRICASASPESEQEKPILDRFTRISQEBSKOPHVIVQDSLPA GPPDIRILKEDTSNGVVSSBNSTSRTLPVKSLAQREAEVARA RKRICASASPESEQEKPILDRFTRISQEBSKOPHVIVQDBLPA GEOGRAPOR 6202 419 1016 DEBESSED ADDESSESD RCPREPATRANASFIDESPFSGTGGEALAGAGAAAPASOHTV TOTAVOTRAMKQTICKTURVASDKETTSHFVKITVVSE KQFSKTILKYLIKKYLKKNILRDWLAVSDKETTSHFVKITVVSE KQFSKTILKYLIKKYLKKNILRDWLAVSDKETTSHFVKITVVSE KQFSKTILKYLIKKYLKKNILRDWLAVSDKETTSHFVKITVVSE KQFSKTILKYLIKKYLKKNILRDWLAVSDKETTSHFVKITVVSE KQFSKTILKYLIKKYLKKNILRDWLAVSDKETTSHFVKITVVSE KQFSKTILKYLIKKYLKKNILRDWLAVSDKETTSHFVKITVVSE KQFSKTILKYLIKKYLKKNILRDWLAVSDKETTSHFVKITVVSE KQFSKTILKYLIKKYLKKNILRDWLAVSDKETTSHFVKITVVSE KQFSKTILKYLIKKYLKKNILRDWLAVSDKETTSHFVKITVVSE KQFSKTILKYLIKKYLKKNILRDWLAVSDKETTSHFVKITVSE KQFSKTILKYLIKKYLKKNILRDWLAVSDKETTSHFVKITVSE KQFSKTILKYLIKKYLKKOLIKURVANSDKETTSHFVKITVSE KQFSKTILKYLIKKYLIKKYLIKURASSHTOLASSHTVANSHKALE KQFSKTILKYLIKKYLIKKYLIKURASSHTOLASSHTVANSHKALE KQFSKTILKYLIKKYLIKKYLIKURASSHTOLASSHTVANSHKALE KQFSKTILKYLIKKYLIKURUR KURSIKYLOHATINASSHTAL KREQHMERSHKARASHTOLASSHTOL	ļ			
HAL* 6200 702 96	Ì	1	1	
Formation	.	ļ	}	
### WUDTHYDPPHHISSIGTYRDRRGQURLYPEWPEVLKRLGSLGV PGGASARTSIERANGLLEIPDLFRYTYMFYGSKITHFERL QKKTGIPSOMT PFDDERRNIUDUSKLGVTCHILIONGMNLQTLS OGLETPAKAGATOPLRSSLESBPPEA 6201 2809 2383 GCTPRVRWKMRSLRAGKRRQTAGRKSKSPPKVDIVIQDDSLPA GPPQIRILKRPTSNGVVSSPNSTSRPTLPVKSLAQREAEYABA RKRILGSASPBEEGGKPLIDRPTRISQEDSRQPMNVIRQPLOP DGSQGFKQRR RKRILGSASPBEEGGKPLIDRPTRISQEDSRQPMNVIRQPLOP DGSQGFKQRR 6202 426 INADRAWASSLLSRPTRKWAPQKDRKPKKSTWRFNLDLTHPVE DGIFDSGMFPGFLREKVKVNGKTGMLGNVVHIRPFKNLTVVSE KOFSKRYLKVLTKKILKKNILRDWLRUVASKETYNLTVVLSE KOFSKRYLKVLTKKILKKNILRDWLRUVASKETYNLTVLYSE KOFSKRYLKVLTKKILKKNILRDWLRUVASKETYNLTVLYSE KOFSKRYLKVLTKIKKILKKNILRDWLRUVASKETYNLTVLYSE KOFSKRYLKVLTKIKKILKKNILRDWLRUVASKETYNLTVLYSE KOFSKRYLKVLTKIKKILKTNILRDWLRUVASKETYNLTVLYSE KOFSKRYLKVLTKIKKILKTHILARNILRDWLRUVASKETYNLTVLYSE LANDOLDAVSKOPTYNILLFARELLGRSPMALSQDIQNTIKKTA RREQLMREABOKRLTATULEQVILDKLGDBOWETDLKGGLNGV PILSEELISLLDBFYKLVDPERDMSLRLINGVSPMASHILDLGL GKKEVCOTTYKVLKEI UPEN PGSWYFDSTHNHONGLCEESEAA SAPAVEDQVPERAPEBASETTEGSEVESTETVURGGMATQGLAV PILSEELISLLDBFYKLVDPERDMSLRLINGVSPMASTHLNDLL GRKEVCOTTYKVLKEI UPEN PGSWYFDSTHNHONGLCEESEAA SAPAVEDQVPERAPEBASETTEGSEVESTETVURGGMATQCHASSTS EGYTASQPLYOPSHATEGOROPOKEP IDQIQATISLNTDLTASSS LPAASGQVTQATSKRULFASGINVANAPOSMOTYFKMNAPV PVNEPPTLKQQNQYQASYNOSFSSQPHQVGPATVPLVSSTS EGYTASQPLYOPSHATEGOROPOKEP IDQIQATISLNTDTTASSS LPAASGQVQTQATSKRUGSGLAQPAGGRGPAGRGGOLQCUTVV TYHGSPDGSKQNTGNNGQPAGNTGPRANGYTYFKMNAPV PVNEPPTLKQGNYGSGSGRGAPAGRGGPAGRGGOPPAPRGMPQM NTQOWN 6204 2933 787 CTHNLISLLGGRALIHFREFLILKIOGGGBINITFCDAYDCFOLV TYRIGSSPTGSSTTLSFPLLRAPAVDCOKGRILEVSEVGHEY XRCTYFEVGLOWSEQSKEMTVEAKKHKFGELDDRMYTYTFK NHEHSYGLEGGRUNDSCHAFTSPENDENTVEAKKHKREGUPPHTIEDAY HVLLKTRRILKGSYYPGFPLPBKTKKEIFFELMGTTDLENVTTDL AQKVNRPVLRTPRHKIIKAACLVQGRQBFLASVASAMSVLHSS SLEDYTPASSRRODSLGAARSLDEEDDRIFTEBDAY HVLLKTRRILKGSYYPGFPLBPKSTKKEIFFELMGTTDLEDWTTDL AQKVNRPVLRTPRHKIIKAACLVQGRQBFLASVASAMSVLHSS SLEDYTPASSRRODSLGAALSSLDEEDDRIFTEBDAY HVLLKTRRILKGSYPGFPLBPKSTKEIFFELMGTDLEBWTEDL LEBRISDSMRVANASSSRRODSTVANPSDFPLQLPRVLEGG LLEBLGSIMHLANGVANDASSBPDDBSGATARACSSPTDLS			1	
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TGTGAVQTEAMKQILGVIDKKLRNLEKKKSKLDDYQERNNKGER LNQDQLDAVSKYQEVTNNLEFAKLDRSYMALSQDIQKTIKKTA RREQLMREBEGKRIKTVLELQYLDKLGDDEVRTDLKQGLNGV PILSEELSLLDEFYKLVDPERDMSLRIMBQVEHASIHLWDLLE GKSKPVCGTTYKVLKEIVERVGSNYFDSTHNDQNGLCESEBAA SAPAVEDQVERAPPBBAEEYTEQSEVESTEYVURQRMAETOFTS GEKCQVDEWTVETVUSVUNSLQQQPQAASPSVPEPHSLTPVAQAD PLVERQRVQDLMAQMGGPVMFIQDSHLDERNQTLDPAIVSAQPM NPTQNNDMPQLVCPPVHSESRLAQPNQVPVQPBATQVPLVSSTS EGYTASQPLVQPBATQERQPRQPVPQVDTAISLNTQOTTASSS LPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMOTVFNMNAPVP PVMEPETLKQQNQYQASYNOSFSSQPHQVEVTBLQQBQLQTVVG GVAGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGTTQSQFSAP RDYSGYQRDGYQQNFKRGSQQSGPRGAPRGRGGPPRPNRGMPQM NTQQVN 6204 2933 787 CTHNLISLLGRALIHFNRFLNKIQEGEANNIFCPAYDCFQLV PGDILKSVVSKEMDKRYLQFDIKAFVENNPAIKWCPTPGCDRAV RLTKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFVBECLGEAHEP CDCQTMKNNLQKITEMKPBELVGVSKAYEDAANCLLINNSKC CCQTMKNNLQKITEMKPBELVGVSKAYEDAANCLLINNSKY NEHSYQLEQRLLKTAKKEMEQLSRALKETEGGCPDTFTEDAV HVLLKTRRILKCSYPYGPFLEPKSTKKEIFELMQTDLENVTEDL AQKYNRPYLAFTRHKI IKAACLVQQKRGFLASVARGVAPADSP PARRSFAGGTMDWEYLGFASPBEXAFFOYRRRGDVBS LLSNPPDPDEPSESTLDIPEGGSSSRPPGTSVVSSASMSVLHSS SLRDYTPASRSKNQDSLQALSSLDEDDPNILLAIQLSLQESGLA LDEETRIFLSNRASLGAGITSPERLDSRVFRTDSFRAALSSSE LLEIGDSLMRLGAENDPFSTDTLSSFFLSRANGVSPABLSS SLRDYTPASRSKNQDSLQALSSLDEDDPNILLAIQLSLQESGLA LDEETRIFLSNRASLGAGITSPERLDSRVFNTDSFRAALSSSE LLEIGDSLMRLGAENDPFSTDTLSSFFLSRATSFCPSSDPDS AGQDPNINDNLLGNIMAMFHDMNPQSIALIPATTEISADSQLP CIKNGSEGVKDVELVLPEDSMFDDASVSGRGTQIEENPLERNIPGGGKGHPQAW PGGKKGHPQAW RAHRGKMALEVGDMEDGQLSDSDDMTVAPSDRPLQLPKVLGGD SAMRAFQNYATACAPVSHYRAVESVDSSEESFSDDDDSCLWKR KRQKCRNPPPKPRPFPFOFGQSSQKPTVAJGKKINNIKGAVLQEQN DAAVTELGILGHGETJDRSRGSSTYNYLLAKKINIKESGEHTKO DAAVATELGILGHGETJDRSRGSSTYNYLLAKKINIKESGEHTKO	6303	419	2550	PCPRPPATAGAAASRPDRSPPSGISGSEAAAGAGAAAPASOHPA
LINGDGLDAVSKYGEVTNNLEFAKELQRSFMALSGDIGKTIKKTA RREQLMREBAGVRIKTVLEIQVIJDKUGDDEVRTDLKGGLNGV PILSEELSLIDEFYKLVDEFROMSLEINBGYBAS IHLWOLLE GKEKPVCGTTYKVLKEIVDEFROMSLEINBGYBAS IHLWOLLE GKEKPVCGTTYKVLKEIVDERFOMSLEINBGYBAS IHLWOLLE GKEKPVCGTTYKVLKEIVDERFOMSLEINBGYBAS IHLWOLLE GKEKPVCGTTYKVLKEIVDERFOMSLEINBGYBAS IHLWOLLE GKEKPVCGTTYKVLKEIVDERFOMSLEINBGYBAS IHLWOLLE GEKEQVDEWTVETVEVVNSLQQDPQBASPSVPEPHSLTPVAQAD PLYRRGRVQDLMAQMGCPYNFIQDSMLDFERGTLDPAIVSAGPM NPTCONDMDMGLVCPPVHSESRIAQPNQVPVQPEATQVPLVSSTS EGYTASQPLYOPSHATEGRPOKEPIDQIQATISINTDQTTASSS LPAASQPQVFQAGTSKPLHSSGINVNAAPFGSMOTVFNNNAPVP PVMEPETLKQQNQYQASYNOSFSSQPHQVEGTELQQEQLQTVVG TYHGSPDGSHQVTGNHQQPPQONTOPPRSNQPYYNSRGYSRGGS RGARGLMNGYRGPANGFRGGYDGYPRSNGPYYNSRGYSRGGS RGARGLMNGYRGPANGFRGGYDGYPRSNDPYYNSRGYSRGGS RGARGLMNGYRGPANGFRGGYDGYPRSNDPYYNSRGYSRGGS RGARGLMNGYRGPANGFRGGYDGYPRSNDPYYNSRGYSRGGS RGARGLMNGYRGPANGFRGGYDGYPRSNDPYNSGGYSQGFRA RDYSGYQRDGYQQNFKRGSGGSGRGAPRGRGGPPRPNRGMPQM NTQQVN CTHNLISLLGGRALIHFNRFLNLKIQEGBAHNIFCPAYDCFQLV PGDIIKSVVSKEMDKRYLQFDIKAFVENNPAIKWCPTPGCDRAV RITKQGSNTSGSDTLSFPLLRAPADVCGKGHLFCWECLGEAHEP CCQTWKNMLKITEMKPBELLWGVSEAY BDAANCLINLINSKPC ANCKSPIQKNEGCNHMQCAKCKYDFCWICLEEMKHSFYHWEVI YRCTRYSVIQHVEEQSKEMTVEAEKKHKRFQELDRFMHYYTRFK NHEHSYQLEGGRLLKTARKEMBQLSRALKETEGGCPDTTFIEDAV HVLLKTRRILKCSYPYGFFLBKSFKKEIFELMOTDLEMVTEDL AQKVNRPYLRTFRHKIIKASLUVQGKRQEFLASVARGVAPADSP EAPRRSFAGGTMDNEYLGFASPEEYAEFQYRRHRQRRGDVHS LLSNPPDPDEBSESTLDIPEGGSSSRRFGTSVVSSASMSVLHSS SLRDYTPASRSUNDEYLGFASPEEYAEFQYRRHRQRRGDVHS LLSNPPDPDEBSESTLDIPEGGSSSRRFGTSVVSSASMSVLHSS SLRDYTPASRSUNDEYLGFASPEDEVAEFCYSSDPDS AGQDPNINDRLICNIMMANPHNPQSIALIPPATTEISADSQUP CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI PGGGKGHPQAW RAHRGKMALEGGDMEDGGLSDSDSDMTVAPSDRPLQLPKVLGGD SAMRAFQNTATACAPVSHYRAVESVDSSESFFSDDDDSCLWKR KRQKCRMPPPKPBPFQFGGGSSGKPVAGGKKINNIMGAVLQEQN ODAVATELGILGMGGTIDFRGOSFTYNYLLAKKLKESQEHTKO DAVATELGILGMGGTIDFRGOSFTYNYLLAKKLKESGEHTKO	6203	419	2330	MCMCANOMERANOTI CALDAAT BALERKKOKI DDAOEBWAKCEB
REQLAREBAEOKRILKTVLELOYVLJAKLGDDEVRTDLKGGLNGV PILSEELSLLDEFYKLVDPERDMSLRINBQYEHASIHLWOLLE GKEKPVCGTTYKVLKEIVERVYGSNYFDSTHNHOMGLCEESEAA SAPAVEDOVPEABPEPAETTEQSEVESTEYVNRQFMAETQFTS GEKEQVDEW-VETVEVVVNSLQQQPQAASFVPEPHSLTPVAQAD PLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAQPM NPTQNMDMPQLVCPPVHSESRLAQPMQVPVPVPBATQVPLVSSTS EGYTASQPLYQPSHATEQRPQKPBIDQIQATISINTDQTTASSS LPAASQPQVPQAGTSKPLHSSGINVNAAPFGSMOTVFNNNAPVP PVNEPETLKQQNQYQASYNQSTSSQPHQVEQTELQQEQLQTVVQ GRAGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTGSQFSAP RDYSGYQRDGYQQNFKRGSGSGPRGAPRGRGPPRPNRGMPQM NTQQVN CTHNLISLLGGRALLHFNRFLNLKIQEGEANNIFCPAYDCFQLV PGDIIKSVVSKEMDKRYLJGPIKAPVENNPAIKWCFTPGCDRAV RLTKQGSNTGSGSTLSFPLLRAPAVDCGKGHLFCMECLGEAHEP CCCQTWKNWLQKITEMKPEELVGVSEAYEDAANCLWLLTNSKPC ANCKSPIQKNEGCNHMQCAKCKYDFCWICLEEWKKHSFVHWEVI YRCTRYEVIGHVEEQSKEMTVEAEKKHKRFQELDRFMHYYTRK NHEHSYQLEGALLKTAKENGLSRALKETEGGCPDTFIEDAV HVLLKTRRILKCSYPYGPFLEPKSTKKEIFELMQTDLEMVTEDL AQKVNRPYLRTPRHKIIKAACLVQQKQGFLASVARGVAPADSP EAPRRSFAGTWDMEYLISFASPEEVAEFGYRRHRORRGDVHS SLEDYTPASRSENQDSLQALSSLEEDDPNILLAIQLSLQESGLA LDEBETRDFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSE LLEIGDSLMKIGAENDPFSTDTLSSPLLSEARSDFCPSSSDPDS AGQDPNINDNLLGNIMAWFHDMNQSIALIPPATTEISADSQLP CIKDGSEGVKDVELVLPEDSMFEDASVEERGRTQIEENPLEENI PGGGKQHPQAW RAHRGKMALEVGDMEDGQLSDSDSDMTVAPSDRPLQLPKVLGGD SAWRAFQNTATACAPVSHYRAVESVDSSESSFSDSDDDSCLWKR KRQKCMPPPKPBPFQFGGSGSKPPVAGGKKINNIMGAVLQEN DAVATELGILGMGSTIDRSROSFTYNVLLAKKLKKESQEHTKO DAVATELGILGMGSTIDRSROSFTYNVLLAKKLKKESQEHTKO DAVATELGILGMGSTIDRSROSFTYNVLLAKKLKKESQEHTKO DAVATELGILGMGSTIDRSROSFTYNVLLAKKLKESGENTKO	į.	1	Ī	
PILSEELSLLDEFYKLVDPERDMSLRLNBQYBHASTHLWDLLE GKEKPVCGTTYKVLKEIVEVPQSNYFDSTHNHQNGLCEEBAA SAPAVEDQVPEAPEPPAEYTEQSEVESTEYVRRQFMAETQFTS GEKEQVDEWTVETUEVVNSLQQQPQAASPSVPBHSLTPVAQAD PLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAQPD NPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPEATQVPLVSSTS EGYTASQPLYQPSHATEQRPQKEPIDQIQATISLNTQQTTASSS LPAASQPVYQAGTSKPLNSGINVNAAPFGSMGTVFKMNAPVP PVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVG TYHGSPDGSHQVTGNHQQPPQQNTGPFRSNQPYNNSGVSRGGS RGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQSQFSAP RDYSGYQRDGYQQNFKRGSGQSGPRGAPRGRGPPRPNRGMPQM NTQQVN 6204 2933 787 CTHNLISLLGGRALIHFNRFLNLKIQEGEAHNIFCPAYDCFQLV PGDIIKSVVSKEMDKRYLQFDIKAFVENNPAIKMCPTPSCDRAV RITKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFCWECLGEAHEP CCCQTWKNWLQKITEMKPEELVGVSRAYEDAANCLMLLTINSKPC ANCKSPIQKNEGCHMQCAKCKXDFCUICLEEMKKHSFVHWEVI YRCTRYEVIQHVEEQSKEMTVEAEKKHKFQELDRFMHYYTRPK NHEHSYQLEQRLLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV HVLLKTRRILKCSYPYGFFLEPKSTKKEIFEIMGTDLEMVTEDL AQKVNRPYLRTPRHKIIKAACLVQQKRQEFLASVARGVAPADSP EAPRRSFAGGTWDMEYLGFASPEEYAAFQYRRRGRRGDVHS LLSNPPDPDEPSESTLDIPEGGSSSRRPGTSVVSSASMSVLHSS SLRDYTPASRSENQDSLQALSSLDEDDDNILLAIQLSLQESGIA LDEETRDFLSNEASLGAIGTSLSPRLDSVPRNTDSPRAALSSE LLELGDSLMRIGAENDPFSTDTLSSFLLSERSDFCPSSDPDS AGQDPNINDNLLGRIMAMFHDNNPQSIALIPPATTEISADSQLP CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI PGGGKQRPQAM 6205 1 1200 RAHRGKWALEWGDMEDGQLSDSDDMTVAPSDRFLQLPKVLGGD SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDDDDSCLWKR KRQKCFMPPPRKPBPPQFGGSSORPVAGGKKINNIWGAVLQEON DAVATELGLILGMEGTIDRSROSETYNYLLAKKLRKESQEHTKD		1	i	
GKEKPVGGTTYKULKEIVERVEGSNYFDSTHNHQNGLCESEAR SAPAVEDQVPEAEPPAEEYTEQSEVESTEYVNRQFMAETQFTS GEREQUDEW~VETVEVVVSLQQQPQAASPSVPEPHSLTPVAQAD PLVRRQRVQDLMAGMQGPYNFIQDSMLDFENQTLDPAIVSAQPM NPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPEATQVFLVSSTS EGYTASQPLYQPSHATEQRPQKEPIDQIQATISLNTDQTTASSS LPAASQPQVFQAGTSKPLHRSGINVNAAPFGSMOTVFKMNAPVP PVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVG TYHGSPDQSHQVTQAGTSKPLHRSGINVNAAPFGSMOTVFKMNAPVP PVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVG TYHGSPDQSHQVTQAGTSKPLHRSGINVNAAPFGSMOTVFKMNAPVP PVNEPETLKQQNQYQASYNQSFSSQPHQRGRGPPRPNRGMPQM NTQQVN NTQQVN NTQQVN OTTHLISLLGGRALIHFNRFLNLKIQEGEAHNIFCPAYDCFQLV PGDIIKSVVSKEMDKRYLQFDIKAFVENNPAIKMCPTPGCDRAV RITKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFCMECLGEAHEP CDCQTMKNWLQKITEMKPBELVGVSEAYEDAANCLWLLITNSKPC ANCKSPIQKNEGCHMMQCAKCKYDFCWICLEEWKKHSFVHWEVI YRCTRYEVIQHVEEGSKEMTVEAEKKHKRFQELDRFMHYYTFFK NHEHSYQLEQRLLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV HVLLKTRRILKCSYPYGPFLEPKSTKKEIFELMQTDLEMVTEDL AQKVNRPYLRTPRIKIIKAACLVQQKRQEFLASVARGVAPADSP EAPRRSFAGGTWMEYLGFASPESYABFGYSRRHRQRRRGDVHS SLRDYTFASRSENQDSLQALSSLDEDDPNILLAIQLSLQESGLA LDEETRIPLSMEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE LLELGDSLMRIGAENDPFSTDTLSSHPLSEARSDFCPSSSDPDS AGQDPNINDLLGNIMAWHDMPQSIALIPPATTEISADSQLP CIKDGSEGVKOVELVLPEDSMFEDASVSEGRGTQIEENPLEENI PGGGKQHPQAW SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDDDDSCLWKR KRQKCFMPPPRKPBPFQFGQSSQRPVARGGKKINNIMGAVLQEQN DAVATEIGLILSMEGTIDRSROSETYNYLLAKKLRKESQEHTKD	1		i	
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SAPAVEDQVPEREPEPAETTEQSEVESTEYUNQCMAETCFTS GEKEQVDEWTVETVEVVNSLQQQPQAASPSVPEPHSLTPVAQAD PJUNRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDFAIVSAQFM NPTQNMMPQLUCPPVHSESRIAQPNQVPVQPEATQVPLVSSTS EGYTASQPLYOPSHATEQRPQKEPIDQIQATISLINTDQTTASSS LPAASQPLYOPSHATEQRPQKEPIDQIQATISLINTDQTTASSS LPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMAPVP PVMEPETLKQQNQYQASYNGSFSSQPHQVEQTELQQBQLQTVVQ TYHGSPDQSHQVTGMHQQPPQQNTPGPRSNQPYYNSRGVSRGGS RGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQSQFSAP RDYSGYQRDGYQNFFRGSQQSGPRGAPRGRGGPPRPNRGMPQM NTQQVN 6204 2933 787 CTHNLISLLGGRALIHFNRFLNLKIQEGEAHNIFCPAYDCFQLV PGDIIKSVVSKEMDKRYLQFDIKAPVENNPAIKWCPTPGCDRAV RLTKQGSNTSGSDTLSPLLKAPAVDCGKGHLFVMECLGEAHEP CDCQTWKNWLQKITEMKPEELVGVSEAYEDAANCLWLLINSKPC ANCKSPIQKNBGCNHWQCAKKYDFCWICLEEWKKHSFVHWEVI YRCTYSEVIGHVEEQSKEMTVEAEKKHKRFQELDRFMHYYTFKK NHEHSYQLEQRLLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV HVLLKTRRILKCSYPYGFFLEBKSTKKEIFELMQTDLEMVTEDL AQKVNRFYLGTPRHKIIKAACLVQQKRQEFLASVARGWAPADSP EAPRRSPAGGTWDWEYLGFASPEEYAEFQYRRHRQRRRGDVHS LLSNPPDPDEESESTLDIPEGGSSSRPGTSVVSSASMSVLHSS SLRDYTPASRSRNQDSLQALSSLDEDDPNILLAIQLSLQESGLA LDEETRDFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE LLELGDSLMRLGAENDPFSTITLSSHPLSEARSDFCPSSSDPDS AGQDPNINDNLIGNINAWFHDMNPQSIALIPPATTEISADSQLP CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI PGGKQHPQAW 6205 1 1200 RAHRGKMALEVCOMEDGQLSDSDSDMTVAPSDRPLQLPKVLGGD SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR KRQKCFRIPPKREPFQFGGSKAPFVNYLLAKKLRKESQEHTKD	ŀ	1	1	GKEKPVCGTTYKVLKEIVERVFOSNYFDSTHNHQNGLCEEEEAA
GEKEQVDEWTVETURVVNSLQQCPQAASBSVPEPHSLTPVAQAD PLVRRQRVQDLMAQMQGPYNFIQDSMLDPENQTLDPAIVSAQPM NPTQNMDMPQLVCPVHSESRLAQPNQVPVQPEATQVPLVSSTS EGYTASQPLYQPSHATEQRPQKEPIDQIQATISLNTDQTTASSS LPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMAPVP PVMEPETLKQQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVG TYHGSPDQSHQVTGRHQQPPQQNTGPPRSNQPYYNSRGVSRGGS RGARGLMNGYRGPANGFRGGYDGYRPSSNPPNSGYTQSFSAP RDYSGYQRDGYQQNFKRGSGQSGPRGAPRGRGGPPRFNRGMPQM NTQQVN 6204 2933 787 CTHNLISLLGGRALTHFNRFLNLKIQEGBAHNIFCPAYDCFQLV PGBIIKSVVSKEMDKRYLQFDIKAPVENNPAIKWCPTPGCDRAV RLTKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFCWBCLGEAHEP CDCQTWKNWLQKITEMKPBELVGVSEAYEDAANCLBULTMNSKPC ANCKSPIJGKNBGCNHAQAKCKVDFCWICLEEWKKHSFVHWEVI YRCTRYEVIQHVEEQSKEMTVEAEKKHKRFQELDRFMHYYTRFK NHEHSYQLEQRILKTAKEKWRGLSRALKETEGGCPDTTFIEDAV HVLLKTRRILKGSYPGPFLEPKSFYKEFIFELMGTDLEMVTEDL AQKVNRPYLRTFRHKIIKAACLVQQKRQEFLASVARGVAPADSP EAPRRSFAGGTWDWEYLGFASPEEVAEFQYRRHRQRRRGDVHS SLENTYTPASRSENQDSLQALSSLDEDDPNILLAIQLSLQESGLA LDBETRDFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE LLEIGDSLMRLGAENDPFSTDTLSSHPLSEARSDFCPSSDPDS AGGDPNINDNLIGNIMAWFHDMNPQSIALIPPATTEISADSQLP CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI PGGGKQHPQAW RAHRGKWALEVCDMEDGQLSDSDSDMTVAPSDRPLQLPKVLGGD SAMRAPQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR KRQKCFNPPPKREPFQFGGSKSPTYNYLLAKKLKKESQEHTKD	1			CADAVEDOVDEARDEDAREVTEOSEVESTRYVNROFMAETOFTS
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PGDIIKSVVSKEMDKRYLQFDIKAFVENNPAIKWCPTPGCDRAV RLTKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFCWECLGEAHEP CDCQTWKNWLQKITEMKPEELVGVSEAYEDAANCLWLLTNSKPC ANCKSPIQKNEGCNHMQCAKCKYDFCWICLEEWKKHSFVHWEVI YRCTRYEVIQHVEEQSKEMTVEAEKKHKRFQELDRFMHYYTRFK NHEHSYQLEQRLLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV HVLLKTRRILKCSYPYGFFLEPKSTKKEIFELMQTDLEMVTEDL AQKVNRPYLRTPRHKIIKAACLVQQKRQEFLASVARGVAPADSP EAPRRSFAGGTWDWEYLGFASPEEYAEFQYRRHRQRRRGDVHS LLSNPPDPDEPSESTLDIPEGGSSSRRPGTSVVSSASMSVLHSS SLRDYTPASRSENQDSLQALSSLDEDDPNILLAIQLSLQESGLA LDEETRDFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE LLEILGDSLMRLGAENDPFSTDTLSSFPLSEARSDFCPSSSDPDS AGQDPNINDNLLGNIMAWFHDMNPQSIALIPPATTEISADSQLP CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI PGGGKQHPQAW 6205 1 1200 RAHRGKMALEVGDMEDGQLSDSDSDMTVAPSDRPLQLPKVLGGD SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR KRQKCFNPPPKPBPFQFGQSSQKPPVAGGKKINNIWGAVLQEQN ODAVATELGILGMEGTIDRSROSETYNVILLAKKLRKESQEHTKD	6204	2933	787	CTHNLISLLGGRALIHFNRFLNLKIQEGEAHNIFCPAYDCFQLV
RLTKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFCWECLGEAHEP CDCQTWKNWLQKITEMKPEELVGVSEAYEDAANCLWLLTNSKPC ANCKSPIQKNEGCNHWQCAKCKYDFCWICLEEWKKHSFVHWEVI YRCTRYEVIQHVEEQSKEMTVEAEKKHKRFQELDRFMHYYTRFK NHEHSYQLEQRLLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV HVLLKTRRILKCSYPYGPFLEPKSTKKEIFELMQTDLEMVTEDL AQKVNRPYLRTPRHKIIKAACLVQQKRQEFLASVARGVAPADSP EAPRRSFAGGTWDWEYLGFASPEEYAEFQYRRHRQRRRGDVHS LLSNPPDPDEPSESTLDIPEGGSSSRPETSVVSSASMSVLHSS SLRDYTPASRSENQDSLQALSSLDEDDPNILLAIQLSLQESGLA LDEETRDFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE LLEILGDSLMRLGAENDPFSTDTLSSFPLSEARSDFCPSSSDPDS AGQDPNINDNLLGNIMAWFHDMNPQSIALIPPATTEISADSQLP CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI PGGGKQHPQAW 6205 1 1200 RAHRGKMALEVGDMEDGQLSDSDSDMTVAPSDRPLQLPKVLGGD SAMRAPQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR KRQKCFNPPPKPBPFQFGQSSQKPPVAGGKKINNIWGAVLQEQN ODAVATELGILGMEGTIDRSROSETYNVILLAKKLRKESQEHTKD	"""		1	
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HVLLKTRRILKCSYPYGFFLEPKSTKKEIFELMQTDLEMVTEDL AQKVNRPYLRTPRHKIIKAACLVQQKRQEFLASVARGVAPADSP EAPRRS FAGGTWDWEYLGFAS PEEYAEFQYRRHRQRRGDVHS LLSNPPDPDEPSESTLDIPEGGSSSRRPGTSVVSSASMSVLHSS SLRDYTPASRSENQDSLQALSSLDEDDPNILLAIQLSLQESGLA LDEETRDFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE LLELGDSLMRLGAENDPFSTDTLSSHPLSEARSDFCPSSSDPDS AGQDPNINDNLLGNIMAWFHDMNPQSIALIPPATTEISADSQLP CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI PGGGKQHPQAW 6205 1 1200 RAHRGKMALEVGDMEDGQLSDSDSDMTVAPSDRPLQLPKVLGGD SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR KRQKCFNPPPKPBPFQGSSQKPPVAGGKKINNIWGAVLQEQN ODAVATELGILGMEGTIDRSROSETYNYLLAKKLRKESQEHTKD	I		1	NHEHSYOLEORLLKTAKEKMEOLSRALKETEGGCPDTTFIEDAV
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LLSNPPDPDEPSESTLDIPEGGSSSRRPGTSVVSSASMSVLHSS SLRDYTPASRSENQDSLQALSSLDEDDPNILLAIQLSLQESGLA LDEETRDFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE LLEIGDSLMRLGAENDPFSTDTLSSEPLSEARSDFCPSSSDPDS AGQDPNINDNLLGNIMAWFHDMNPQSIALIPPATTEISADSQLP CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI PGGGKQHPQAW 6205 1 1200 RAHRGKMALEVGDMEDGQLSDSDDMTVAPSDRPLQLPKVLGGD SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR KRQKCFNPPPKPBPFQFGQSSQKPPVAGGKKINNIWGAVLQEQN ODAVATELGILGMEGTIDRSROSETYNYLLAKKLRKESQEHTKD	1	1	1	
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PGGGKQHPQAW 6205 1 1200 RAHRGKMALEVGDMEDGQLSDSDSDMTVAPSDRPLQLPKVLGGD SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR KRQKCFNPPPKPBFFQFGQSSQKPPVAGGKKINNIWGAVLQEQN ODAVATELGILGMEGTIDRSROSETYNYLLAKKLRKESQEHTKD	1	1	1	CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEENI
6205 1 1200 RAHRGKMALEVGDMEDGQLSDSDSDMTVAPSDRPLQLPKVLGGD SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR KRQKCFNPPPKPBPFQFGQSSQKPPVAGGKKINNIWGAVLQEQN ODAVATELGILGMEGTIDRSROSETYNYLLAKKLRKESQEHTKD	1	1	1	PGGGKOHPOAW
SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR KRQKCFNPPPKPEPFQFGQSSQKPPVAGGKKINNIWGAVLQEQN ODAVATELGILGMEGTIDRSROSETYNYLLAKKLRKESQEHTKD	6305		1200	RAHRGKMALEVGDMEDGOLSDSDSDMTVAPSDRPLOLPKVLGGD
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QDAVATELGILGMEGTIDRSRQSETYNYLLAKKLRKESQEHTKD LDKELDEYMHGGKKMGSKEEBNGQGHLKRKRPVKDRLGNRPEMN	1	1	1	KKÖKCEMPBEKBRBEÖEGÖSZÖKBBAWGGKYTMUTMGWAPÖEÖM
LDKELDEYMHGGKKMGSKEEBNGQGHLKRKRPVKDRLGNRPEMN	1	1	1	QDAVATELGILGMEGTIDRSRQSETYNYLLAKKLRKESQEHTKD
	ı	1	1	LDKELDEYMHGGKKMGSKEEENGQGHLKRKRPVKDRLGNRPEMN

SEQ	Predicted	1 7 32 3	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid E_
1	location	corresponding	Glucamic Acid, F=Phenvlalanine G=Glucine
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
Į	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	Bequence	Codon, /=possible nucleotide deletion,
· · · · · · · · · · · · · · · · · · ·	-		\=pcssible nucleotide insertion)
1			YKGRYEITAEDSQEKVADEISFRLQEPKKDLIARVVRIIGNKKA
ł			IELLMETAEVEQNGGLFIMNGSRRRTPGGVFLNLLKNTPSISEE
	į		QIKDIFYIENQKEYENKKAARKRRTQVLGKKMKQAIKSLNFQED
i		•	DDTSRETFASDTNEALASLDESQEGHAEAKLEAEEAIEVDHSHD
6206	10	1442	IISERRERSCLHLVCIRCSCDVVEMGSVLGLCSMASWIPCLCGS
	Ì		APCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQ
1			LNKIPGFCENEKGVVPCNILVGYKAVYRLCFGLAMFYLLLSLLM
1	1		IKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIPEGTFTTVW
	}		FYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKMEEGNSRCWYA
			ALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLC
į.			VGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTWSAMTNEPE
1			TNCNPSLLSIIGYNTTSTVPKEGQSVQWWHAQGIIGLILFLLCV
			FYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
	1		RAVDNERDGVTYSYSFFHFMLFLASLYIMMTLTNWYRYEPSREM
<u> </u>			KSQWTAVWVKISSSWIGIVLYVWTLVAPLVLTNRDFD
6207	2924	1471	TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG
1			GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSPY
1			SVVCKYFQRGYCIYGDRCRYEHSKPLKOEEATATELTTKSSLAA
1			SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNATEFVP
. 1			GQPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA
1 '			VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
			HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERRFGILSNCN
1			HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVEE
]]			KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
1	i		GRREEPQRQKVGTSSRYRAQRRNHFWELIEERENSNPFDNDEEE
6208	2924	1471	VVTF3LGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDL
1 1	1		TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSPY
1 /	1		SVVCKYFQRGYCIYGDRCRYEHSKPLKQEEATATELTTKSSLAA
		•	SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEFVP
1 1	i		GQPYCGRTAPSCTEAPLQGSVTKEESEKEQTAVETKKQLCPYAA
1 1	1		VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
1 1			HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERRFGILSNCN
i !	į		HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVER
[[KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
[GRREEPQRQKVGTSSRYRAQRRNHFWELIEERENSNPFDNDEER
6209	1370		VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDI.DI.
02.05	1758	829	ERLCFPCMQSKIYSYMSPNKCSGMRFPLQEENSVTHHEVKCQGK
		.	PLAGIYRKREEKRNAGNAVRSAMKSEEOKIKDARKGPLVPFPNO
[1		KSBAAEPPKTPPSSCDSTNAAIAKQALKKPIKGKQAPRKKAQGK
ļ.,	1		TQQNRKLTDFYPVRRSSRKSKABLQSEERKRIDELIESGKEEGM
j			KIDLIDGKGRGVIATKQFSRGDFVVEYHGDLIEITDAKKREALY
ł	j		AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ
			TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIEAHPWL KH
6210	3761	387	
į.			IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT SSIGGTDKELRLVDGENKCSGRVEVKVQEEWCTVCNNGWSMEAV
· · · i		. i	SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD
[. 1	CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE
1	j	İ	IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG
1		}	SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG
1		1	ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK
1		İ	QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHE
Ī	ļ		WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEIQRL
		ŀ	LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWL
			The state of the s

Segonating nucleotide location locat								
No. nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence seque	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide				
nucleotide location corresponding to first samino acid residue of samino acid residue of samino acid residue of samino acid sequence	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=				
to first amino acid residue of amino acid residue of amino acid sequence Septime	NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,				
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to first amino acid residue of amino acid residue of amino acid amino acid amino acid amino acid acquence P=Proline, Q=Glutamine, R=Arginine, acquence Codon, /=possible nucleotide deletion,	1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,				
amino acid residue of amino acid sequence solve nce solve of the sequence solve of the sequence solve of the sequence solve of the sequence solve of the sequence solve of the sequence solve of the sequence solve of the sequence solve of the sequence solve of the sequence solve of the sequence solve of the sequence solve of the sequence solve of the sequence solve of the sequence solve of the sequence solve of the sequence solve of the sequence solve of the sequence				P=Proline, Q=Glutamine, R=Arginine,				
residue of amino acid sequence	1			S=Serine, T=Threonine, V=Valine,				
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SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRFETCSH SRDVGVVCSRYTEIRLVNGKTPCBGRVELKTLGAWGSLCNSHWD IEDAHVLCQQLKCGVALSTPGGARFGKCNGQIWRHMFHCTGTEQ HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT RPTIPEESAVACIESGQLRLVNNGGRCAGRVEIYHEGSWGTICD DSWDLSDAHVVCRQLGCEAINATGSAHFGEGTGPIWLDEMKCN GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP ASLDKAMSIPMWDDNVQCPKGPDTLWQCPSSPWERKLASFSEET WITCDNKIRLQEGFTSCSGRVEIWHGGSWGTVCDDSWDLDDAQV VCQQLGCGPALKAFKEABFGQGTGPIWLMEVKCKGNESSLWDCP ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR EMNSCLNADDLDLMNSSGHSEPH LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSFGYTEVTIIEKPPAERHMISSWE QKNNCVWPEDVKNFYLMINGFHMTWSVKLDEHIIPLGSMAINSI SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK GPSGPSGPSTSTSTSSSSGGNPTRK LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCWMEDFDVKNFYIMTNGFHMTWSVKLDEHIIPLGSMAINSI	1		1	FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLV				
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VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR EMNSCLNADDLDLMNSSGHSEPH LKWBLRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSGPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK GPSGPSGPSTSSTSKSSSGGNPTRK G213 1 1134 LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSGPPPAPARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI	1	1		ACCOMPACTABLY ANY CALL CANADA VALLED CODUCCALY				
EMNSCLNADDLDLMNSSGGHSEPH EMNSCLNADDLDLMNSSGGHSEPH	1	1		AKKWGHSECGHKEDAAVICIDISVQKIPQAAIIGASSKQSSIA				
6212 1 1134 LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSGPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCVMPEDVKNFYLMTINGFHMTWSVKLDEHIIPLGSMAINSI SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK GPSGPSGPSTSSTSKSSSGSGNPTRK CPSGPSGPSTSSTSKSSGSGNPTRK RELPFPACHEIGLGAEAGSGPPAPARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI	1							
RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS VIFELDSCNGSGKVCLVYKSGKPALAEDTELWFLDRALYWHFLT DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK GPSGPSGPSTSSTSKSSSGSGNPTRK CPSGPSGPSTSSTSKSSGSGNPTRK RELPFPACHEIGLGAEAGSGPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCWMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI	1			EMNSCLNADDLDLMNSSGGHSEPH				
RELPFPACHEIGLGAEAGSGPPAPARESRSRAMEEEASSPGL GCSKPHLEKITLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCVMPEDVKNFYLMTINGFHMTWSVKLDEHIIPLGSMAINSI SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK GPSGPSGPSTSSTSKSSSGSGNPTRK CPSGPSGPSTSSTSKSSGSGNPTRK LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSCPPAPARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCWMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI	6212	1	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR				
QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK GPSGPSGPSTSTSKSSGSGNPTRK LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI			1	RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL				
QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK GPSGPSGPSTSTSKSSGSGNPTRK LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI	1	1	1	GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE				
SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK GPSGPSGPSTSTSKSSGSGNPTRK LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI	ı	1	l	OKNNCVMPEDVKNFYLMINGFHMTWSVKLDEHIIPLGSMAINSI				
VIFELDSCNGSGKVCLVYKSGKPALAEDTEIMFLDRALYWHFLT DTFTAYYRLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK GPSGPSGPSTSTSKSSGSGNPTRK LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI	ı		Į.	SKITOLTOSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS				
DTFTAYYRLITHLGLPQWQYAFTSYGISPQAKQRVSMYKPITY NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK GPSGPSGPSTSSTSKSSSGSGNPTRK LKWELRPGGAVWGTGRGAGTGPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSGPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI	1			VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT				
NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK GPSGPSGPSTSSTSKSSSGGNPTRK 6213 1 1134 LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCUMPEDUKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI	{		1	DYFTAYYRLLITHLGLPOWOYAFTSYGISPQAKQRVSMYKPITY				
GPSGPSGPSTSSTSKSSSGSGNPTRK 6213 1 1134 LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSGPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCUMPEDUKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI	ł			NTNI.I.TEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK				
6213 1 1134 LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCUMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI	1		1	CDCCDCCDCTCCTCKSSSGSGNPTRK				
RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCUMBEDUKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI	L			T WHET BROCKWAGTGPGAGTGADPSCCCOTNPGPPSSI.RRAFRR				
GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE OKNNCVMDEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI	6213	1	1134	DEWELLEPGGAVWG TORGAG TOAPROCCOQ THE OF FOODINGSPRACEDOS.				
OKNINCYMDEDVKNEYI.MTNGFHMTWSVKLDEHIIPLGSMAINSI	1	1		RELPHPACHEIGIGAEAGSUPPPAPAAKESKSKWEBEASSFOR				
QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI SKLTOLTOSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS				GCSKPHLEKLTLGITRILESSPGVTEVTITEAFFAEAAMISSWE				
I SKI TOLTOSSMYSLPNAPTLADLEDDTHEASDDQPERPHFDSRS	- [1	QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI				
V.W. 2	1			SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS				

SEQ	Predicted	Predicted end	Tool
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H-Histidine, I=Isoleucine, K-Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
]	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
1			VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT
1			DTFTAYYRLLITHLGLPQWQYAFTSYGISPOAKORVSMYKPTTY
1			NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVOPAGGOK
6214	 		GPSGPSGPSTSSTSKSSSGSGNPTRK
0214	2	460	HELAPSAIRRAARLGLGPARWQSRAAAFYFVRGFRTGWSFVGWV
1			VLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRESKRFSAYN
1			YRTYAVRRIRDAFRENKNVKDPVEIQTLVNKAKRDLGVIRRQVH
6215	2	1849	IGQLYSTDKLIIENRDMPRT
	1	1049	FVAGGPRGSGSAAETMPEIRVTPLGAGQDVGRSCILVSIAGKNV
1			MLDCGMHMGFNDDRRFPDFSYITQNGRIJTDFLDCVIISHFHLDH
1	1		CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDYRKIAVDXKGE
į.			ANFFTSQMIKDCMKKVVAVHLHQTVQVDDELEIKAYYAGHVLGA
			AMFQIKVGSESVVYTGDYNMTPDRHLGAAWIDKCRPNLLITEST YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGRAQELC
İ			ILLETFWERNNLKVPIYFSTGLTEKANHYYKLFIPWTNQKIRKT
ł			FVQRNMFEFKHIKAFDRAFADNPGPMVVFATPGMLHAGQSLQIF
İ			RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRQVLEVK
			MOVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKMEFLKQ
1			KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKREMAOGI.
			LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEHOLRFTC
Ì			RVHLHDTRKEQETALRVYSHLKSVLKDHCVOHLPDGSVTVESVI.
6216	11		LQNANPSEDPGTKVLLVSWTYQDEELGSFLTSLLKKGLPQAPS
0210	11	393	QTTRPEPRNSALRQSRSKMAVVGVSSVSRLLGRSRPQLGRPMSS
İ			GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGEHERPE
6217	9	1178	FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYEDE
		11/0	TRVGRGESGLKMEVKPPPGRPQPDSGRRRRRRGEEGHDPKEPEQ
1			LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQTKRSRG FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDSVKPGA
			HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEDRQSGK
1			KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSKQEMQS
	·		AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGGRGGYGGGG
1			GGSRGSYGGGDGGYNGFGGDGGNYGGGPGYSSRGGYGGGGPGYG
1 1			NQGGGYGGGGYDGYNEGGNFGGGNYGGGGNYNDFGNYSGOOG
<u> </u>			NYGPMKGGSFGGRSSGSPYGGGYGSGGGGGGGGGGGGGGGG
6218	1305	906	SCERRGFIMADDLKRFLYKKLPSVEGLHAIVVSDRDGVPVIKVA
			NDNAPEHALREGELSTFALATDQGSKLGLSKNKSIICYYNTYOV
6219			VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELROVVEVS
0213	2	890	AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADR PHORDET.
1 1	ŀ		IGVSGGTASGKSTVCEKIMELLGQNEVEQRQRKVVILSQDRFYK
]			VLTABQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEGKTVEVP
]]	Ī		TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDMFHLRLF
1 1			VDTDSDVRLSRRVLRDVRRGRDLEQILTQYTTFVKPAFEEFCLP
	İ		TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWHRGGSNG
6220	227	764	RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH
]	•	*	EQNISLEMSCTIEKALADAKALVERLRDHDDAAESLIEQTTALN KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQIRELQQ
1			ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDDPGIIMK
1 1	}		LKEQHSKIDMVHRNKSEGFFLDASRHILEAPOHGLERRHLEANO
	i		NVH
6221	98	916	RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGLYQGVTP
	i i		NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLVSAAEAG
	•		AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDTLVKIYK
	j		YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQHINRLPE
1	1	İ	AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHMFYSGVI
	1		DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYENVSHFL
			LDLREKRK

		La de al ana	New- park compat companies of continuous
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence	1	\=possible nucleotide insertion)
6222	2	2116	MARELRALLLWGRRLRPLLRAPALAAVPGGKPILCPRRTTAQLG
0222	-	1 2220	PRRNPAWSLOAGRLFSTQTAEDKEEPLHSIISSTESVQGSTSKH
1	i	ĺ	EFOAETKKLLDIVARSLYSEKEVFIRELISNASDALEKLRHKLV
}	ł	l	SDGOALPEMEIHLQTNAEKGTITIQDTGIGMTQEELVSNIGTIA
Į			
			RSGSKAFLDALQNQAEASSKIIGQFGVGFYSAFMVADRVEVYSR
ì			SAAPGSLGYQWLSDGSGVFEIAEASGVRTGTKIIIHLKSDCKEF
{	1	l	SSEARVRDVVTKYSNFVSFPLYLNGRRMNTLQAIWMMDPKDVRE
1	!	f	WQHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKPSM
1		1	FDVSRELGSSVALYSRKVLIQTKATDILPKWLRFIRGVVDSEDI
ì	1		PLNLSRELLQESALIRKLRDVLQQRLIKFFIDQSKKDAEKYAKF
	}	i	FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTSLS
		1	EYASRMPAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLFCF
1	1	1	EOFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPAAE
ì	1		CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEMG
1	1		AARHFLRMQQLAKTQEERAQLLQPTLEINPRHALIKKLNQLRAS
1	1		EPGLAQLLVDQIYENAMIAAGLVDDPRAMVGRLNELLVKALERH
6223	3	715	DAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGCY
6223	, ,	/13	RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDSCYKLGAYYVTGK
1]	GGLTQDLKAAARCFLMACEKPGKKSIAACHNVGLLAHDGQVNED
ł	}		GOPDLGKARDYYTRACDGGYTSSCFNLSAMFLQGAPGFPKDMDL
}	3		
	1	i	ACKYSMKACDLGHIWACANASRMYKLGDGVDKVEAKAEVLKNRA
	<u> </u>	<u> </u>	QQVHKEQQKGVQPLTFG
6224	1	133	LRTISSMAWGPLLLTLLAHCTGSWAQSVLTQPPSVSGARIPHEK
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT
ļ	j	}	QKEWRLLSPAQRALYREVTLENYSHLVSLGILHSKPELIRRLEQ
İ	i	1	GEVPWGEERRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD
1	1	1	QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES
Į.	ļ	l .	SQGQRENPTEIDKVLKGIENSRWGAFKCAERGQDFSRKMMVIIH
1	1	1	KKAHSROKLFTCRECHOGFRDESALLLHONTHTGEKSYVCSVCG
1		[RGFSLKANLLRHQRTHSGEKPFLCKVCGRGYTSKSYLTVHERTH
ļ	l .	1	TGEKPYECOECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT
1	1	í	NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK
ł	1		PFACROCKOSFSVKGSLLRHORTHSGEKPFVCKDCERSFSQKST
	1	}	LVYHORTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC
ŀ			KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH
i	1	1	LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE
1		1	
I	1	1	KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH
1		1	SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN
Ī	1	1	WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE
ı			KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS
			YYSKHLKRHLREKRFCTGSVGEASS
6226	29	266	TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS
Į.	1		IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA
6227	2581	890	MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP
			NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS
ł	1]	YGOLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS
1		1	AWGNNSSOGOSTOSSGYSSNYAYAPSSLGGAMIDGQSAFANETL
1	j .	1	NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI
} .		1	VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL
I		i	
l l			PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG
1	1		QQANNSPPVAQASVGQQTQPLPPPPPQPAQLSVQQQAAQPTRWV
1	Į.		APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN
	i	1	NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK
Ì		1	RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG
ſ		1	VWSQDKWKGRFDVRWIFVKDVPNSQLRHIRLENNENKPVTNSRD
		1	
	1	1	TQEVPLEKAKQVLKIIASYKHTTSIPDDFSHYEKRQ

SEQ Predicted Predicted end Amino acid segment	containing signal peptide
	containing signal peptide eine, D=Aspartic Acid, E=
	nenylalanine, G=Glycine,
location corresponding H=Histidine, I=Isol	lengian & funia
	onine, N=Asparagine,
amino acid P=Proline, O=Glutan	nine D-Arginine
amino acid residue of S=Serine, T=Threoni	ine V-Valino
residue of amino acid W=Trvptophan V=Tvv	cosine, X=Unknown, *=Stop
amino acid sequence Codon, /=possible r	nucleotide deletion,
sequence \=possible nucleoti	de insertion
6228 47 1978 GRRCRRGAVMELAGEARE	LGCWAVEEMGVPVAARAPESTLRRL
CLGOGADIWAYILOHVHSC	PRIVKKIRGNLLWYGHQDSPQVRRKL
ELEAAVTRLRAEIOELDOS	LELMERDTEAQDTAMEQARQHTQDT
ORRALLLRAOAGAMRROOF	TLRDPMQRLQNQLRRLQDMERKAKV
DVTFGSLTSAALGLEPVVI	RDVRTACTLRAQFLQNLLLPQAKRG
SLPTPHDDHFGTSYOOWLS	SVETLLINHPPGHVLAALEHLAAER
EAEIRSLCSGDGLGDTEIS	RPQAPDQSDSSQTLPSMVHLIQEGW
RTVGVLVSORSTLLKEROV	LTORLOGLVEEVERRVLGSSEROVL
ILGLRRCCLWTELKALHDO	SQELQDAAGHRQLLLRELQAKQQRI
LHWRQLVEETOEOVRLLIK	GNSASKTRLCRSPGEVLALVQRKVV
PTFEAVAPQSRELLRCLEE	EVRHLPHILLGTLLRHRPGELKPLP
TVLPSIHQLHPASPRGSSF	TALSHKLGLPPGKASELLLPAAASL
RQDLLLLQDQRSLWCWDLL	HMKTSLPPGLPTOELLOIOASORKO
QKENLGQALKRLEKLLKQA	LERIPELOGIVGDWWEOPGOAALSE
ELCQGLSLPQWRLRWVQAQ	GALQKLCS
GPSLLGTRGTPNPARTLQI	FFLIIGRRLTGRMAAVDDLQFEEFG
NAATSLTANPDATTVNIED	PGETPKHQPGSPRGSGREEDDELLG
NDDSDKTELLAGQKKSSPF	WTFEYYQTFFDVDTYOVFDRIKGSI.
LPIPGKNFVRLYIRSNPDL	YGPFWICATLVFALAISGNLSNFLT
HLGEKTYHYVPEFRKVSIA	ATIIYAYAWLVPLALWGFLMWRNSK
VMNIVSYSFLEIVCVYGYS	LFIYIPTAILWIIPHKAVRWILVMI
ALGISGSLLAMTFWPAVRE	DNRRVALATIVTIVLLHMLLSVGCL
6230 1723 600 SKMSGPSGVVVMSVI GROOM	NQTVAAAKSS
SKMSGRSGRKKMSKLSRSAI	RAGVIFPVGRLMRYLKKGTFKYRIS
VGAPVYMAAVIEYLAAEILI	ELAGNAARDNKKARIAPRHILLAVA
DDEPENDENCEMENT	LPRIHPELLAKKRGTKGKSETILSP
SEPONDENT ROWS IN	KAAKPRTSKKSKPKDSDKEGTSNST
TTAETOLVEDTOVALTIVA	GQKLSLTQSDISHIGSMRVEGIVHP
SOSSGLAREUTUCHTPOW	GKEFLETVKELRKSQGPLEVAEAAV GSDKCEEQLEETIKNCLSAAEDKKL
KSVAFPPFDSGPMCEPKOTI	AAQVILKAISAHFDDSSASSLKNVY
FLLFDSESIGIYVQEMAKLI	ACVILKAISAHFUUSSASSLKNVY
6231 149 870 LIFSSSTMDRSLPNULVUS	GFLLLFTAYGGLQSLQSSLYSEEG
LGVTALSTI, VGGMI, I, SSMET	LPPLLIERLGCKGTIILSMCGYVAF
SVGNFFASWYTI.IPTSILLO	SLGAAPLWSAQCTYLTITGNTHAEK
AGKRGKDMVNOYFGIFFI.TF	FQSSGVWGNLISSLVFGQTPSQETL
PEEQLTSCGASDCIMATTTT	INSTORPSOOLVYTLIGIYTGSGVL
AVLMIAAFLQPIRDVORESE	2
6232 3679 1476 FVAGTTMAGFWVGTAPLVAA	GRRGRWPPOOLMLSAALRTLKHVI.
YYSRQCLMVSRNLGSVGYDF	NEKTFDKILVANRGEIACRVIRTC
KKMGIKTVAIHSDVDASSVH	IVKMADEAVCVGPAPTSKSYT,NMDA
IMEA1KKTRAQAVHPGYGFL	SENKEFARCLAAEDVVFIGPDTHA
IQAMGDKIESKLLAKKAEVN	TIPGFDGVVKDAEEAVRTARETGY
PVMIKASAGGGKGMRIAWD	DEETROGFRLSSOEAASSFGDDRI.
LIEKFIDNPRHIEIQVLGDK	HGNALWLNERECSIORPNOKTORE
APSIFLDAETRRAMGEQAVA	LARAVKYSSAGTVEFLVDSKKNEV
FLEMNTRLQVEHPVTECITG	LDLVQEMIRVAKGYPLRHKOADTD
INGWAVECRVYAEDPYKSFG	LPSIGRLSOYOEPLHT.PGVRVDSG
IQPGSDISIYYDPMISKLIT	YGSDRTEALKRMADALDNYVIRGV
THNIALLREVIINSRFVKGD	ISTKFLSDVYPDGFKGHMLTKSEK
NQLLAIASSLFVAFQLRAQH	FQENSRMPVIKPDIANWELSVKLH
DKVHTVVASNNGSVFSVEVD	GSKLNVTSTWNLASPLLSVSVDGT
QRTVQCLSREAGGNMSIQFL	GTVYKVNILTRLAAELNKFMLEKV
TEDTSSVLRSPMPGVVVAVS	VKPGDAVAEGQEICVIEAMKMONS
6233 1 2654 HETTERN MACHINERO	GEGDLLVELE
6233 1 2654 HSTRENLNAGNFNFPSEGHL	VRSTGPGGSFAKHMVAQCVSPKGP

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ľ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		· · · · · · · · · · · · · · · · · · ·	LACSRTYFFGATHVPYLGGDSKLPKKTEOIRLLSQIYAAVIEAV
l			LAGIACYAKTSSLTKAKEVAEOTLGSGLDSFELIPFKAALRSKM
ł		[TFHIHAVNNQGRIVPLDSEDSLSFVKTACMAVYDIPDLLGGNGC
1		l	LGSVVFSESFLTSQILVKEKDGTVTTETSSVVLTAAVPRFCSWL
			VEDNEVKLSEKTHQAVRGDESFLGTYLTGGEGAYLYSSNLQSWP
1	ł	i	EEGNVHFFSSGLLFSHCRHGSIIISKDHMNSISFYDGDSTSTVA
		1	ALLIDFKSSLLPHLPVHFHGSSNFLMIALFPKSKIYQAFYSEVF
1	1		SLWKQQDNSGISLKVIQEDGLSVEQKRLHSSAQKLFSALSQPAG
1			EKRSSLKLLSAKLPELDWFLQHFAISSISQEPVMRTHLPVLLQQ
1	1		AEINTTHRIESDKVIISIVTGLPGCHASELCAFLVTLHKECGRW
i		1	MYYRQIMDSSECFHAAHFQRYLSSALEAQQNRSARQSAYIRKKT
			RLLVVLQGYTDVIDVVQALQTHPDSNVKASFTIGAITACVEPMS
j.	1	ŀ	CYMEHRFLFPKCLDQCSQGLVSNVVFTSHTTEQRHPLLVQLQSL
	1		IRAANPAAAFILAENGIVTRNEDIELILSENSFSSPEMLRSRYL
1	ľ	[MYPGWYEGKLNAGSVYPLMVQICVWFGRPLEKTRFVAKCKAIQS
1	1	1	SIKPSPFSGNIYHILGKVKFSDSERTMEVCYNTLANSLSIMPVL
	ļ		EGPTPPPDSKSVSQDSSGQQECYLVFIGCSLKEDSIKDWLRQSA
ļ	1	l	KOKPORKALKTRGMLTQQEIRSIHVKRHLEPLPAGYFYNGTQFV
ĺ		İ	NFFGDKTDFHPLMDQFMNDYVEEANREIEKYNQELEQQEYHDLF
İ			ELKP
6234	1731	404	PRVREDMDHKSPGNKGSLVYAGIKSIVKSSLGMVESSRHNWSGL
0234	1/31	101	DKOSDIONLNEERILALQLCGWIKKGTDVDVGPFLNSLVQEGEW
1	†	1	ERAAAVALFNLDIRRAIQILNEGASSEKGDLNLNVVAMALSGYT
1	ł	1	DEKNSLWREMCSTLRLQLNNPYLCVMFAFLTSETGSYDGVLYEN
			KVAVRDRVAFACKFLSDTQLNRYIEKLTNEMKEAGNLEGILLTG
l .	1		LTKDGVDLMESYVDRTGDVQTASYCMIQGSPLDVLKDERVQYWI
		1	ENYRNLLDAWRFWHKRAEFDIHRSKLDPSSKPLAQVFVSCNFCG
			KSISYSCSAVPHQGRGFSQYGVSGSPTKSKVTSCPGCRKPLPRC
ļ	İ		ALCLINMGTPVSSCPGGTKSDEKVDLSKDKKLAQFNNWFTWCHN
1			CRHGGHAGHMLSWFRDHAECPVSACTCKCMQLDTTGNLVPAETV
			OP
6235	1	571	EKRDHRLPSWPRAALKVPGRGGRVGTTPELAAGGIMATRNPPPQ
1 3232	_		DYESDDDSYEVLDLTEYARRHQWWNRVFGHSSGPMVEKYSVATQ
1			IVMGGVTGWCAGFLFQKVGKLAATAVGGGFLLLQIASHSGYVQI
ı			DWKRVEKDVNKAKRQIKKRANKAAPEINNLIEEATEFIKQNIVI
1			SSGFVGGFLLGLAS
6236	1 1	703	WDONKGAAAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF
1	_		NLKFAAKBLSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAE
i			NAIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK
1			SMDATLKTMNLEKISALMDKFEHQFETLDVQTQQMEDTMSSTTT
1 -			LTTPQNQVDMLLQEMADEAGLDLNMELPQGQTGSVGTSVASAEQ
1		· ·	DELSQRLARLRDQV
6237	312	720	PTAMAEEGIAAGGVMDVNTALQEVLKTALIHDGLARGIREAAKA
"""	1 746	/~~	LDKROAHLCVLASNCDEPMYVKLVEALCABHQINLIKVDDNKKL
1		1	GEWYGLCKIDREGKPRKVVGCSCVVVKDYGKESQAKDVIEEYFK
l	1		CKK
6238		4666	ERVPTOESVKWEINVIIKNPEIVFVADMTKNDAPALVITTQCEI
6236	ż	******	CYKGNLENSTMTAAIKDLOVRACPFLPVKRKGKITTVLOPCDLF
			YOTTOKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE
			TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP
1			KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL
	1		INLHCOLELEVHYYNEMFGVWEPLLEPLEIDQTEDFRPWNLGIK
1			
		1	MKKKAKMAIVESDPEEENYKVPEYKTVISFHSKDQLNITLSKCG
1		1	LUMLNNLVKAFTEAATGSSADFVKDLAPFMILNSLGLTISVSPS
	1		DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK
L	<u> </u>		LFFILLTPVNHSTADKIPLTKVGRRLYTVRHRESGVERSIVCQI

Deginning nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Aparagine, P=Poline, Q=Glutamic, Acid, P=Phenylalanine, R=Aparagine, L=Leucine, M=Methionine, N=Aparagine, P=Poline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, Codon, /=possible nucleotide deletion, \possible nuc	ID	beginning nucleotide location corresponding to first amino acid residue of amino acid	nucleotide location corresponding to first amino acid residue of amino acid	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDTLLGTASPENEFN IPLGSYRSFIFLKPEDENYQMCEGIDFEEIIKNDGALLKKKCRS KNPSKESFLINIVPEKDNLTSLSVYSEDGWDLPYIMHLWPPILL RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQLGKARLHLKL LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT
NO: nucleotide location corresponding to first amino acid amino acid residue of amino acid sequence se		nucleotide location corresponding to first amino acid residue of amino acid	location corresponding to first amino acid residue of amino acid	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \ -possible nucleotide insertion) DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDTLLGTASPENEFN IPLGSYRSFIFLKPEDENYQMCEGIDFEEIIKNDGALLKKKCRS KNPSKESFLINIVPEKDNLTSLSVYSEDGWDLPYIMHLWPPILL RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQLGKARLHLKL LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT
Location Corresponding Lofirst amino acid Location Loc		location corresponding to first amino acid residue of amino acid	corresponding to first amino acid residue of amino acid	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDTLLGTASPENEFN IPLGSYRSFIFLKPEDENYQMCEGIDFEEIIKNDGALLKKKCRS KNPSKESFLINIVPEKDNLTSLSVYSEDGWDLPYIMHLWPPILL RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQLGKARLHLKL LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT
corresponding to first amino acid serious of session of the session of the session of amino acid sequence seque		corresponding to first amino acid residue of amino acid	to first amino acid residue of amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDTLLGTASPENEFN IPLGSYRSFIFLKPEDENYQMCEGIDFBEIIKNDGALLKKKCRS KNPSKESFLINIVPEKNNLTSLSVYSEDGWDLPYIMHLWPPILL RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQLGKARLHLKL LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT
to first amino acid residue of residue of amino acid residue of amino acid sequence Serine, T=Threonine, V=Valine, amino acid sequence Codon, /=possible nucleotide deletion, -possible nucleotide insertion) DTVEGSKKVTTRSPVQTRNHFSVPLSTYGEGTLLGTASPENEF IPLGSYRSFIFLREDENYGMCEGIDFEIIKNDGALLKKKCR KNPSKESFILNIVDEKUNLTSLSYVSEDGUDLPYIMHLMPPIL RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQIGKARLHLK LDYLNHDWKSEYHIKPNQODISPYSTCVTEMEKTDLDIAVHM YNTGQTVVAPHSPYWMVMKTGRMLQYKADGIHRKHPPNYKKPV FSFQPNHFFNNNKVQLMVTDSELSNQFSIDTVGSHGAVKCKGL MDYQVGVTIDLSSENITRIVTFTFYMIKKKSKHISVABEGN KWHSLDLEGCIPFWPEYASSKLLIQVERSEDPPRIYNKYMCEN KWHSLDLEGCIPFWPEYASSKLLIQVERSEDPPRIYNKYMCEN KWHSLDLEGCIPFWPEYASSKLLIQVERSEDPPRIYNKYMCEN HGEVTQXDDMMMPIDLGEKTIYLVSFFEGLQRILLFTEDPRVF VTTESBKAELAEGBIAVALQDVGISLVMNYTKQEVAYIGITSS VVWBTKPKKKARMKMPMSVKHTEKLEREPKEVTESSPSDKVIQ DTNVPVRLTPTGHMMKILQPHVIALRRNYLPALKVEYNTSAHQ SFRIQIYRIQIQNQIHGAVFFVFYVFVKPFKSVTMDSAPKFFT VSIVMRSAGRSQISRIKYFKVLIQEMDLKLDLGFIYALTDLMT AEVTENTEVELFHKDIEAFKEEYTTASLVDQSQVSLYEYFHIS IKHLSVSLSSGREEAKDSKQNGGIPVHSLNLLKSIGATLT VQDVVFKLAFFELNYQFHTTSDLQSEVIRHYSKQAIKQMYVLII GLDVLGNPFGLIRBFSEGVEAFFYEPYQGAIQGPEFVEGMAL LKALVGGAVGCLACAASKITCAMAKGVAAMTMDEDYQKRREA NKQPAGFREGITRGGKGLVSGFYSGITTGIVTKPIKGAQKGGAA FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESL DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDTRYPRENITMTHSSSD DDDDDDDDDDDDDDDDDDDDDDDDDRYNH FCRUVKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESL PPRFFREGOTRPTLRPGTGNOMLQKIQFYRENITMTHSSSD DDDDDDDDDDDDDDDDDDDDDDDDCRYPRENITMTHSSSD DDDDDDDDDDDDDDDDDDDDCRYPRENITMTHSSSD DDDDDDDDDDDDDDDDDDDCRYPRENITMTHSSSD DDDDDDDDDDDSDLNH FCRUVTAMQPHLMFYCTRTLPNVLALPAVULLALAANLRHEWARF WISAFAIIVERVSLCLEIGLLLLALARKVSVVPAARARPAPA		to first amino acid residue of amino acid	amino acid residue of amino acid	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDTLLGTASPENEFN IPLGSYRSFIFLKPEDENYQMCEGIDFBEIKNDGALLKKKCRS KNPSKESFLINIVPEKDNLTSLSVYSEDGWDLPYIMHLWPPILL RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQLGKARLHLKL LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT
amino acid residue of amino acid sequence Codon, -possible nucleotide deletion, -possible nucleotide deletion, -possible nucleotide deletion, -possible nucleotide deletion, -possible nucleotide deletion, -possible nucleotide insertion) DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDEDILIGTASPENEF, IPLEGSYRSF1FLKPEDEDENYQMCEGIDFEEIKNNGALLKKKCR, KNPSKESFLINIVPEKDNLTSLSVYSEDGMDLPYIMHLWPPIL RNLLPYKIAYYIEGIENSVFTLSGGHSAGICTAQIGKARHLK LDVINHDWKSSYHIKPNQQDISPVSFTCVTEMEKTDLDIAVHM YNTGQTVVAFHSPYWMVNKTGRMLQYKADGIHRKHPDNYKKPV FSFQPRHFFNNNKVQLMVTDSELSNGFSIDTVGSHGAVKCKGL MPDYQUGVTIDLSSENHITRIVTFTPFYMIKNKSKYHISVAEEGN KWILSLDLEGCIPFWPEYASSKLLIQVERSEDPPRRIYFNKQEN KWILSLDLEGCIPFWPEYASSKLLIQVERSEDPPRRIYFNKQEN LILLDNELGGIIAEVNLABHSTVITFLDYHDGAATFLLINHT NELVQYNQSSLSEIEDSLPPGKAVFYTWADPVGSRRLKWRCKK HGEVTQKDDMMMPIDLGEKTIYLVSFFEGLQRIILFTEDPRVF VTYESEKAELAEQEIAVALQDVGISLVNNYTKQEVAYIGITSS VVWETKFKKKARWKRMSVKHTEKLEEFKSYTESSPSEDKVIQ DTMVPVKLTPTGHNNKILQPHVIALRRNYLPBALKVEYNTSAHQ SPRIQIYQIQNGHGAVPFPVFYYPVKPKSVATWDSAPKPFT VSIVMSAGHSQISSKIKFKVLIQEMDLRLDLGFIYALTDLMT AEVTENTEVELFHKDIEAFKEFYKTASLVDQSQVSLVEYFHIS IKLHLSVSLSGREERAKDSKQNGGLIPHSLAULSIGATITI VQDVVFKLAFFELNYQFHTTSDLQSEVIRFYSKQAIKQMYVLI GLDVICMPFGLIREFSEGVEAFFYEFYQGAIQGFEBFVEGMAL LKALVGGAVGLAGAASKITGAMAKGAVAMTMDEDYQKKREBA NKQPAGFREGITRGCKGLVGAASKITGAMAKGAVAMTMDEDYQKKREBA NKQPAGFREGITRGCKGLVGAASKITGAMAKGAVAAMTMGRYQKKREBA NKQPAGFREGITRGCKGLVGAASKITGAMAKGAVAAMTMGRYQKKREBA NKQPAGFREGITRGCKGLVGAASKITGAMAKGAVAAMTMGRIGYFREWIMTHSSSSD DDDDDDDDDDDDDLDSDLNH 634 KPGMAGKGSSGRRPLLGLLVALVAVVVLLALAAWLRHEWARF FKGVUKMQPHLMFYCTRILPVVLLALPVVLLALAAWLRHEWARF WLSAFAILVFRVSLGIGUFFGWTLQKEVRRHGAMVAT FCWVTAMQPHLMFYCTRILPVVLLALPAVLLAAAWLRHEWARF WLSAFAILVFRVSLGIGUFFGWTLLAAAWLRHEWARF WLSAFAILVFRVSLGIGUFFGWTLLAAAWLRHEWARF WLSAFAILVFRVSLGIGUFFGWTLLAAAWLRHEWARF WLSAFAILVFRVSLGIGUFFGWTLLAAAWLRHEWARF WLSAFAILVFRVSLGIGUFFGWTLLAAAWLRHEWARF		amino acid residue of amino acid	residue of amino acid	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDTLLGTASPENEFN IPLGSYRSFIFLKPEDENYQMCEGIDFEEIKNDGALLKKKCRS KNPSKESFLINIVPEKDNLTSLSVYSEDGWDLPYIMHLWPPILL RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQLGKARLHLKL LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT
residue of amino acid sequence (Codon, /=possible nucleotide deletion, \-possible nucleotide deletion, \-possible nucleotide dinsertion) DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDTLLGTASPENEF IPLGSYRSFIFLKFEDENYQMCEGIFFEIIKNDGALLKKKCR KMPSKESFIFLKNPEDANYATSSUYYEGDTLLGTASPENEF IPLGSYRSFIFLKFEDENYQMCEGIFFEIIKNDGALLKKKCR KMPSKESFIFLNIVPEKDNITSLSVYSEDGWDLPYTMHIMPPIL RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQLGKARLHLK LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHM YNTGQTVVAFHSPYMMVMKTGRMLQVKADGIHRKHPNNYKRPV FSFQNHFFNNNKVQLMVTDSBLSNGFSIDTVGSHGAVKCKGL MDYQVGVTIDLSSFNITRIVSTFTPFYMIKMSXHISVAEEGN KWISLDLEQCIPFWFEYASKLLIQVERSEDPPKRIYHNQEGN ILLRLDNELGGIIAEVNLAEHSTVITFLDYHDGAATFILIUNIT NELUQYNQSSLSEINSPEGKAVFTWADPVGSRRIKWRCKK HGEVTQKDDMMMPIDLGEKTIYLVSFFEGLQRILLFTEDPRVF VTYESEKAELAEQEIAVALQDVGISLVNNYTKQEVAYIGITSS VVWETKPKKKARWKFWAKHTEKLEEFEKSYTESSPEDKVIQ DTNVPVRLTPTGHNMKILQPHVIALRRNYLPALKVEYNTSAHQ SFRIQIYRIQIQNGHGAVFFPVFYVKPKSVTMDSAPKFFT VSITVMSSAGSHSQISRIKYFKVLIQEMDLRILDLGFIYALTDLMT AEVTENTEVELFHKDIEAFKEEFSKTFSSPSDKVIQ GTVIPTSAGAGNGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG		residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDTLLGTASPENEFN IPLGSYRSFIFLKPEDENYQMCEGIDFEEIKNDGALLKKKCRS KNPSKESFLINIVPEKDNLTSLSVYSEDGWDLPYIMHLWPPILL RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQLGKARLHLKL LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT
amino acid sequence Codon, /=possible nuclectide deletion, \possible nuclectide insertion) DTVEGSKKYTISPYOQIRNEFSVPLSVYEGOTLLGTASPENEF IPLGSYRSFIFLKPEDENYQMCEGIDFEEIIKNDGALLKKKCR KNPSKESFLINIVPEKDNLTSLSVYSEGOMDLPYIMHLWPPIL RNLLPYKLAYYIEGIRSVFTLSEGHSAQICTACLGKARLHLK LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHM YMTGQTVVAFHSPYWMVNKTGRMLQYKADGIHRKHPPNYKKPV FSFQPNHFPNNKVQLMVTDSHLSNQFSIDTVSGHGAVKCKGL MDYQVGVTIDLSSFNITRIVTFTPFYMIKNKSKYHISVAEEGN KWLSLDLEQCIPFWEYASSKLLQVERSEDPPKRIYFNKQEX HGBVTQKNDMMMPIDLGEKTIYLVFFFEGLQRILLFTEDPRVF VTYESEKABLASQEIAVALQDVGISLVNNYYKQEVAYIGITSS VVWETKPKKKARWKPMSVKHTEKLEREPKEYTESSPSEDKVIQ DTMVPVRLTPTGHNMKILQPHVIALRRNYLPALKVEYNTSAHQ SFRIQIYRIQIQNGIASVFFFVFYVKPFKSYTMDSAPKPFT VSIVMRSAGHSQISRIKYFKVLIQEMDLRLDLGFIYALTDLMT ABVTENTEVELFHKDIEAFFKEYKTASLDQSCVSLYEYFHIS IKHHLSVSLSSGEBEAKDSKQNGGLIPVHSLNLLLKSIGATLT VQDVVFKLAFFELNYQFHTTSDLQSEVTRIYSKQAIKQMYVLI GLDVLGNPFGLIREFSEGVEAFFYEPYQCAIQGPEFVEGMAL LKALVGGAVGCLAGAASKITGAMAKGVAAMTMDEDYQQKREAA NKQPAGFREGITGGKGLVSGFVSGITGIVTKPIKGAQKGGAA FFKGVGKGLVGAAASKITGAMAKGVAAMTMDEDYQQKREAA NKQPAGFREGITGGKGLVSGFVSGITGIVTKPIKGAQKGGAA FFFKGVGKGLVGAAASKITGAMAKGVAAMTMDEDYQQKREAA NKQPAGFREGITGGKGLVSGFVSGITGIVTKPIKGAQKGGAA FFFKGVGKGLVGAVARPTGGIDMASSTFQGIKRATETSEVESL DDDDDDDDDEDESDLNH 634 KPGMAGKGSSGRZPFLLIGLLVAAVATVHLVICPYTKVEESFRLQ THDLLYHMQDLEQYDHLEFFGVVPRTFLGPVVLAVFSSPAYVY SLLEMSKFYSQLIVRGVIGGVIGGUTGUMTLQKEVRRHFGAMYAT FCWVTAMQPHLMFYCTRTLPDVLALPVVLLALAAMLRHEWARF FCWVTAMQPHLMFYCTRTLPDVLALPVVLLALAAMLRHEWARF FCWVTAMQPHLMFYCTRTLPDVLALPVVLLALAAMLRHEWARF FCWVTAMQPHLMFYCTRTLPDVLLALPAVLLALAAMLRHEWARF FCWVTAMQPHLMFYCTRTLPDVLLALPAVLALAAMLRHEWARF FCWVTAMQPHLMFYCTRTLPDVLLALAGRRKVSVVRALRHAVPA		amino acid		Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DTVEGSKKVTIRSPVQIRNHFSVPLSVYEGDTLLGTASPENEFN IPLGSYRSFIFLKPEDENYQMCEGIDFEEIKNDGALLKKKCRS KNPSKESFLINIVPEKDNLTSLSVYSEDGWDLPYIMHLWPPILL RNLLPYKIAYYIEGIENSVFTLSEGHSAQICTAQLGKARLHLKL LDYLNHDWKSEYHIKPNQQDISFVSFTCVTEMEKTDLDIAVHMT
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	[1		GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI
	1	1 .		DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA
		1		PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL
ERLPRPS ERLPRPS]	
	6340	2202	1176	HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF
	3240	2202	11/0	DPLSSGSRSSSLKSAOGTGFELGOLOSIRSEGTTSTSYKSLANO
	1			TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL
l l l l l l l l l l l l l l l l l l l	Ī			
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1				AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREXL
	l	1		LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP
1 1		1		LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS
			1	SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS
				
				ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV
l (6241	3	1341	RNAKEKKRISLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT
	6241	3	1341	RNABEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEBLTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR
1 1 · · · · · · · · · · · · · · · · · ·	6241	3	1341	RNABEKKRLSLQREKI IARVSI DNRTRALVQALRRTTDPKLCIT RVEBLTFHLLBFPEGKGVAVKER I I PYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRĞIRILSI DGGGTRGVVALQTLKKLVELTQ
l ! = = =	6241	3	1341	RNABEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEBLTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR
TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYK	6241	3	1341	RNABEKKRLSLOREKI IARVSI DNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERI I PYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRĞIRILSI DGGGTRGVVALQTLKKLVELTQ KPVHQLFDYI CGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVI VGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP
WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECK	6241	3	1341	RNABEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRĞIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV
LWPDVPLECIVSLGTGRYESDVRNTVTYTSLKTKLSNVINSAT	6241	3	1341	RNABEKKRLSLOREKI IARVSI DNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERI I PYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRĞIRILSI DGGGTRGVVALQTLKKLVELTQ KPVHQLFDYI CGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVI VGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP
TEBVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQL:	6241	3	1341	RNABEKKRLSLOREKI IARVSI DNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERI I PYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSI DGGGTRGVVALQTLKKLVELTQ KPVHQLFDYI CGVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVI VGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM
GLKYIERNEQKMKKVAKILSQEKTTLQKINDWIKLKTDMYEGL	6241	3	1341	RNABEKKRLSLOREKI IARVS I DNRTRALVQALRRTTDPKLCIT RVEBLTFHLLEFPEGKGVAVKER I I PYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIR I LS I DGGGTRGVVALQTLKKLVELTQ KPVHQLFDYICGVSTGAI LAFMLGLFHMPLDECEELYRKLGSDV FSQNVI VGTVKMSWSHAFYDSQTWEN I LKDRMGSALMIETARNP TCPKVAAVSTIVNRGITPKAFVFRNYGHFPGINSHYLGGCQYKM WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
10.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	1)	
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
· }	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence		\=possible nucleotide insertion)
			FFSKL
6242	198	1310	QHFLPGAETWSPGAAVCTARRFPGRSLAAFPRPAAPRRAVEMGE
1	i		SSEDIDOMFSTLLGEMDLLTQSLGVDTLPPPDPNPPRAEFNYSV
	Ì	i	GFKDLNESLNALEDQDLDALMADLVADISEAEQRTIQAQKESLO
}	Į.		NQHHSASLQASIFSGAASLGYGTNVAATGISQYEDDLPPPPADP
1]		VLDLPLPPPPPPEPLSQEEEEAQAKADKIKLALEKLKEAKVKKLV
1	ł		VKVHMNDNSTKSLMVDERQLARDVLDNLFBKTHCDCNVDWCLYE
-	Ì		IYPELQIERFFEDHENVVEVLSDWTRDTENKILFLEKEEKYAVF
			KNPONFYLDNRGKKESKETNEKMNAKNKESLLEVRLILOSGRKE
1	İ		KDVCSIFKSFASENNGKI
6243	1509	614	RSASRFSGCWSRDSTCCCCPSTCWSRSSASCPRARWPPSSAPAT
1 25.43	1303	074	TSRASSRRLACGPQTRAGAETRSTAMIRANSAARDTRRATCRSA
	1		<u>-</u>
j			AGTPSPTTMTCLTDVPTGCAAVEPTARLPAAAWASTITTGCCPA
			MGQAGAGPAGRKGSEAGGGPGRAHHAHPSPLPREPRVRTGPPAH
1	<u> </u>		SPTPGSIDPSPELSWGSAGVTQESPLLDPVDFLLFRTRAVDPLR
}	}		RVFFFFYQHLTFFSIQPQPPPCHAFHPRDPPAGTKRQLILVPLK
			GPPILAPILSLTPILSRWSCYFPRSRIAQGWHLS
6244	2119	1745	FEHAYASQFGTFLGNNESERCKLKLQQKTMSLWSWVNQPSELSK
	l .	i	FTNPLFEANNLVIWPSVAPQSLPLWEGIFLRWNRSSKYLDEAYE
		l	EMVNIIEYNKELQAKVNILRRQLAELETEDGMQESP
6245	81	1148	LSLRNAKYSFPQELISLFSMTDLNDNICKRYIKMITNIVILSLI
1	ļ		ICISLAFWIISMTASTYYGNLRPISPWRWLFSVVVPVLIVSNGL
	1	1	KKKSLDHSGALGGLVVGFILTIANFSFFTSLLMFFLSSSKLTKW
1	1	1	KGEVKKRLDSEYKEGGQRNWVQVFCNGAVPTELALLYMIENGPG
1		l .	EIPVDFSKOYSASWMCLSLLAALACSAGDTWASEVGPVLSKSSP
1	1	İ	RLITTWEKVPVGTNGGVTVVGLVSSLLGGTFVGIAYFLTQLIFV
		İ	NDLDISAPQWPIIAFGGLAGLLGSIVDSYLGATMQYTGLDESTG
1		l	MVVNSPTNKARHIAGKPILDNNAVNLFSSVLIALLLPTAAWGFW
		1	PRG
6246	1177	359	SLWPWILMDDSLMOISLOLLCVYTANFPNGCSSLCWSSCGOHPV
"		, ,,,	QATHRGAVSNSLMLCILKLASQMPLENTTVQQMVFMLLSNLALS
1	j	l	HDCKGVIQKSNFLQNFLSLALPKGGNKHLSNLTILWLKLLLNIS
	1		· · · · · · · · · · · · · · · · · · ·
1	1		SGEDGQQMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCFS
	1		PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ
i			KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN
			LVQLLNSS
6247	3	1678	NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP
1		ł	PGPGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL
[YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV
i			SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS
			LQAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG
Ì	J.	}	QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL
1			LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVBEVL
1	1		AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA
1			IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL
1			GRRPLDIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI
1		Ì	IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNPAVG
1	}	J	LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI
1			SOAFSKRNKAYPPEEKIDSAVTDGKINGRP
6248		1773	
0240	56	1773	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI
ŀ			AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL
	}	·	ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP
	<u>[</u>	[SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII
1	1	Ì	LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP
)	I .		YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF
-		j	LINEQSPRASEETLLGISKKAKQMKINVQNNVDLGQPVKNKRVF
	1	I	

SEQ	I b 32 3		
ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO.	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	residue of	S=Serine, T=Threonine, V=Valine,
l	i	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sedneuce	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	ļ		KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
	1		VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAQAI
į.	l.		FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
i .	1		TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
			ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
L	<u> </u>		HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6249	56	1773	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI
Į.	1		AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL
i	ì		ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP
1	1		SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII
}			LNLVMVGLVSRLWVLYKGVLKRLILLYBPLFGLLQEVARIQPMP
1	1		YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF
1	1		LINEQSPRASEETLLGISKKAKQMKINVQNNVDLGQPVKNKRVF
1			KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
Į.	1		VIGTPHAKSFVQRFREAESFTQLSEEIQMAVVWCRSKKLKAQAI
ł .	i l		FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
1			TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
	i ·		ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
1			HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6250	232	1306	LAALHIMALPFRKDLEKYKDLDEDELLGNLSETELKQLETVLDD
ł	{		LDPENALLPAGFRQKNQTSKSTTGPFDREHLLSYLEKEALEHKD
			REDYVPYTGEKKGKIFIPKQKPVQTFTEEKVSLDPELEEALTSA
ł			SDTELCDLAAILGMHNLITHTKFCNIMGSSNGVDQEHFSNVVKG
l			EKILPVFDEPPNPTNVEESLKRTKENDAHLVEVNLNNIKNIPIP
ŀ			TLKDFAKALETNTHVKCFSLAATRSNDPVATAFAEMLKVNKTLK
i			SLNVESNFITGVGILALIDALRDNETLAELKIDNQRQQLGTAVE
			LEMAKMLEENTNILKFGYQFTQQGPRTRAANAITKNNDLVRKRR
			VEGDHO VEGDHO
6251	62	972	TPGSGPMSAWAAASLSRAAARCLLARGPGVRAAPPRDPRPSHPE
l			PRGCGAAPGRTLHFTAAVPAGHNKWSKVRHIKGPKDVERSRIFS
1			KLCLNIRLAVKEGGPNPEHNSNLANILEVCRSKHMPKSTIETAL
			KMEKSKDTYLLYEGRGPGGSSLLIEALSNSSHKCQADIRHILNK
1			
l			NGGVMAVGARHSFDKKGVIVVEVEDREKKAVNLERALEMAIEAG
Į			AEDVKETEDEEERNVFKFICDASSLHQVRKKLDSLGLCSVSCAL
6252	27	1897	EFIPNSKVQLAEPDLEQAAHLIQALSNHEDVIHVYDNIE
	- "	107/	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
[[ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
			PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR
			KLPHSKAKTRSRLEVARAREEETSIKAARSELLLAEEPGFLEGE
			DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG
			RHLAFGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL
			AVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFLLATASE
			TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
	†		TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
'			KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA
			GQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT
]		SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPARLIC
			LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
ĺ	Ì		SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS
			ALDRFVR
6253	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
			ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
	ĺ		PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR
			KLPHSKAKTRSRLEVAEABEEETSIKAARSELLLAEEPGFLEGE
l]		DGEDTAKICOADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG
	ļ		RHLAFGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	ooguunio	\=possible nucleotide insertion)
	Doguesia		AVAONRWLHIYDNOGIELHCIRRCDRVTRLEFLPFHFLLATASE
Ì		<u> </u>	TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
		{	TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
\		[KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA
1		j	GOGKASPPSLEOPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT
Į.	1	ì	SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPAELIC
]	ļ		LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
I	l .	İ	SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS
1	}		ALDREVR
6354	100	1139	HALGREGGSOELSAAACGCFALRLEAPGSGRPALAPGAAAFAGL
6254	155	. 1139	GGAPRFPPRGSAAGCGCFALKEKAPGSGRPALAPGAAAFAGU
1	ł		SHEOSDRGEGVEVVONEPFEDPHHGNGQFTEKRVYLNSKLPSWA
1		1	RAVVPKIFYVTEKAWNYYPYTITEYTCSFLPKFSIHIETKYEDN
1	1	1	KGSNDTIFDNEAKDVEREVCFIDIACDEIPERYYKESEDPKHFK
1	1	1	SEKTGRGQLREGWRDSHQPIMCSYKLVTVKFEVWGLQTRVEQFV
i	1	1	HKVVRDILLIGHRQAFAWVDEWYDMTMDDVREYEKNMHEQTNIK
	Ì		VCNOHSSPVDDIESHAOTST
6255	1	1444	PTRPOOELLVSLATVIFVASOKALSVESKAVIKQOLESVSNGWT
6255	1	1444	VYRIAROASRMGNHDMAKELYOSLLTOVASKHFYFWLNSLKEFS
			HAEQCLTGLQEENYSSALSCIAESLKFYHKGIASLTAASTPLNP
1		Ì	LSFQCEFVKLRIDLLQAFSQLICTCNSLKTSPPPAIATTIAMTL
1		İ	GNDLQRCGRISNOMKQSMEEFRSLASRYGDLYQASFDADSATLR
j		1	NVELQQQSCLLISHAIEALILDPESASFQEYGSTGTAHADSEYE
1		{	RRMMSVYNHVLEEVESLNGKYTPVSYMHTACLCNAIIALLKVPL
			SFORYFFOKLOSTSIKLALSPSPRNPAEPIAVQNNQQLALKVEG
Ì		1	VVOHGSKPGLFRKIQSVCLNVSSTLQSKSGQDYKIPIDNMTNEM
			EQRVEPHNDYFSTQFLLNFAILGTHNITVESSVKDANGIVWKTG
ļ	1	Į.	PRTTIFVKSLEDPYSQQIRLQQQQQQPLQQQQQRNAYTRF
6256	1	1542	CRGAGAEPAANPRSPRSLVPSLESTSTSVPPAPGTMATDSWALA
0250	1 -	1342	VDEOEAAAESLSNLHLKEEKIKPDTNGAVVKTNANAEKTDEEEK
Į.	1	Į.	EDRAAOSLLNKLIRSNLVDNTNQVEVLQRDPNSPLYSVKSFEEL
	1		RLKPQLLQGVYAMGFNRPSKIQENALPLMLAEPPQNLIAQSQSG
1	1	1	TGKTAAFVLAMLSQVEPANKYPQCLCLSPTYELALQTGKVIEQM
	1 ,		GKFYPELKLAYAVRGNKLERGQKISEQIVIGTPGTVLDWCSKLK
			FIDPKKIKVFVLDEADVMIATQGHQDQSIRIQRMLPRNCQMLLF
1			SATFEDSVWKFAQKVVPDPNVIKLKREEETLDTIKQYYVLCSSR
1	1		DEKFOALCNLYGAITIAOAMIFCHTRKTASWLAAELSKEGHQVA
Į.	İ		LLSGEMMVEQRAAVIERFREGKEKVLVTTNVCARGIDVEQVSVV
1			INFDLPVDKDGNPDNETYLHRIGRTGRFGKRGLAVNMVDSKHSM
ł			NILNRIQEHFNKKIERLDTDDLDEIEKIAN
6357	210	615	AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE
6257	410	673	NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI
l		•	TAEIKRYESOLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG
1			KA
6359	210	615	AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE
6258	210	615	NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI
1			TAEIKRYESOLRDLEROSEOORETLAQLQQEFQRAQAAKAGAPG
i	1		
6350	ļ	1540	KA
6259	2	1540	ILEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV
1		1	SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII
1			SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDQKRNAI
1			NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK
1			YNECGRIFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH
1			QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD
Į.			KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTQLRRAHT
1	l	i	GEKTFECGECGKTFWEKSNLTQHQRTHTGEKPYECTECGKAFCQ

Degimning nucleotide location corresponding contion corresponding control contro	SEQ	Predicted	Predicted end	Amino acid coment control
NO: mucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence	_		**	Amino acid segment containing signal peptide
coxtesponding	1 .		1	Glutamic Acid R-Phonylol-sine Collection
Corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence S-Serine, T-Threonine, V-Valine, M-England S-Equence S-Serine, T-Threonine, V-Valine, M-England S-Equence S-Serine, T-Threonine, V-Valine, M-England S-Equence S-Serine, T-Threonine, V-Valine, M-England S-Equence S-Serine, T-Threonine, V-Valine, M-England S-Equence S-Serine, T-Threonine, V-Valine, M-England S-Equence S-Serine, T-Threonine, V-Valine, M-England S-Equence S-Serine, T-Threonine, V-Valine, M-England S-Equence S-Serine, M-England	1	i		H-Wistidine T-Toolougine V I-wine
to first amino acid residue of amino acid residue of amino acid amino acid amino acid sequence Refirence Refirence Ref				LeLeucine M-Methionine N-Acromatine
amino acid residue of amino acid sequence solvence sequen	ļ			P=Proline O=Glutamine P-Arginine
residue of amino acid sequence (adon, /possible nucleotide deletion, /possible nucleotide deletion, /possible nucleotide deletion, /possible nucleotide insertion) REPHITMIQUENTICER PYEKCE(CARTECVESNITERIORITICER) FOR ACOMITY OF THE PROPERTY OF THE PROP	1		1	S=Serine T-Threonine V-Voline
sequence Codon, /-possible nucleotide deletion, /-possible nucleotide dinsertion	1	residue of	1	Watryotophan, Yatryosine Yalinknown tacton
Sequence Apossible nucleotide insertion		amino acid		Codon. /=possible nucleotide deletion
KPHLTINIQRTHITGER YYECKGCKTFCVKSNLTHEIGRTHTGERP (1	sequence		\=possible nucleotide insertion)
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SPACEPCRPDFAFRRALLLIRSGPRSAPATIGKPALKGQPGPWPG MAEVSIDGSKLEGVEKVCRDPALVLAGLOGE TEHTLAS NVORNRIJORGHIJOVAKGLOGEBLIKADAGLOKYYKDLEQODCE IA OBIQEKLAIEAERRRIQEKKDEDIARILQEKELQEEKKRKKHPP EFPATRAYADSYYYEDGGMKPRWAKEAVSTPSRMAHRDGSWYDA EIRAKLQEBELLATQVDWRAAQVAQDEEIARLIMAEEKKAYKKA KERKKSSLDKRRQDPEWKPKTWAKAANSKSKEDDEPHISKMERPA RPPPPTIMTDGBDADTHFTINQSSTRHFSKESSSHKGFHYKH 6262 2 1759 PECHSGOLCSVHRPGKVPOAMSKLOGRDEPAGHRLISGELIL GSTELVSGGLEALRSHDAVLQSISGTIECLQOGHBEGGLYHEK ARQLRRSMENIELGISEAQVMLALUGGDEPAGHRLISGELIL GSTELVSGGLEALRSHDAVLQSISGTIECLQOGHBEGGLYHEK ARQLRRSMENIELGISEAQVMLALUGGDEPAGHRLISGELIL CQENQWLRDELAGTQQRLQRSEQAVAQLEEEKKHLEPIGQLRQ YDEDGHISBEKBGDATKDSLDDLFPRNEEEDPSNCLERGGGATA AQGGGVEIPARLRTHHINLVIQYARGYKSVAPLKCQALEDLER TSGRGHEDVATMLINLALLVYEDGNKYKEAHLLINDALSIRESTL GPDHPAVAATLINILAVYENGGKYAPERVENYVORALLAIPRESTL GPDHPAVAATLINILAVYENGGKYAPERVENYVORALLAIPRESTL GPDHPAVAATLINILAVILYGKGKYAPERPLICGRALETREVLGT NHIPDVAKGINNIALLCONGGKYEAVERYYQRALAIPREGGGPON PNVARTKINILASCIVKGGKYAPERKEPLICGRALETREVLGT NHIPDVAKGINNIALLCONGGKYEAVERYGGFSVAPUENSGGDSTUQR SGSLGKIRDVURR FELDSSCRTSGEGFGDSVKFREGGBASVAVENSGGSGSTUQR SGSLGKIRDVURR FELDSSCRTSGEGFGDSVKFREGGBASVAVENSGGSGSTUGR GSGLGKIRDVURR FELDSSCLGFGCSSEKNIKURADPILSTRTDSTPCT LEVRCSMPSVICEHTKGFGTISEESNGGSLLTVPGGTSFSPKP EVFSNVPERDLSNNVSNIHISSFATSGANSKYVSARNILIKNT APVNTVMDSPVHLEPSSQVGVIGNKSMEMPUDRIETISTRDFIC PNSNI PDQSSLGGFGCNSEKNUKLABADELSLRQTELPGNSCAQ DPASFMPPQQPCSPPSQSLSDARSISKHMSLSYVAMQBEGILQQ KNAVQIISSALDTDNESTKDTENTFVLGDVKTDAFVPVYSSST IQEASFNPFKAYTILPVLPSSKOPUENDSDASTGLNTNYAMPSKLTIK SSSGHEVENSTIDTQVISHEKENKLESUVLTHLSRCDSDLCEMN AGMYKGNLNEODPHKPTKKKLEENAEDDKTENO PROMTENNANTMA NGKGILASCTLLSEKDSSSSSPREDESSGOSILSISLENISQ QSTQPEMHKYGGLVKVELEENAEDDKTENO PROMTENNANTMA NGKGILASCTLLSEKDSSSSSPREDESSGOSILGTRUTDHPTKKK VSSVPOPPUQVSPSLLQAKEKTQGSLAAIVDSLKLDEIQPYSSER ANPYPEYLHIRKKIEEKKLLCSVI PQAPQYVBDYTPTNGSYLL DONPLSKICITTITPPSSLSDPLKEDIFRQGEVVENKURQHSIE REKLIVSNEGSVLRVHYRAARTLANOTLPFSSCTVLLDAEVYNV PLDSGSDDSKTSVRORRNARAPGMWDDKFFIKKTCLLMRG QHEAALANAVQRLEWQLKLQELDPATYKSISIYSIQEFYVPLVD VNDDFELTPI WHOOVPHRKYB	6261	3	1188	
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NVORNRIJOHOLOVARIOLOGEELIKAROLOGEELIKAROLOGEELIKA GEIGEKAI FERBERR TOEKIGETARILOGEELGEKKRKHEP EFPATRAYADSYYYEDGGMEPRIMKEAUSTPSRMAHROQEMYDA ETARKLOGEELLATQVDMRAQOVAQDEETARLIMAEEKKAYKKA KEREKSSLDKRKQDEWKEAVAKAANSKSKSDEPHISKNERPA REPENTRAYADSYYYEDGGMEPRAKAANSKSKSDEPHISKNERPA REPENTRAYADSYYYEDGGMEPRAKAANSKSKSDEPHISKNERPA REPENTRAYADSYYYEDGGMEPRAKAANSKSKSDEPHISKNERPA REPENTATOEDGADYTHETTNOQSSTHEPSKEESHKOFHYKH GETKUNGOGEELIKA GETKUNGOGLEALRESHQAVLQSISGTTECLQOGGHEEGLVHEK ARQURRSMENIELGISAQVMLASHISTYDESEKOKLRAQVER LCQENQUALRELKHLEPLGQLROW YDEDGHTSEEKEGDATKDSLDDLPFNEEEEDPSNGLSGGGATA AQQGGYEIPARIRTILINIJVIQYAQGRIVEVAVPLCKQALEDLER TSGRGHEDVATHINILAVYARQGRIVEARPLCKQALEDLER TSGRGHEDVATHINILAVYARQGRIVEARPLCKQALEDLER TSGRGHEDVATHINILAVYARQGRIVEARPLCKGALETIREKVLGT NHEDVAKQLINILAVLYCKGKARABPLCVKKABPLCQRALETIREKVLGT NHEDVAKQLINILAVLYCKGKARABPLCVKKABPLCQRALETIREKVLGT NHEDVAKQLINILAVLYCKGKARABPLCVKKABPLCQRALETIREKVLGT NHEDVAKQLINILAVLYCKGKARABPLCVKKABPLCQRALETIREKVLGT NHEDVAKQLINILAVLYCKGKARABPLCVKALETIRECGTDYSGVKACKVSSPTV NTTLRINGALYRGCGKLEARFLECALISRERGCTDPISGTKVA ELLGESDGRRTSQEGGGDSVKPEGGEDASVAVEWSCDGGGTLQR SGSLGKIRDVLRR ELLGESDGRRTSQEGFDGSVKFEGGEDASVAVEWSCDGGGTLQR SGSLGKIRDVLRR FELLGESDGRRTSQEGFDSVKFEGGEDASVAVEWSCDGGGTLQR SGSLGKIRDVLRR FELLGESDGRRTSQEGFDSVKFEGGEDASVAVEWSCDGGGTLQR FOLGENTY STATEMPT OF NON 19DOBSSLGSFONSENKVKRAKVSADRILIKNT APVATVMDSPVILLEPSQUGVIQNKSWBMPDDRLETLSTRDPIC PNSN 19DOBSSLGSFONSENKVKRANDPSLIGATELPONSCAQ DPASFMPPQOPCSPSPGGLISDAESISKHMSLSVVANQEPGILQQ KNAVQIISSALDTDNESTROTENTFULDOVRITARVEPTYSDST 1QEASNPEKATTLEVLSESEKDFRNSDASTQLINTARPSKLTYK SSSGHEVENSTDTOVISHEKENKLESLVUTHLSRCDSDLCEMM AGMPKONLNEODPKICPSSEKTLSTEDBSGGSTLSSLENNSQ QSTQPEMHKYGGLVKVELBENAEDDKTENQIPQRTRARATMAM NOSKGILASCTLLSKOSESSPRITATEDDPOTHIPRKRK VSRVPQDPUQVSPSLLQAALVDSLKLDEIQPYSSER ANDYFEYLHIKKIEEKKLLCSVIPQAPYDEVTYTRGSYLL DCRYGSDDKKTSVERDRRARAFMSMLODVDKKPDGVIKKTCLIMRQ QHEAAALNAVGRLEKPRLYRABATLANOTLPSACTVLLDAEVYNV PLDSGDDSKTSVERDRRARAFMSMLODVDKRPSLKKTLLIMRQ QHEAAALNAVGRLEKPRUNGLEBUVANDFALKILGRI EREKLUSADDSLICHTARGELVANDFALKILGRI VVIDDFELIPI	1			
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EFPATRAYADSYYYEDGGKPRWKEAUSTESRAHENDGEWTDA EIARKLOEBELLATOYUMRAADODE IARLIWABEKKAYKKA KEREKSSLDKRKQDPEWKPKTAKAANSKSKESDEPHHSKNERPA RPPPPIMTOEDADYTHFTNQGSSTRHFSKESSHKGFHYKH 6262 2 1759 PECHSOGGLESVHFGKFVFQARNSGLVLGGREPFAGHLSGUELL GSTELVSOGLEALRSHHQAVLQSISQTIECLQOGGHEEGLVHEK ARQLERSMENIELGLSEAQVMLASHISGHTSECLQOGGHEEGLVHEK ARQLERSMENIELGLSEAQVMLASHISGHTSEKOKLRAQVER LCQENQULRDELAGTQQRLQRSEQAVAQLEBEKKHLEFLGQURQ YDEDGHTSBEKEGDATKDSLDDLFFNEBEBPSNGLSRGGGATA AQGGYEIPARLETHINLVIVQAAQGRVEVAVPLCKQALEDLER TSGRGHEDVATMINILALVYRDQNSYKEAAHLIMDALSTRESTL GPDHPAVAATLINALAVLYGKGKYAEAHLINTAHLSGQLGDDN PNVARTKNNILASCYLKQGKYAEAHTLYKRLITRAHVQERGSUDD HEKPIMHAEEREEMSKSHHESGTPYAEYGGWKACKVSSTVV NTTLRNILGALYRRQGKLEAAETLEECALRSRGCGTDFISGTKVA ELIGESDGRTTSGCGFGDSVKFEGGGDASVAVEWSGDGSGTLQR SGSLGKIRDVLRR 6263 1 2408 RELDSLADLFERIKPPYANGLSTSHLRSSSVEDVKLIISEGRPT IEVRRCSMESVICBHTKOFQTISESSNGGSLLTVPGGTSPSSKP EVVSNVPERBLSNVSNIHISSFATSFTGASNSKYVSADRNILINT APVNTYMDSFYWLIEDSQUGYGNSWEMPUPDLETLSTRDFIC PNSNIPDGSSLQSFCNSENKVLKKNADFISLROTELPGNSCAQ DPASFMPPQQPCSFPSQSLSDAESISKHMSLSYVANQEPGILQQ KNAVQIISSALDTDNESTKDTENTFVLGDVQKTDAFVPYYSDST IQEASFNFEKAYTLEVLISEKDFNGSDASTQLNTHYAFSKLTYK SSGHEVENSTTDTVQVISHEKENKLESLVITHLSFCDSDLCEMN AGMPKONLINGOPPKICPBSEKCLLSIEDBESQGS ILGSLENHSQ CSTOPBMHKYQGLVKVELBENAEDDKTENQIPQNFTRNKANTMA NQSKQILASCTLLSEKDSESSSPRGTRLTEDDDPQTHHPRKRK VSRVPQPVQVSPSLLQAKEKTQQSLAAIVDSLKLDBIQPYSSER ANSYFSYLJHIRKKLEEKKKLLCSPQQSVVARMLRCHSHIE PRELIVSNDSEVLRYHYRAARTLANOTLPFSACTVLLDAEVYNV PLDSGSDDSKTSVRDRRNARGFMUQDVDKRFDKLTCLLMRQ QHEAAALNAVQRLEWQLKLQELDPATYKSISTEQEFYVPLVD VNDDFELTFI REKLIVSNDSEVLRYHYRAARTLANOTLPFSACTVLLDAEVYNV PLDSGSDDSKTSVRDRRNARGFMSUQDVDRKDRLKTCLLMRQ QHEAAALNAVQRLEWQLKLQELDPATYKSISTEQEFYPLVLVD VNDDFELTFI KHGGENNALDMAPBIHMTGPMCLIENTNGELVANPEALKKILSAT TQPVVVVAIVGLYRTGKSYLMNKLASKNKGFSLGSTVKSHTKGII WMCVPHFKCEEHTLVLULDTEGLOUKKGDNQMDSWIFTLAVLL	1			QEIQEKLAIEAERRRIQEKKDEDIARLLQEKELQEEKKRKKHFP
KEREKSSLDKRKQDPEWFKTYAKAANSKSKESDEPHHSKNERPA RPPPPINTDGBDADYTHFTNOGSTRIPFSKESSHKGHYKH 6262 2 1759 PECHSOGLCSVHRPGKVFQARMSGLVLGGRDEPAGHRLSQEUL GSTKLVSGGLEALRSHKQAVLQSISGYTIECLQQGGHEEGLVHEK ARQLRSMENIELGLSEAQVMALLASHLSTVESEKOKLKAQVRR LCQENQHLRDELAGTQQRLQRSEQAVAQLEEEKKHLEPLGQLRQ YDEEDGHTSBEKEGDATKDSLDDLPPNEEEBDPSMGLSRGQGATA AQQGYEIPARLRTLHNLVIQYAAQGRYEVAVPLCKQALEDLER TSGRGHEDVATMLNILALVSKRGKYKEAHALLINDALSIRESTL GPDHPAVAATINALALVIGKRGKYKEAHALLINDALSIRESTL GPDHPAVAATINALALVIGKRGKYKEAHALLINDALSIRESTL HPDVARQLMNILALLCONQCKYEAVERYQRALAIYEGGLGPDN PNVARTKNNLASCYLKGGKVAEABRILVKEILTHAHVQEEGSVDD DHK9IWHAEEREEMSKSRHHEGGTPYAEYGGWYKACKVSSPTV NTTLRNLGALYRRQGKLEAAETLEECALRSRRGGTDPISQTKVA WHEN SEGLIGSTGRTSGGEGGDSVAVEWSGGGSGTLQR SGSLGKIRDVLRR RELDSLADLEPERIKPPYANGLSTSHLRSSSVEDVKLIISEGRPT IEVRRCSMPSVICEHTKQPQTISEESNQGSLLTVVGDTSFSFKP EVFSNVPERDLSNVSNIHSSFATSPTGASNSKXVSADRNLIKNT APVNTVMDSPVILEPSSQVGVIQNKSWEMPUDRIETISTPPIC PNSNIPDQESSLQSFCNSENKVLKENAADFLSLRGTELPONSCAQ DEASFMPPQOPCSFPSGSLSSEIGKMPLSEVANQBERGIQQ KNAVQIISSALDTDNESTKDTENTFVLGDVQKTDAFVEVYSDST IQEASINFERATTLEVULPSEKDFNGSDASTQLNTHYAPSKLTYK SSSGHEVENSTIDTOVISIEKEKKLESLVLITHISRCDSDLCEMN AGMPKGNLNEODPKHCPESEKCILISIEDESQQSLLSLESLENHSQ OSTOPEMHYKGQLVKVELEENDEDDFTGENITHISRCDSDLCEMN AGMPKGNLNEODPKHCPESEKCILISIEDESQQSLLSLESLENHSQ OSTOPEMHYKGQLVKVELERADDDFTGNITHISRCDSDLCEMN AGMPKGNLNEODPKHCPESEKCILISIEDESQQSLLSLESLENHSQ OSTOPEMHYKGQLVKVELERADDDFTGNITHISRCDSDLCEMN AGMPKGNLNEODPKHCPESEKCILISIEDESQQSLUNTHYAPSKLTYK VSRVPQPVQVSPSLLQAKEKTQQSLAAIVDSLKLDEIQPYSSER ANDYFSYLLIKKKIEEKKRLLCSVIPQAPQYVDEVYTNEGSYLL DGMPLSKICIPTITPPPSLSDPLKELFRQGEVVRNKLRLQHSIE REKLIVSNDGGVLVVVELERAGROFFANTANOTLPFSACTVLLDAFVYNV PLDSQSDDSKTSVRDFNARQFMSMLQDVDRFFEKLKTLLMRQ QHEAAALANQRLEWQLKLQELDPATYKSISIYEIQEFYVPLVD VNDDFFELTTI DGMPLSKICLEPTITPPPSLSDPLKELFRQGEVVRNKLRLGHSIE REKLIVSNDGGVLRVVELRARGFMSMLQDVDRFFEKLKTLLMRQ QHEAAALANQRLEWQLKLQELDPATYKSISIYEIQEFYVPLVD VNDDFFELTTI G264 143 1960 KHRQENNALDMAPEIHMTGPMCLIENTNGELVANDEAGLKILSAT TQPVVVVAVGPHPKKEPBHTLJVLLDTBGLGDVKKGDNONSWIFTLAVLL	1			EFPATRAYADSYYYEDGGMKPRVMKEAVSTPSRMAHRDQEWYDA
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PECHSOGLCSVHRPGKVPQARMSGLVLGGRDEPAGHRLSQEELL GSTRLVSQGLEALRSHQAVVQSLSQTIECLQQGGHEEGLVHEK ARQLRRSMENIELGLSEAQVMLALSHLSTVESEKQKLRAQVRR LCQENQMLRDELAGTQQLLQRSBGDVAQLEERKHLEPIGQLRQ YDEDGHTSBERGGDATNOSLDDLPNNEEEDPSNGLSRAGQATA AQQGYEIPARLRTLHNIVIQYAAQGRYEVAVPLCKQALEDLER TSGRGHEPVATMLANILALVYRDQMYKKEAAHLLINDALSIRESIL GPDHPAVAATILNILALVYRKGKKYKEAEPLCQRALEIREKVLGT MHPDVAKQLINILALLCONOGKYEAVERYYQRALAIYEGQLGPDN PNVARTKINILASCYLKQGKYAEAEPLCYRALEIREKVLGT MHPDVAKQLINILALLCONOGKYEAVERYYQRALAIYEGGLGPDN PNVARTKINILASCYLKQGKYAEAEPLCYRALEIREKVLGT MHPDVARGLENAGSKERABETLEEGALRSRRQGTDPISQTKVA ELLGSSDGRRTSQGEPGDSVKFEGGEDASVAVEWSGDGSGTLQR GSLGKIRDVLRR 6263 1 2408 RELDSLADLEFRIKPPYANGLSTSHLRSSSVEDVKLIISEGRPT IEVRCSMPSVICHTKGFQTISEBSNQGSLLTVFGGDTSPSFKP EVFSNVERDLSNVSNIHSSFATSPTGASNSKYVSADRNLIKNT APVNTVMDSPVHLEPSSQVGVIKKSMEMPVDRIETLSTRDFIC PNSNIPPOGESSLQSFCNSENKVLKSMEMPDRIETLSTRDFIC PNSNIPPOGESSLQSFCNSENKVLKSMEMPDRIETLSTRDFIC PNSNIPPOGPSSLQSFCNSENKVLKSMEMPDRIETLSTRDFIC PNSNIPPOGPSSLQSFCNSENKVLKSMEMPDRIETLSTRDFIC PNSNIPPOGPSSSQSSLSDASSISKHMSLSVVANQEBGILQQ KNAVQIISSALDTDNESTKDTENTFVLGDVQKTDAFVPVVSDST IQEASPHPERAYTLPVLPSEEDFRGSDASTGLNTHYAFSKLTYK SSSGHEVENSTTDTQVISHEKENKLISSLVLTHLISCDSDLCEMN AGMPKGHLINGDPKHCPESEQGSILVISTLSCDSLGEMN QGRQFKGHLINGDPKHCPESEQGSILVISTLSCDSLGEMN QGRQFKGHLINGDPKHCPESEQGSILVISTLSCDDLCEMN AGMPKGFULTSCOPPSLQAKERTQGSLAIVDSLKDELQPYSSER ANPYFEVLHTRKKIEEKRKLLCSVIPQAPQYYDEYVTFNGSYLL DGNPLSKICIPTITPPPSLSDFGRIRLITEDDDPQIHHPRKRK VSSVQPDFVQVSPSLLQAKERTQGSLAIVDSLKDELQPYSSEL ANPYFEVLHTRKKIEEKRKLLCSVIPQAPQYYDEYVTFNGSYLL DGNPLSKICIPTITPPPSLSDFACTVLLDBETYVPLVD PLDSGSDBSKTSVRDRNARGFMSWLQDVDDKFPKLKTCLIMRQ QHEAAALNAVQRLEWQLKLQELDPATYKSISTYLEIQEFYVPLVD VNDDFELTII FERLITSNEGEVLRVHYRAARTLANOTLPFSACTVLLIDETYVPLVD VNDDFELTIT				KEREKSSLDKRKQDPEWKPKTAKAANSKSKESDEPHHSKNERPA
GSTRLVSGGLEALRSHAQAVLQSISQTIECLQQGGHEEGLVHEK ARQLRRSMENIELGLSEAQVMLALSHLSTVESEKQKLRAQVRR LCQENGMLRDELAGTQQLQRSBQAVAQLEBEKKHLEHGQLRQ VDEDGHTSBEKEGDATKDSLDDLPPNEEEDPSNGLSRGQGATA AQQGYEIPARLRTHNIVIQYAAQGRYEVAVPLCKQALEDLER TSGRGHPVATMLNILALVYRDQNSYKEAAHLINDALSIRESTL GPDHPAVAATINNILAVYRDQNSYKEAAHLINDALSIRESTL GPDHPAVAATINNILAVYRDQRKYKEAFELCORALEITEKKVLGT NHPDVAKOLNILALLCONGKYEAVERYYQRALAIYEGGLGPDN PNVARTKNNLASCYLKQGKYAAEABTLYKEILTRAHVQEFGSVDD DHKF IMMHAEEREEMSKSRHHEGGTPYAEYGGWYKACKVSSBTV NTTIRNICAGLYRRGGKLEAARTLEECALRSRRQGTDPISQTKVA ELIGESDGRRTSQBGFGDSVKFEGGEDASVAVEWSGDGSGTLQR SGSLGKKRDVLIRR 6263 1 2408 RELDSLADLPERIKPPYANGLSTSHLRSSSVEDVKLIISEGRPT IEVRRCSMPSVICHTKOFOTISEENQGSLLTVVGDTSSFSKP EVPSNVPERDLSNVSNIHNSSFATSPTGRANSKYVSADRNLIKNT APWNTVMDSPYHLEPSSQVGVIQNKSWEMPUDRLETLSTRDFIC PNSNIPDQESSLQSFCNSENKVKLKENADFLSLRGTELFGNSCAQ DPASFMPPQQPCSFPSSGSLSDABEISKMSLSYVANQBEPGILQQ KNAVQIISSALDTDNESTKDTENTFVLGDVQKTDAFVPVYSDST IQEASPMPEKAYTLPVLPSEDFNGSDASTQLNTHKYAFSKLTYK SSSGHEVENSTTDTQVISHEKENKLESLVLTHLSRCDSDLCEMN AGMPKGNLNBQDPKHCPESEKCLLSIEDESSQOSILSSLENHNSQ QSTQPEMHKYGQLVKVELEEMAEDDKTENGT PQMMTKKANTMA NGSKGILASCTLLSEKDSESSSPRGRIRLTEDDDPQIHHPRKRK VSRVPQDPVQWSPSLLQAKEKTQGSLAAIVDSLKLDEIQPYSSER ANPYFFYLHIRKKIEEKRKLLCSVIPQAPQYYDBYVTPNGSYLL DCMPLSKICTPTITPPSLSDPLKELFRQQEVVMKLRLQHSIE REKLIVSNEGBVLRVHTKAARATLANOTLPFSACTVLLDAEVYNV PLDSGSDDSKTSVRDRFNARQFMSWLQDVDDKFDKLKTCLLMRQ QHEAAALNAVQRLEWGLKLQELDPATYKSISIYEIQEFYVPLVD VNDDFBLITPI 6264 143 1960 KRRQENNALDMAPEIHNTGPMCLIENTNGELVANPEALKILSAI TQPVVVAIVGLYRTGKSYLIMKKLAGKNKGFSLGSTVKSTKKGI WMWCVPHPKKPBHTULLIDTGGLGDVKKKGNNQNDSWIFTLAVLI MWCVPHPKKPBHTLULLIDTGGLGDVKKKGNNQNDSWIFTLAVLI MWMCVPHPKKPBHTULLIDTGGLGDVKKKGNNQSTVKSTTKKGI MWMCVPHPKKPBHTULLIDTGGLGDVKKKGNNQNDSWIFTLAVLI MWMCVPHPKKPBHTULLIDTGGLGDVKKKGNNQNDSWIFTLAVLI MWMCVPHPKKPBHTULLIDTGGLGDVKKKGNNQNDSWIFTLAVLI				RPPPPIMTDGEDADYTHFTNQQSSTRHFSKSESSHKGFHYKH
ARGIRRSMENTELGISEAQVMALAISHISTUSEKKOKIRAQVRR LCQENQWIRDELAGTQQRIQRSBQAVAQLEEEKKHLEPLGQLRQ YDEDGHTSEEKEGDATKDSLDDLFPNEEEEDFSNGLSRGQGATA AQGGYETPARLRTHHNLVIQVAAQGRYEVAVPLCKQALEDLER TSGRGHPDVATMINILALVYRQDNKYKEAAHLLNDAISIRESTL GPDHPAVAATINNLAVLYGKRGKYKEAAHLLNDAISIRESTL GPDHPAVAATINNLAVLYGKRGKYKEAAHLLNDAISIRESTL GPDHPAVAATINNLAVLYGKRGKYKEAAPLLNDAISIRESTL GPDHPAVARTINNLASCYLKGGKYAEABTLKKELUTRAHVOEFGSVDD DHKP HWMIAEREEMSKSRHHEGGTPVAEYGGWYKACKVSSPTV NTTLRNLGALYRRGGKLEAAETLEECALRSRRGGTDDISGYKVA ELIGESDGRRTSQEEGFGSVKFEGGEDAVAVEWSGDGSGTLQR SGSLGKIRDVLRR 6263 1 2408 RELDSLADLPERIKPPYANGLSTSHLRSSSVEDVKLIISEGRPT IEVRRCSMESVICEHTKOPGTISEESNQGSLLTVPGDTSPSPKP EVFSNVERDLSNVSNIHSSFATSPTGASNSKYVSADRNLIKNT APVMTVMDSPVHLEPSSCVGVGVIQNKSWEMPVDRIETLSTROFIC PNSNIPDQESSLQSFCNSENKVLKRADFISLRGTELFGNSCAQ DPASFMPPQQPCSPPSQSLSDABSISKHMSLSYVANQEBGILQO KNAVQIISSALDTDNESTADTENTFYLDDVKTDAFFVVYSDST IQEASPNFEKAYTLPVLPSEKDFNGSDASTQLNTHYAFSKLTYK SSSGHEVENSTTDTQVISHEKENKLESLVITHLSRCDSDLCEMN AGMPKGHLNBOPPKHCPSEKCLLSIEDESQOSILSSLENHSQ QSTOPEMHKYGQLVKVELEENABDDKTENQIPQRMTRNKANTMA NQSKQILASCTILSEKDSESSSPRGRIRLTEDDDPQTHHPKRK VSRVPQPVQVSPSLLQAREKTQQSLVAMLRIQHSIE ANPYFEVLHIRKKLEEKRLLCSVIPQAPQYVDEYVTPNGSYLL DGNPLSKICIPTITPPPSLESDPLKELFRQQEVVMKLRIQHSIE REKLIVSNEGBVLRVHYRAARTLANOTLPFSACTVLLDAEVYNV PLDSQSDDSKTSVRDRFNARQFMSWLQDVDDKFPKLKTCLLMRQ QHEAAALNAVQRLEWQLKLQELDPATYKSISIYEIQEFYVPLVD VNDDFELIPI 6264 143 1960 KHRQENNALDMAPBIHMTGFMCLIENTNGELVANPEALKILSAT TQPVVVVAJVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI WMWCVPHPKKPEHTLVLLDTBGLGDVKKGRONQNSWIFTILAVLL	6262	2	1759	PECHSOGLCSVHRPGKVPQARMSGLVLGQRDEPAGHRLSQEEIL
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ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT	<u> </u>			ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
140.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		amino acid	P=Proline, Q=Glutamine, R=Arginine,
	to first		S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	S=Serine, 1=infedime, v-value,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		1 2	\=possible nucleotide insertion)
	sequence		SOKDKNENLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE
	l	1	ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
	1	1	INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ
	1	l	INAISRGDLPCMENAVLALAQIENSAAVQAATAATDQQAGQAVQ
	ŀ		LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFQKKLAAQL
	1		DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG
	ļ	1	YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL
	Į.		QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK
	1		EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER
)	1	EKSYORHYKOLTEKMERERAODBEOEKIDISKOSKIVI
	1	1	CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6265	143	1960	KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI
5265	1 -3-5	1	TOPWWWAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
	1	1	WMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAVLL
1	1	1	SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS
		1	ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT
İ	1	1	ADEADLA ALL CALLED SEDENTAL SELECT DIEDAL VOLENI ODE
1		1	SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE
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l	1	ı	L.PAETT.OELLDLHRVSEREATEVYMKNSFKDVDHLPQKKLAAQL
	i e	ļ	DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG
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}	1	1	EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER
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		1	CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6366	276	1421	GSHOKOMLVPCFLYSLONRKPSLYGSLTCQGIGLDGIPEVTASE
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GRTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GRTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLJVLSGGMDAOLKIWSAEDASCVVTFKGHKGGILDTAIVDR
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKINQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINIGSPEOMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVVADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LEIGSDAFNCCTFLSGFLLLAGTODGNIYQLDVRSPRAPVQVIH
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTODGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD
			GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD
6266	276	622	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL IGMMKKNNSAKRGPODGNOOPAPPEKVGWVRKFCGKGIFREIWK
			GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDOLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS
			GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFTVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK PSKKNHSKFTLAHSKOPGNTAPNLIFLAVSPEEKESWINALNSA
			GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA
			GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKINQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIGEEDPSPEEPTSLC
6267	3	622	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC UDBLCONLAGGLSSALIDNPLTLLLSIDTYWNLQEPVTFQDVAV
			GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC UDBLCONLAGGLSSALIDNPLTLLLSIDTYWNLQEPVTFQDVAV
6267	3	622	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLILIAGTODGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPUTFQDVAV DESPERWGLLGPTORTEYRDVMLETFGHLVSVGWETTLENKELA
6267	3	622	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQDGSCFTVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLISIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA
6267	3	622	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFTVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQFAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKOMESAORKDLPOKKHFDNRESOANSGALDTNQVSLQKIDNPE
6267	3	622	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFTVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLSITTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SOANSGALDTNOVLLHKIPPKRKRRDSQVKSMKHNSRVKIHQ
6267	3	622	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLSIDTYWMLQEPUTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCFROKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK
6267	3	622	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLSIDTYWMLQEPUTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCFROKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK
6267	3	622	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFFNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS
6267	3	622	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLILIAGTODGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPUTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GEPPFECOECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ
6267	3	622	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFFNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS
6267	3	622	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFTVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR
6267	160	1368	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFTVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQFAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DPSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS
6267	3	622	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFTVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLSITTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPRKRLSKOSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL TOVVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT
6267	160	1368	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFTVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLSITTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPRKRLSKOSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL TOVVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT
6267	160	1368	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT
6267	160	1368	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLSIDTYVMLQEPUTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN FDKACELWEGILODHPTDMLALKFSHDAYFYLGYQEQMRDSVAR
6267	160	1368	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGRIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR TVPFWTPDIDISSSVKGIYSFGLMETNFYDQABKLAKEALSINP
6267	160	1368	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCONLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQCSSSLTQHQRVHS GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKELDLAVKTMVEISRTQPLTRREQHLVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKEALSINP
6267	160	1368	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFTVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQFAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCONLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPKKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSHDAYFTJGYQEQMRDSVAR IYPFWTDIPLSSYVKGIYSFGLMETNFYDQAEKLAKEALSINP TDAWSVHTVAHIHEMKAEIKDGLEFMQHSETLWKDSDMLACHNY
6267	160	1368	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLQSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFTVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQFAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR IYPFWTPDIPLSSYVKGIYSFGLMETNFYQABKLAKEALSINP TDAWSVHTVAHIHEMKAEITYDTHILPSLQANDAMLDVVDSCSML VPLOMEGVSVGORWODVLPVARKHSRDHILLFNDAHFLMASLGA
6267	160	1368	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCONLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQEKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQCSSSLTQHQRVHS GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKELDLAVKTMVEISRTQPLTRREQHLVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKEALSINP

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine
- 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Ct
1	amino acid sequence	sequence	Codon, /=possible nucleotide deletion
	sequence :		\=possible nucleotide insertion)
ı			DGNPDRVLELLLPIRYRIVQLGGSNAQRDVFNQLLIHAALNCTS
6270	23	2086	SVAKNVARSLLMERDALKPNSPLTERLIRKAATVHLMO
ı	1	2000	SVTVTLGSEGDGRPPTYHLEEMEQEPQNGEPAEIKIIREAYKKA
-		}	FLFVNKGLNTDELGQKEEAKNYYKQGIGHLLRGISISSKESEHT
- }			GPGWESARQMQQKMKETLQNVRTRLEILEKGLATSLQNDLQEVP KLYPEFPPKDMCEKLPEPQSFSSAPQHAEVNGNTSTPSAGAVAA
			PASLSLPSQSCPAEAPPAYTPQAAEGHYTVSYGTDSGEFSSVGE
		ļ	EFYRNHSQPPPLETLGLDADELILIPNGVQIFFVNPAGEVSAPS
1			YPGYLRIVRFLDNSLDTVLNRPPGFLOVCDWLVDLVDDDCDVIV
1			CTAGAYMFPDTMLQAAGCFVGVVLSSFI.DEDDDEL FEDI I DOMG
1	1	1	DERLOANWIRAEEENEFOIPGRTRPSSDOLKEASGTDUVOLDOG
			NKDVKHKGKRGKRAKDTSSEEVNLSHIVPCEPVDEFVDVDI DPM
	İ		SEKVAHNILSGASWVSWGLVKGAEITGKAIQKGASKLRERIQPE
1			EKPVEVSPAVTKGLYIAKQATGGAAKVSQFLVDGVCTVANCVGK
			ELAPHVKKHGSKLVPESLKKDKDGKSPLDGAMVVAASSVQGFST VWQGLECAAKCIVNNVSAETVQTVRYKYGYNAGEATHHAVDSAV
1			NVGVTAYNINNIGIKAMVKKTATQTGHTLLEDYQIVDNSQRENQ
6271	30		EGAANVNVRGEKDEQTKEVKEAKKKDK
62/1	32	1058	GCGVKTAGMVGREKELS IHFVPGSCRLVEEPVN I PMPPVI ATTCA
1			TGLLGRAVHKEFQQNNWHAVGCGFRRARPKFEOVNLLDGNAVER
!			IIHDFQPHVIVHCAAERRPDVVENOPDAASOLNVDASCNLAKEA
i			AAVGAFLIYISSDYVFDGTNPPYREEDIPAPLNLYGKTKLDGEK
			AVLENNLGAAVLRIPILYGEVEKLEESAVTVMFDKVQFSNKSAN
			MDHWQQRFPTHVKDVATVCRQLAEKRMLDPSIKGTFHWSGNEQM TKYEMACAIADAFNLPSSHLRPITDSPVLGAQRPRNAQLDCSKL
- 6000			ETLGIGQRTPFRIGIKESLWPFLIDKRWRQTVFH
6272	1136	528	GAVMEDAAAPGRTEGVLEROGAPPAAGOGGALVELTETEGGLAT
1 1			VSPYHTHRAGDPLDLVALAEOVOKADEFTRANATNYTTYL A BOT
}			QHLQEQARKVLEDAHRDANLHHVACNIVKKPGNIVVIVVPECO
1 1			QIFSIISPKEWGTSCPHDFLGAYKLOHDLSWTPYEDIEKODAKI
6273	256	843	SMMDTLLSQSVALPPCTEPNFQGLTH
	1	043	SCPRVSPECRSLGCQVMFSLPLNCSPDHIRRGSCWGRPQDLKIA
			SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS
			ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME
6274			LAHVEHYAEVRDNTYCVLPT
02/4	56	1142	AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVCGEVEAUDM
	1		VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMAPALYOSI
1 1	İ		LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVEKKIINDKCD
1 1			DVFEPARAQFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS
1	}	1	AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED
1	}		LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTRBEVVS ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTDIYSI
1 1		i	SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA
6275			QSLHRVFQKS
02/3	20	565	SRRGRARCLARGSRRPVPRPAKTMAFMVKTMVGGQLKNLTGSLG
] [ļ	GGEDKGDGDKSAAEAQGMSREEYEEYOKOLVEEKMEDDAORTOD
!!	ļ	1	KAERATLRSHFRDKYRLPKNETDESOIOMAGGDVELDDELDVAL
			EEDTEEEEKASVLGQLASLPGLNLGSLKDKAQATLGDLKOSAF
6276	797		KCHVM
! !		31	TLLPLPPLPDTEGMILLNTGLEGTVAENPVPIVHTPSGMILTLE
			SCLQQLATHPGHWGIHLQIAEPAALRPSLALLARLSSLGLLHWP
		1	VWVGAKISHGSFSVPGHVAGRELLTAVAEVFPHVTVAPGWPEEV LGSGYREQLLTDMLELCQGLWQPVSFQMQAMLLGHSTAGAIGRL
	}	1	LASSPRATVIVEHNPAGGDYASVRTALLAARAVDRIRVYYRLPQ
			GYHKDLLAHVGRN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
2.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}		to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding		P=Proline, Q=Glutamine, R=Arginine,
1	to first	amino acid	
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 304	\=possible nucleotide insertion)
		L	MAFRIEMGLYYSYFKTIVEAPSFLNGVWMIMNDKLTEYPLVINT
6277	4600	2744	
1	1	ĺ	LKRFNLYPEVILASWYRIYTKIMDLIGIQTKICWTVTIGEGLSP
		Ť	TESCEGLGDPACFYVAVIFILNGLMMALFFIYGTYLSGSRLGGL
		ì	VTVLCFFFNHGECTRVMWTPPLRESFSYPFLVLQMLLVTHILRA
1	i	1	TKLYRGSLIALCISNVFFMLPWQFAQFVLLTQIASLFAVYVVGY
1		1	IDICKLRKIIYIHMISLALCFVLMFGNSMLLTSYYASSLVIIWG
l	l .	Į.	ILAMKPHFLKINVSELSLWVIQGCFWLFGTVILKYLTSKIFGIA
	Į		
	1	ł	NDAHIGNLLTSKFFSYKDFDTLLYTCAAEFDFMEKETFLRYTKT
1	1	\$	LLLPVVLVGFVAIVRKIISDMWGVLAKQQTHVRKHQFDHGELVY
	1	i	HALQLLAYTALGILIMRLKLFLTPHMCVMASLICSRQLFGWLFC
ļ	1	Į.	KVHPGAIVFAILAAMSIQGSANLQTQWNIVGEFSNLPQEELIEW
1	í		IKYSTKPDAVFAGAMPTMASVKLSALRPIVNHPHYEDAGLRART
i	1	I	KIVYSMYSRKAAEEVKRELIKLKVNYYILEESWCVRRSKPGCSM
ļ	1	İ	
1	1	li e	PEIWDVEDPANAGKTPLCNLLVKDSKPHFTTVFQNSVYKVLEVV
1	1	1	KE
6278	3	823	ILFRLVLLSLVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLLL
	l .		IRIILEYCQGVDNIPSVTTDMLTRLSDLLKYFNSRSCQLVLGAG
1		1	ALQVVGLKTITTKNLALSSRCLQLIVHYIPVIRAHFEARLPPKQ
1		1	YSMLRHFDHITKDYHDHIAEISAKLVAIMDSLFDKLLSKYEVKA
1	1	1	PVPSACFRNICKOMTKMHEAIFDLLPEEQTOMLFLRINASYKLH
	1	I	
1		1	LKKQLSHLNVINDGGPQNGLVTADVAFYTGNLQALKGLKDLDLN
	1	}	MAEIWEQKR
6279	127	1687	GGAMASDGARKQFWKRSNSKLPGSIQHVYGAQHPPFDPLLHGTL
1	<u> </u>	(LRSTAKMPTTPVKAKRVSTFQEFESNTSDAWDAGEDDDELLAMA
	l]	AESLNSEVVMETANRVLRNHSQRQGRPTLQEGPGLQQKPRPEAE
i	Ī	į.	PPSPPSGDLRLVKSVSESHTSCPAESASDAAPLQRSQSLPHSAT
Į.	1	1	VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELRR
	1	1	
Ì	1		LSWSGIPKPVRPMTWKLLSGYLPANVDRRPATLQRKQKEYFAFI
1	1	i	EHYYDSRNDEVHQDTYRQIHIDIPRMSPEALILQPKVTEIFER:
Į	l	ļ	LFIWAIRHPASGYVQGINDLVTPFFVVFICEYIEAEEVDTVDVS
1	}	[GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVKMLE
1.	j		ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIR
	İ		LWDTYQSEPDGFSHFHLYVCAAFLVRWRKEILEEKDFQELLLFL
1			QNLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYKK
L			
6280	857	2515	ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEDE
1	1	1	DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA
1	1		WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA
1	1		QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS
1	1		YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA
1	1	1	RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD
	l l	1	
1	1	l	LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ
l	1	1	IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK
1	1		PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR
	i	1	EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH
1	l	}	GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK
1		}	LINHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM
-	1		
			PESEECASAPAPVPQSSTPFSSPQ
6281	857	2515	ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEBEEEDE
1	1		DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA
	i contract of the contract of	1	WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA
	Į		
			OKHSFPRMLHORERGLCHRGSFSLGEOSRVISHFLPNDLGFTDS
			QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS
			QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA
			QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD
			QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ
			QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD

SEQ	Predicted	Predicted end	
DI	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
ľ	amino acid	residue of	S=Serine, T=Threonine, V=Valine
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine X=Unknown +-Stor
1	amino acid	sequence	Codon, /=possible nucleotide deletion
 	sequence		\=possible nucleotide insertion)
			EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH
			GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK
			LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM
6282	125	906	PESEECASAPAPVPQSSTPFSSPQ
İ		1	RMAACRALKAVLVDLSGTLHIEDAAVPGAQEALKRLRGASVIIR FVTNTTKESKQDLLERLRKLEFDISEDEIFTSLTAARSLLERKQ
1			VRPMLLVDDRALPDFKGIQTSDPNAVVMGLAPEHFHYQILNQAF
İ			RLLLDGAPLIAIHKARYYKRKDGLALGPGPFVTALEYATDTKAT
İ		İ	VVGKPEKTFFLEALRGTGCEPEEAVMIGDDCRDDVGGAQDVGML
			GILVKTGKYRASDEEKINPPPYLTCESFPHAVDHILOHLL
6283	140	1043	LSLFGIHVMNPFWSMSTSSVRKRSEGEEKTI.TGDVKTSDDDTAD
}			KKQLPSIPKNALPITKPTSPAPAAOSTNGTHASYGDEVIEVELI
į.			AEFTLVVKQKLPGVYVQPSYRSALMWFGVTFTRHGT.YODGUEKE
i			TVYIPDNYPDGDCPRLVFDIPVFHPLVDPTSGELDVKRAFAKWR
)		RNHNHIWQVLMYARRVFYKIDTASPLNPEAAVLYEKDIQLFKSK
			VVDSVKVCTARLFDQPKIEDPYAISFSPWNPSVHDEAREKMLTQ KKKPEEQHNKSVHVAGLSWVKPGSVQPFSKEEKTVAT
6284	1	2879	RSVIPGSTISSRWPGLSRPRFMAAHEWDWFQREELIGQISDIRV
İ			QNLQVERENVQKRTFTRWINLHLEKCNPPLEVKDLFVDIQDGKI
			LMALLEVLSGRNLLHEYKSSSHRIFRLNNIAKALKFLEDSNVKL
	İ		VSIDAAEIADGNPSLVLGLIWNIILFFOIKELTGNLSDNSDSSS
1			LAPGSGGTDSDSSFPPTPTAERSVAISVKDORKATKALLAWVOD
1			KTRKYGVAVQDFAGSWRSGLAFLAVIKAIDDSTADMKOATEMET
			RENLEKAFSIAQDALHIPRLLEPEDIMVDTPDEOSIMTVVAORI
			ERFPELEAEDIFDSDKEVPIESTFVRIKETPSEQESKVFVLTEN
			GERTYTVNHETSHPPPSKVFVCDKPESMKEFRLDGVSSHALSDS
			STEFMHQIIDQVLQGGPGKTSDISEPSPESSILSSRKENGRSNS LPIKKTVHFEADTYKDPFCSKNLSLCFEGSPRVAKESLRQDGHV
1 1			LAVEVAEEKEQKQESSKIPESSSDKVAGDIFLVEGTNNNSQSSS
1			CNGALESTARHDEESHSLSPPGENTVMADSFQIKVNLMTVEALE
1			EGDYFEAIPLKASKFNSDLIDFASTSOAFNKUPSPHETKDDEDA
i i			EAFENHAEKLGKRSIKSAHKKKDSPEPOVKMDKHEDHODSGPFA
j [EGCPSAPEETPVDKKPEVHEKAKRKSTRPHVEREGEDDDLOGUG
	1		EELSSSPPSSCVSLETLGSHSEEGLDFKPSPPLSKVSVTPHDLE
1 1	i	ĺ	YFPHYEVPLAAVLEAYVEDPEDLKNEEMDLEEPEGYMPDLDSRE
1			EEADGSQSSSSSSVPGESLPSASDQVLYLSRGGVGTTPASEPAP
[]	-		LAPHEDHOORETKENDPMDSHOSOESPNLENIANPLEENVTKES ISSKKKEKRKHVDHVESSLFVAPGSVQSSDDLEEDSSDYSIPSR
<u> </u>			TSHSDSSIYLRRHTHRSSESDHFSLCSVEERSRSG
6285	2157	1331	SCKTENLLEMWWFOOGLSFLPSALVIWTSAAFIFCVITAUTTIU
			IDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATIYVRYKOVH
[ALSPEENVIIKLNKAGLVLGILSCLGLSIVANFOKTTLFAAHVS
		İ	GAVLTFGMGSLYMFVQTILSYQMOPKIHGKOVFWIRLLIVIWCC
	1		VSALSMLTCSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMTTTDA
j i		!	EWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLTLYDTAPCPIN
6286	1619	276	NERTRLLSRDI
		2,3	KAGASCCGSANPYVSVGKSCVLLAMAQLQTRFYTDNKKYAVDDV
	}	1	PFSIPAASEIADLSNIINKLLKDKNEFHKHVEFDFLIKGOFLRM PLDKHMEMENISSEPRAFIERVERVATA DODGO CANTILONIO
[İ	·	PLDKHMEMENISSBEVVEIEYVEKYTAPQPEQCMFHDDWISSIK GAEEWILTGSYDKTSRIWSLBGKSIMTIVGHTDVVKDVAWVKKD
' [SLSCLLLSASMDQTILLWEWNVERNKVKALHCCRGHAGSVDSIA
1			VDGSGTKFCSGSWDKMLKIWSTVPTDEBDEMEESTNRPRKKQKT
·	ł	1	EQLGLTRTPIVTLSGHMEAVSSVLWSDAEEICSASWDHTIRVWD
1		ŀ	VESGSLKSTLTGNKVFNCISYSPLCKRLASGSTDRHIRLWDPRT
1		j.	KDGSLVSLSLTSHTGWVTSVKWSPTHEOOLISGSLDNIVKLWDT
			RSCKAPLYDLAAHEDKVLSVDWTDTGLLLSGGADNKLYSYRYSP

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ĺ	sequence	Sequence	\=possible nucleotide insertion)
	Bequeinee		TTSHVGA
6287	278	1402	
0207	278	1482	MQFFFNFQIGLRSTSGKEKYSGDAGFLGDALQLFLQCLALDEDF
}	4		APAKLQVQKILCDLLLPENLKEGLKESSWSSLPCTKNRPFDFHS
ł			VMEESQSLNEPSPKQSEEIPEVTSEPVKGSLNRAQSAQSINSTE
]	MPAREDCLKRVSSEPVLSVQEKGVLLKRKLSLLEQDVIVNEDGR
ł	†	ļ	NKLKKQGETPNEVCMFSLAYGDIPEELIDVSDFECSLCMRLFFE
			PVTTPCGHSFCKNCLERCLDHAPYCPLCKESLKEYLADRRYCVT
1	1 .	İ	QLLEELIVKYLPDELSERKKIYDEETAELSHLTKNVPIFVCTMA
į	1 '		YPTVPCPLHVFEPRYRLMIRRSIQTGTKQFGMCVSDTQNSFADY
ļ			GCMLQIRNVHFLPDGRSVVDTVGGKRFRVLKRGMKDGYCTADIE
6288	 		YLEDV
0288	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
Ì			MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM
1	Į.	ł	HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM
l	ì	1	KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM
		1	PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM
6289	<u> </u>	·	RSEDPRSVINLLRNVCSEAAQKRSLDR
6289	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
ł	ł		MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM
1			HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM
1	\$		KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM
1	!		PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM
6290			RSEDPRSVINLLRNVCSEAAQKRSLDR
6290	3	1856	TLGRWLLGVYETVAPTLACLPRPRLRRRRRRRRRRRRRRRRMISRYTRKA
	1		VPQSLELKGITKHALNHHPPPEKLEEISPTSDSHEKDTSSQSKS
l	1	j	DITRESSFTSADTGNSLSAFPSYTGAGISTEGSSDFSWGYGELD
Í	1		QNATEKVQTMFTAIDELLYEQKLSVHTKSLQEECQQWTASFPHL
]	· ·		RILGRQIITPSEGYRLYPRSPSAVSASYETTLSQERDSTIFGIR
1]		GKKLHFSSSYAHKASSIAKSSSFCSMERDEEDSIIVSEGIIEEY
l	Į.		LAPDHIDIEEGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY
1		1	VFDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV
j			LSELHPLVLPRVPQSKVLYITSNPMSLCQASRHQPNVNDLLVHG
			MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS
]	i		TSSLSYTVQSTRRRNPPPRTLHPISTSHSCAETPRSVEEILRGA
]			RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK
1	1		PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTQSFLLDT
	ļ		QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG
6291	1732		P
0231	1/32	602	LVAKMASSASARTPAGKRVINQEELRRLMKEKQRLSTSRKRIES
1			PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG
1	· ·		AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST
 			SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEGD
•			GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK
			APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV
1			RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ
			IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN
6300	4.00		ADSDDEGELQDLLSQDWRVKGALL
6292	1835	1142	TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV
			LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI
			LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN
			SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY
			LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA
			AKEPPPPYVSA
6293	2382	1035	FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL
	1		1 7700000 07700000000000000000000000000
			VGSRTLPVDFHIKMVESMKYPFRQGMRLEVVDKSQVSRTRMAVV
			DTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIK

SEO	Predicted	Predicted end	I have a second and a second an
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
- {	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
			MSERRSDMAHHPTFRKIYCDAVPYLFKKVRAVYTEGGWFEEGMK
İ	1		LEAIDPLNLGNICVATVCKVLLDGYLMICVDGGPSTDGLDWFCY
	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	l	HASSHAIFPATFCQKNDIELTPPKGYEAQTFNWENYLEKTKSKA
i	1	i	APSRLFNMDCPNHGFKVGMKLEAVDLMEPRLICVATVKRVVHRL
		ŀ	LSIHFDGWDSEYDQWVDCESPDIYPVGWCELTGYQLQPPVAAEP
	1		ATPLKAKEATKKKKKQFGKKRKRIPPTKTRPLRQGSKKPLLEDD
İ			PQGARKISSEPVPGEIIAVRVKEEHLDVASPDKASSPELPVSVE
	İ		NIKQETDD
6294	354	1814	AQLTTRGRTVAGGVRWIPSPFPDLBLYSCCLGTDRGFPELSHHC
1			KNVIATASDYDMAEITNIRPSFDVSPVVAGLIGASVLVVCVSVT
]			VFVWSCCHQQAEKKHKNPPYKFIHMLKGISIYPETLSNKKKIIK
}			VRRDKOGPGREGGRRNLLVDAAEAGLLSRDKDPRGPSSGSCIDQ
1			LPIKMDYGEELRSPITSLTPGESKTTSPSSPEEDVMLGSLTFSV
	[DYNFPKKALVVTIQEAHGLPVMDDQTQGSDPYIKMTILPDKRHR
1			VKTRVLRKTLDPVFDETFTFYGIPYSQLQDLVLHFLVLSFDRFS
1	,		RDDVIGEVMVPLAGVDPSTGKVQLTRDIIKRNIQKCISRGELQV
1	ì		SLSYQPVAQRMTVVVLKARHLQKMDIAGLSGNPYVKVNVYYGRK
1			RIAKKKTHVKKCTLNPIFNESFIYDIPTDLLPDISIEFLVIDFD
1			RTTKNEVVGRLILGAHSVTASGAEHWREVCESPRKPVAKWHSLS
			EY
6295	2795	617	VSSALLTGATSGSDAAKSEGASASPLSCTNAVAMDRPDEGPPAK
1	ĺ		TRRLSSSESPQRDPPPPPPPPPLLRLPLPPPPQQRPRLOEETEAA
			QVLADMRGVGLGPALPPPPPYVILEEGGIRAYFTLGAECPGWDS
			TIESGYGEAPPPTESLEALPTPRASGGSLEIDFOVVOSSSFGGE
	i		GALETCSAVGWAPQRLVDPKSKEEAIIIVEDEDEDERESMRSSR
			RRRRRRRRKQRKVKRESRERNAERMESILOALEDIOLDLEAVNT
1			KAGKAFLRLKRKFIQMRRPFLERRDLIIQHIPGFWVKAFLNHPR
1 .	·		ISILINRRDEDIFRYLTNLQVQDLRHISMGYKMKLYFQTNPYFT
łi			NMVIVKEFQRNRSGRLVSHSTPIRWHRGQEPQARRHGNQDASHS
1			FFSWFSNHSLPEADRIAEIIKNDLWVNPLRYYLRERGSRIKRKK
1	1		QEMKKRKTRGRCEVVIMEDAPDYYAVEDIFSEISDIDETIHDIK
1			ISDFMETTDYFETTDNEITDINENICDSENPDHNEVPNNETTDN
1 1	1		NESADDHETTDNNESADDNNENPEDNNKNTDDNEENPNNNENTY
} <u> </u>	1		GNNFFKGGFWGSHGNNQDSSDSDNEADEASDDEDNDGNEGDNEG
1			SDDGNEGDNEGSDDDDRDIEYYEKVIEDFDKDQADYEDVIEII
1	1		SDESVEEEGIEEGIQQDEDIYEEGNYEEEGSEDVWEEGEDSDDS DLEDVLQVPNGWANPGKRGKTG
6296	727	1199	RHCGCDAQGACDSLPPTGTSSPVTARNAIPEARCCVWLLDGTTV
1 1	•		EAVRPARERLARKELRQKRMQQFSRDSAYSSNKDSTCLLTERDT
1	1	i	LGTSLQFPSPFSGTISFGSFSDSGIFPLGSQCCLGFQQFSISGK
i 1			KWALIHKRVRLSVFGARWGRIYFGK
6297	1	922	QRAAAAS PSSCGPRGAEYGALMAMEGYWRFLALLGSALLVGFLS
		-	VIFALVWVLHYREGLGWDGSALEFNWHPVLMVTGFVFIQGIAII
, 1			VYRLPWTWKCSKLLMKSIHAGLNAVAAILAIISVVAVFENHNVN
]		j	NIANMYSLHSWVGLIAVICYLLQLLSGFSVFLLPWAPLSLRAFL
	1		MPIHVYSGIVIFGTVIATALMGLTEKLIFSLRDPAYSTFPPEGV
1	1	ļ	FVNTLGLLILVFGALIFWIVTRPQWKRPKEPNSTILHPNGGTEQ
	1	ļ	GARGSMPAYSGNNMDKSDSELNNEVAARKRNLALDEAGORSTM
6298	3	985	SVPLRRLSLSGTLQGAGTTTKMAVARLAAVAAWVPCRSWGWAAV
	1		PFGPHRGLSVLLARI PQRAPRWLPACRQKTSLSFLNRPDLPNLA
] [1	1	YKKLKGKSPGIIFIPGYLSYMNGTKALAIEEFCKSLGHACIRFD
		ļ	YSGVGSSDGNSEESTLGKWRKDVLSIIDDLADGPQILVGSSLGG
	}	1	WLMLHAAIARPEKVVALIGVATAADTLVTKFNQLPVELKKEVEM
i 1]	KGVWSMPSKYSEEGVYNVQYSFIKEAEHHCLLHSPIPVNCPIRL
1	İ	İ	LHGMKDDIVPWHTSMQVADRVLSTDVDVILRKHSDHRMREKADI
i	1	İ	QLLVYTIDDLIDKLSTIVN
			Z

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ĺ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
j	sequence	Bequence	\=possible nucleotide insertion)
6299	512	814	ECDLEGIMPNVTISLSLPTNGSPLODILVHPCVTSLDSAILTSS
0233		""	SIDAMDDSAFSGPYKFFFTPPLESFNLCFYTSQVPVPPILGFYQ
	1		MKEEEVQLRNNH
6300	121	692	AAPSCWSORGVPAAGTPSSPRLLVSRAAAPSAGPWGAWROGARA
1 0500	1	0,72	AQSPFSIPNSSSVPYGSQDSVHSSPEDGGGGGRDRPVGGSPGGPR
t	İ	f	LVIGSLPAHLSPHMFGGFKCPVCSKFVSSDEMDLHLVMCLTKPR
		ļ	ITYNEDVLSKDAGECAICLEELQQGDTIARLPCLCIYHKGCIDE
		•	WFEVNRSCPEHPSD
6301	516	304	GKFVPVNWEPPOPLPFPKYLRCYRCLLETKELGCLLGSDICLTP
0301	616	284	AGSSCITLHKKNSSGSDVMVSDCRSKEQMSDCSNTRTSPVSGFW
}	[]	IFSQYCFLDFCNDPQNRGLYTP
6302	490	745	I
0302	1 ****	/45	IFGFLHLFHMEHSFLLVCALFAHVFFSSSCGSSVALHSDPCLLS
6303		1063	PVLLNCLPGDLRPLDELYAQKLKYKAISEELDHALNDMTSL
6303	2	1961	YWNEYGGGLLWQSWQEKHPGQALSSEPWNFPDTKEEWEQHYSQL
Į.			YWYYLEQFQYWEAQGWTFDASQSCDTDTYTSKTEADDKNDEKCM KVDLVSFLSSPIMGDNDSSGTSDKDHSEILDGISNIKLNSEEVT
		į	
	i	1	QSQLDSCTSHDGHQQLSEVSSKRECPASGQSEPRNGGTNEESNS
		İ	SGNTNTDPPAEDSQKSSGANTSKDRPHASGTDGDESEEDPPEHK
Į	1		PSKLKRSHELDIDENPASDFDDSGSLLGFKYGSGQKYGGIPNFS HROVRYLEKNVKLKSKYLDMRROIKMKNKHIFFTKESEKPFFKK
[(1	
	1	1	SKILSKVEKFLTWVNKPMDEEASQESSSHDNGHDASTSCDSEEQ
		1	DMSVKKGDDLLETNNPEPEKCQSVSSAGELETENYERDSLLATV PDEQDCVTQEVPDSRQAETEAEVKKKKNKKKNKKVNGLPPEIAA
ļ			VPELAKYWAQRYRLFSRFDDGIKLDREGWFSVTPEKIAEHIAGR
1		İ	VSQSFKCDVVVDAFCGVGGNTIQFALTGMRVIAIDIDPVKIALA
Į	ł.	ł	RNNAEVYGIADKIEFICGDFLLLASFLKADVVFLSPPWGGPDYA
1		ĺ	TAETFDIRTMMSPDGFEIFRLSKKITNNIVYFLPRNADIDQVAS
	•	İ	LAGPGGQVEIEQNFLNNKLKTITAYFGDLIRRPASET
6304	1	1438	HRARVDRSRESPGGDLRHPGRVRRDITLSGHPRLSTOHVVLLRE
0504	i *	1430	DEVGDPGTKDLGHPQHGSPIQETQSEVVTLVSPLPGSDMAALPA
l	}	l	WRATSGLTLWPHTAEGRDLLGAENRALTGGQQAEDPTLASGAYQ
			WPGSVEKLOGSVWCDAETLLSSSRTGGQAPPWLTDHDVQMLRLL
j	1		ACCEVVDKARVPAHGOVLOVGFSTEAALODLSSPRLSOLCSOGL
1		1	CGLIKRPGDLPEVLSFHVDRVLGLRRSLPAVARRFHSPLLPYRY
1	1	1	TDGGARPVIWAPDVOHLSDPDEDONSLALGWLOYOALLAHSCN
	1		WPGQAPCPGIHHTEWARLALFDFLLQVHDRLDRYCCGFEPEPSD
1		[PCVEERLREKCRNPAELRLVHILVRSSDPSHLVYIDNAGNLOHP
1			EDKLNFRLLEGIDGF?ESAVKVLASGCLQNMLLKSLQMDPVFWE
ļ			SQGGAQGLKQVLQTLEQRGQVLLGHIQKHNLTLFRDEDP
6305	99	420	NMIWRGRSTYRPRPRRSVPPPELIGPMLEPGDEEPOOEEPPTES
1 3303	1	120	RDPAPGOEREEDOGAAETQVPDLEADLQELSQSKTGDECGDGPD
			VQGKILTKSEQFKMPEGR
6306	1	1874	PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC
0300	*	10/4	FTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD
			ESEDSGVIPGSHSENALHASEEEEGGGKAOSSLGYIPLMRVVO
}	!		
1	ł		SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFQ
			NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA
1	Į.		TYFVGEMPGGTPGGPSGQGAEAARGWETAIRQALMPVILQDAPS
			APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVLGSGQF
ļ			GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR
l			HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL
			TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC
			DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG
	1		VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID
l			LINNLLQVKMRKRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER YITHESDDARWEQFAAEHPLPGSGLPTDRDLGGACPPQDHDMQG
			TV CERREINADWENEAAFBULDGSGLDTDDDLGGACUDNHNMOG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Clutamic Arid P. Phanalalania
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	1	L=Leucine, M=Methionine, N=Asparagine,
	1	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ī	amino acid	sequence	Codon, /=possible nucleotide deletion.
}	sequence	1	\=possible nucleotide insertion)
			LAERISVL
6307	2136	589	CFLLPRGRDPEPPEAGAAAPCAPGAPDMSFRKVVRQSKFRHVFG
1			QPVKNDQCYEDIRVSRVTWDSTFCAVNPKFLAVIVEASGGGAFL
1	i		VLPLSKTGRIDKAYPTVCGHTGPVLDIDWCPHNDEVIASGSEDC
I	1	ļ	TIMINOT DENCE TO DE TODO DE TO
1	ì	1	TVMVWQIPENGLTSPLTEPVVVLEGHTKRVGIIAWHPTARNVLL
		İ	SAGCDNVVLIWNVGTAEELYRLDSLHPDLIYNVSWNHNGSLFCS
1	i	ľ	ACKDKSVRIIDPRRGTLVAEREKAHEGARPMRAIFLADGKVFTT
1	1		GFSRMSERQLALWDPENLEEPMALQELDSSNGALLPFYDPDTSV
}	1	[VYVCGKGDSSIRYFEITEEPPYIHFLNTFTSKEPQRGMGSMPKR
j.	1		GLEVSKCEIARFYKLHERKCEPIVMTVPRKSDLFQDDLYPDTAG
			PEAALEAEEWVSGRDADPILISLREAYVPSKQRDLKISRRNVLS
ŀ	l .		DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGEAGKLEEVM
		<u></u>	QELRALRALVKEQGDRICRLEEQLGRMENGDA
6308	. 2	1118	GRPTRPEKMLLSLVLHTYSMRYLLPSVVLLGTAPTYVLAWGVWR
l			LLSAFLPARFYQALDDRLYCVYQSMVLFFFENYTGVQILLYGDL
1			PKNKENIIYLANHQSTVDWIVADILAIRQNALGHVRYVLKEGLK
1			WLPLYGWYFAQHGGIYVKRSAKFNEKEMKNKLQSYVDAGTPMYL
1			VIFPEGTRYNPEQTKVLSASQAFAAQRGLAVLKHVLTPRIKATH
1	Į.		VAFDCMKNYLDAIYDVTVVYEGKDDGGQRRESPTMTEFLCKECP
			KIHIHIDRIDKKDVPEEQEHMRRWLHERFEIKDKMLIEFYESPD
	{		PERRKRFPGKSVNSKLSIKKTLPSMLILSGLTAGMLMTDAGRKL
			YVNTWIYGTLLGCLWVTIKA
6309	220	563	LVAEVKEPCSLPMLSVDMENKENGSVGVKNSMENGRPPDPADWA
1	·		VMDVVNYFRTVGFEEQASAFQEQEIDGKSLLLMTRNDVLTGLQL
			KLGPALKIYEYHVKPLQTKHLKNNSS
6310	36	979	CDDCWVRI II CONVOCATA DIGWINDOS
]	373	GPRCWKFLILSSVNCETLRIGKAWPQSSGQERYWTPRTHSSASE
1 1	1		AQRGSLAELNVAAAGLWADCDQPLYDCPMCGLICTNYHILQEHV
i i			DLHLEENSFQQGMDRVQCSGDLQLAHQLQQEEDRKRRSEESRQE
1 1			IEEFQKLQRQYGLDNSGGYKQQQLRNMEIEVNRGRMPPSEFHRR
1			KADMMESLALGFDDGKTKTSGIIEALHRYYQNAATDVRRVWLSS
)			VVDHFHSSLGDKGWGCGYRNFQMLLSSLLQNDAYNDCI,KGMLIP
1			CIPKIQSMIEDAWKEGFDPQGASQLIIRLQGTKAWIGACEVYIL
6311			LTSLRV
9311	ı	675	PVWWNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL
			ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLVKEVAELEANL
			PCTCKVHFPDPNKLHCFQLTVTPDEGYYQGGKFQFETEVPDAYN
			MVPPKVKCLTKIWHPNITETGEICLSLLREHSIDGTGWAPTRTL
1 1		ı	KDVVWGLNSLFTDLLNFDDPLNIEAAEHHLRDKEDFRNKVDDYI
			KRYAR
6312	213	1400	GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW
	1		GKTEERAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT
<u> </u>			RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN
]	1		VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC
1 1	Ī		DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA
1 1	į		IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV
1 1	į		GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPOD
j l	į		VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL
[1	Į	YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL
6313		2071	OBSCAADI A EL DODESDA CHIDONI CONTOCIONA
	-	2011	QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL
			FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD
] [RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF
[]			TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE
[[J		FLQMLEAIKALEVRNKENSAPLEENTTGKNBAKKRKIAETSNVI
			TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASAKQSVK
			YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK
Ll			QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE
· ·			

SEQ Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence seq	, E= ne, Stop KIHVC TLKCH HTGDK ETRVQ LLQDS ERVNQ EDHED PLGVL IKMILD IFFQEF WKAAE
NO: nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence P-Proline, Q-Glutamine, R-Arginine, S-Serine, T-Threonine, N-Asparagine, P-Proline, Q-Glutamine, N-Asparagine, M-Proline, Q-Glutamine, N-Asparagine, P-Proline, Q-Glutamine, N-Asparagine, M-Proline, Q-Glutamine, N-Paparagine, M-Proline, Q-Glutamine, N-Paparagine, M-Proline, Q-Glutamine, N-Paparagine, M-Proline, Q-Glutamine, N-Paparagine, M-Proline, Q-Glutamine, N-Paparagine, M-Proline, Q-Glutamine, N-Paparagine, M-Proline, Q-Glutamine, N-Paparagine, M-Proline, Q-Glutamine, N-Paparagine, M-Proline, Q-Glutamine, N-Paparagine, M-Proline, Q-Glutamine, N-Paparagine, M-Proline, Q-Glutamine, N-Paparagine, M-Proline, N-Paparagine, M-Proline, Q-Glutamine, N-Paparagine, M-Proline, Q-Glutamine, N-Paparagine, M-Proline, Q-Glutamine, N-Paparagine, M-Proline, M-Paparagine, M-Proline, Q-Glutamine, N-Paparagine, M-Proline, M-Paparagine, M-Paparagine, M-Proline, M-Paparagine, M-Proline, M-Paparag	Stop KIHVC TLKCH HTGDK ETRVQ LLQDS ERVNQ EDHED PLGVL IKMILD IFFQEF WKAAE
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amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, residue of amino acid sequence Codon, /=possible nucleotide deletion, \=possible QVGKVHVLPLLQVQVDSAQVTVEQVHPF QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHV MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAR AEDLETKPTVDSEAEKABHEDRTALPVLE 6314 2 2071 QRSGAARLAFLPSPSFSPACVHRSPLSFHGCWFYFVVVFM FHRRAHGCTLSCSFVEQPTAMEAEETMECLQEFPEHR RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYY TQSPLVEIECVSKWAFRRLIEFTYTAKLMTQGEEEANDV FLQMLEAIKALBVRNKENSAPLEENTTGKNEAKKRKIAF TESLPSAESEPVEIEVEIAGGTIEVEDEGIETLEEVASF YTQSTGSSDDSALALLADITSKYRQCDRKGQIKEDGCE QVEGIETVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMM SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGF QYCEKQPDHFGHFKEHLRKHTGEKGFECFNCHERFARMS LTACQTGVGAKKGRKKLYECQVCNSVFNSDOFKDHLVY PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSV TEPVTSNTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPI QVHDSHMSELPEQVQVSYLEVGRIQTEGGTEVHVEELH MPVVEQTELLEADLDHVTPEIMNQEERESSQADAAEAA AEDLETKFTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGGAVNVVTTLVLISYCPTATEERPWTYLLCALGLFT IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIA PDWFFSCSFIGMFVFYCAHWQTVYSGMLRGKKVDVTEIG VFVLSARGGATWWDYTIPILEIKLKLIPVLGFLGGVIF HVVLLAGGGVGRNGSTIAGTSVLSPGLHIGLIILAIMIYI VFFKKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQD	KIHVC TLKCH HTGDK ETRVQ LLQDS ERVNQ EDHED IPLGVL KMILD LFFQEF WKAAE
residue of amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide insertion) sequence SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGK QYCEKOFDHFGHFKEHLRKHTGEKPFECPNCHERFARNS LTACQTGVGAKKGRKKLYEQQVCNSVFNSWQPKDHLUY PNHCTLCDLWFMQGNELRHLSDAHNISERLVTEEVLSV TEPVTSHTIIEQVGKVHVLPLLQQVQVDSAQVTVEQVHPL QVHSHSSLPBQVQVSYLEVGRIQTEEGTEVHVEELHW MPVEVQTELLEADLDHVTPEIMNQERESSQADAAEAAR AEDLETKPTUDSEAEKAENEDRTALPVLE 6314 2 2071 QRSGARALAFLPSPFSPACVHRSPLSFHGCWFYFVVVFM FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHR RLNEQREQDRFTDITIIVDGHHFKAHKAVLAACSKFFYM TOSPLVEIEGVSKMFRHLIEFTTTAKLMIQGEEANDV FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAF TESLPSAESEFVEIEVEIABGTIEVEDEGIETLEEVASS YTIGSTGSDDSALALLADITSKYRGDRKGQIKKDGCDE QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMM SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGF QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMM SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGF QVEGIEIVELQLGHVVQFUSAQVTVEQVHDI QVYCSKQFDHFGGJFKHLSDAHNISERLVTEEVLSV TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHDI QVHDSHMSELPEQVQVSYLEVGRIGTEEGTEVHVEELH MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAH AEDLETKFTVDSEAEKAENEDRTALPVLE LGLAVNVVTTLVLISYCPTATEEAPFWTYLLCALGIFT IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAH PDWFFSCSPIGMFVYCAHMQTYVSGMLRRGKVDVTEIU VFFLISAFGGATMMDYTTPILBIKKLILPVLGFLGGVIFK HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYI VFFKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQV	KIHVC TLKCH HTGDK ETRVQ LLQDS ERVNQ EDHED IPLGVL KMILD LFFQEF WKAAE
amino acid sequence Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) SFKCEICNKRYIRESAWKOHLNCYHLEEGGVSKKQRTGK QYCEKQFDHFGHFKEHLRKHTGEKFFECPNCHERFARNS LTACQTGVGAKKGRKKIYEQVCNSVFNSWDQFKDHLVI PNHCTLCDLWFMQGRERFRHLSDAHNISERLVTEVLSV TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPI QVHDSHMSBLFEQVQVSYLEVGRIQTEEGTEVHVEELHV MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAR AEDLETKPTVDSEAEKAENEDRTALPVLE 6314 2 2071 ORSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFP FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHE RLNEQREQDRFTDITLIVDCHHFKAHKAVLAACSKFFYX TQBPLVEIEGVSKMAFRHLLEFTYTAKLMIQGEEEAND FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAE TESLPSAESEPVELVEIABGTIEVEDEGIETLEEVASS YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPE QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHM SFKCEICNKFYLRESAWKOHLNCYHLEEGGVSKKQRTGT QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNS LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVJ PNHCTLCDLWFMQGRELRRHLSDAINISERLYTEVESV TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPI QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHN MPVEVQTELLEADHVTPEIMNGERESSQADAAEAAA AEDLETKFTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGGAVNVVTTLVLISYCPTATEEAPFWTYLLCALGLFI UDGKQARRTNSCSPLGBLFDHGCDSLSTVFWAVGASIA PDWFFSCSFIGMFVFYCAHWGTYVSGMLRFGKVDVTEIQ VFYLSAFGGATMWDYTTPILEIKLKILPVLGFLGGVIFR HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYI VFEKHPCLYIIMFGCVFAKVSQKLVVAHMTKSELYLQV	KIHVC TLKCH HTGDK ETRVQ LLQDS ERVNQ EDHED IPLGVL KMILD LFFQEF WKAAE
amino acid sequence Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) SFKCEICNKRYIRESAWKOHLNCYHLEEGGVSKKQRTGK QYCEKQFDHFGHFKEHLRKHTGEKFFECPNCHERFARNS LTACQTGVGAKKGRKKIYECQVCNSVFNSWDQFKDHLVI PNHCTLCDLWFMQGRERRHLSDAHNISERLVTEVLSV TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPI QVHDSHMSBLFEQVQVSYLEVGRIQTEEGTEVHVEELHV MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAR AEDLETKPTVDSEAEKAENEDRTALPVLE 6314 2 2071 QRSGAARLAFLFSPFSPACVHRSPLSFHGCWFYFVVVFP FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFFEHE RLNEQREQDRFTDITLIVDCHHFKAHKAVLAACSKFFYX TQBPLVEIEGVSKMAFRHLLEFTYTAKLMIQGEEEAND FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAE TESLPSAESEPVELEVEIABGTIEVEDEGIETLEEVASS YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPE QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHM SFKCEICNKFYLRESAWKQHLNCYHLEEGGVSKKQRTGF QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNS LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVJ PNHCTLCDLWFMQGNELRRHLSDAINISERLYTEVESV TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPI QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHM MPVEVQTELLEADHVTPEIMNGERESSQADAAEAAA AEDLETKFTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGGAVNVVTTLVLISYCPTATEEAPFWTYLLCALGLFI UGKQARRTNSCSPLGBLFDHGCDSLSTVFMAVGASIA. PDMFFSCSFIGMFVFYCAHMQTYVSGMLRFGKVDVTEIQ VFYLSAFGGATMWDYTTPILEIKLKILPVLGFLGGVIFR HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYI VFEKHPCLYIIMFGCVFAKVSQKLVVAHMTKSELYLQV	KIHVC TLKCH HTGDK ETRVQ LLQDS ERVNQ EDHED IPLGVL KMILD LFFQEF WKAAE
Sequence SpkceIcnkryLresawkQhLnCyHLeEGGVSKKQRTGK	TLKCH HTGDK ETRVQ LLQDS ERVNQ EDHED PLGVL KMILD FFQEF
SFKCEICNKRYLRESAWKQHLMCYHLEEGGVSKKQRTCK QYCEKQFDHFGHFKEHLKHTGEKPFECPNCHERFARNS LTACOTGYGAKKGRKKLYECQVCNSVFNSWDQFKDHLVI PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSV TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPEL QVHDSHMSBLPEQVQVSYLEVGRIQTEEGTEVHVEELHV MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAR AEDLETKPTVDSEAEKAENEDRTALPVLE 6314 2 2071 QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFN FHRRAHGCTLSCSSFVEQPTAMMEAETMCCLQEFPEHL RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYR TQEPLVEIEGVSKMAFRRLIEFTYTAKLMIQGEEANDV FLQMLEAIKALEVNKENSAPLEENTTGKKNEAKKKIAF TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASA YIGSTGSSDSALALLADITSKYRQGDRKGQIKEDGCDE QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHM SFKCEICNKRYLRESAMKQHLKCYHLEEGGVSKKQRTGF QYCEKQFDHFGHFKEHLKKHTGEKPFECPNCHERFARNS LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVI DPNHCTLCDLWFMQONELRRHLSDAHNISERLVTEEVLSV TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPI QVHDSHMSELPPCVQVSYLEVGRIQTEEGTEVHVEELHK MPVEVOTELLEADLDHVTPEIMNQEERESSQADAAEAAF AEDLETKPTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGGAVNVTTLVLISYCPTATEEAPYWTYLCALGLFTI LDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAF PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQ VFVLSAFGGATMWDYTIPLIEIKLKLIEPULGFLGGVIFF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIY VFEKHPCLYLIMFGCVFAKVSQKLVVAMMTKSELYLQD	TLKCH HTGDK ETRVQ LLQDS ERVNQ EDHED PLGVL KMILD FFQEF
QYCEKQFDHFGHFKEHLRHTGEKPFECPNCHERFARNS LITACQTGVCAKKGRKKIYECQVCNSVFNSMDQFKDHLVI PNHCTLCDLWFMQGNELRHLSDAHNISERLVTEEVLSV TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPD QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHV MPVEVQTELLEADLDHVTPEIMNQERESSQADAAEAR AEDLETKPTVDSEABKAENEDRTALPVLE 6314 2 2071 QRSGARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFM FHRRAHGCTLSCSSFVEQPTAMBAEETMECLQEFPEH RLNEQREQREQTTITLIVDGHHFKAHKAVLAACSKFFYK TQSPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDV FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAF TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASS YIQSTGSSDDSALALLADITSKYRQGDRKGOIKEDGCEE QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHM SFKCEICNRYLRESAWKQHLNCYHLEEGGVSKKQRTGE QYCEKQFDHFGHFKKEHLRKHTGEKPFECPNCHERFARNS LTACQTGVGAKKGRKKLYECQVCNSVYNSWDQFKDHLVJ PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSV TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVQCVHUP QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELH MPVEVQTELLEADLDHVTPEIMNQERESSQADAAEAAR AEDLETKPTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGGARATMSCSPLGELFDMGCDSLSTVFMAVGASIAJ PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEI(VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFS VFVLSAFGGATMWDTTIPILEIKLKLLPVLGFLGGVIFS HVILHGGVGKNGSTIAGTSVLSSPGLHIGLIILIAIMIYI VFFEKHPCLYLIMFGCVFAKVSQKLVVAHMTKSELYLQDD	TLKCH HTGDK ETRVQ LLQDS ERVNQ EDHED PLGVL KMILD FFQEF
ITACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVI PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSV TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPI QVHDSHMSELPEQVQVSYLEVGRIQTEGGTEVHVEELHV MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAR AEDLETKPTVDSEAEKAENEDRTALPVLE 6314 2 2071 QRSGAARLAFLPSPFSACVHRSPLSFHGCWFYFVVVFM FHRRRHGGTLSCSSFVEQPTAMEAEETMECLQEFPEHE RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYK TQSPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDV FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAE TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASS YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPS QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHM SPKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGE QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARMS LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVI PNHCTLCDLWFMQGNELRRHLSDAINISERLUTEEVLSS TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHDI QVHDSHMSELPPQVQVSYLEVGRIQTEGGTEVHVEELHV MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAF AEDLETKPTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFII IDGKQARRTNSCSPLGELFDNGCDSLSTVFMAVGASIAF PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIL VFVLSAFGGATMWDTTIPILEIKLKLIPVLGFLGGVIF VFVLSAFGGATMSTIAGTSVLSPGLHIGLIILLAIMIYI VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQDI	HTGDK ETRVQ LLQDS ERVNQ EDHED PLGVL IKMILD IFFQEF WKAAE
PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSV TEPVTSMTIIEQVGKVHVIPLLQVQVDSAQVTVEQVHPD QVHDSHMSBLPEQVQVSYLEVGRIQTEEGTEVHVEELHV MPVEVQTELLEADLDHVTPEIMMQEERESSQADAAEAAR AEDLETKPTVDSEAEKAENEDRTALPVLE 6314 2 2071 QRSGARLAFIPSPFSPACVHRSPLSFHGCWFYFVVVFM FHRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEH RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYV TQEPLVEIEGVSKMAFRHLIEFTYTAKLMIQGEEEANDV FLOMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAE TESLPSAESEPVEIEVEIAEGTIEVEDEGIETLEEVASF YIGSTGSSDDSALALLADITSKYRQGDRKGGIKEDGCPE QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHM SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGE QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNS LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVI PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSV TEPVTSMTIIEQVGKVHVLPLQVQVDSAQVTVEQVHPI QVYNSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHM MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAF AEDLETKFTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGLAVNVTTLVLISYCPTATEEAPYWTYLLCALGLFII IDGKQARRTNSCSPLGELFPHGCDSLSTVFMAVGASIAF PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIG VFVLSAFGGATMWDYTIPILEIKLKLIPVLGFLGGVIRF HVILHGGVGKRGSTIAGTSVLSPGLHIGLIILAIMIYI VFFKKHPCLYILMFGCVFAKVSQKUVAHMTKSELYLQD	ETRVQ LLQDS ERVNQ EDHED PLGVL KMILD FFQEF WKAAE
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LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVJ PNHCTLCDLWFMQGMELRRHLSDAHNISERLVTEEVLSV TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPI QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHV MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAH AEDLETKPTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIY IDGKQARRTNSCSPLGELPDHGCDSLSTVFMAVGASIAI PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIG VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFS HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYI VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQD	
PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSV TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPI QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHV MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAI AEDLETKPTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIY IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAI PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQ VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYI VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQD	TLKCH
TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPI QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHV MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAI AEDLETKPTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFII IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAI PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIG VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFS HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYI VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQD	HTGDK
QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHV MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAFAAH AEDLETKPTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIY IDGKQARRINSCSPLGELFDHGCDSLSTVFMAVGASIAH PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIG VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYN VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQD	ETRVQ
QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHV MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAFAAH AEDLETKPTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIY IDGKQARRINSCSPLGELFDHGCDSLSTVFMAVGASIAH PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIG VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFF HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYN VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQD	LLODS
MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAFAAF AEDLETKPTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIY IDGKQARRINSCSPLGELFDHGCDSLSTVFMAVGASIAN PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIG VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFS HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYI VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQD	
AEDLETKPTVDSEAEKAENEDRTALPVLE 6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLCALGLFI' IDGKQARRTNSCSPLGELPDHGCDSLSTVFMAVGASIA' PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEI' VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFS HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYI VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQD	
6315 1 1015 LGLAVNVVTTLVLISYCPTATEEAPYWTYLLCALGLFIY IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAI PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQ VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFS HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILLAIMIYI VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQD	
IDGKQARRTNSCSPLGELFDHGCDSLSTVFMAVGASIAI PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEI(VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFS HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILLAIMIYI VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQD	TOCT DA
PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIQ VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFS HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILLAIMIYI VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQD	
VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFS HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYI VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQD	
HVILHGGVGKNGSTIAGTSVLSPGLHIGLIILAIMIYI VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQD	
VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQD:	
GLLFLDQYFNNFIDEYVVLWMAMVISSFDMVIYFSALCI	JQISRH
LHLNIFKTACHQAPEQVQVLSSKSHQNNMD	
6316 1503 792 VSAGAGTGIMGGTTSTRRVTFEADENENITVVKGIRLSI	NVIDR
MKESSPSGSKSQRYSGAYGASVSDEELKRRVAEBLALE	AKKES
EDOKRIKOAKELDRERAAANEQLTRAILRERICSEEERI	
AROLEEKDRVLKKODAFYKEQLARLEERSSEFYRVTTE:	
EEVEAKFKRYESHPVCADLQAKILQCYRENTHQTLKCS	
MHCVNHAKQSMLEKGG	
)CCDAN
6317 102 839 PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKI	CDDRAIN 1997AN
FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVG	
TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILI	
EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERV	
QHLGEQLGFEFFETSAKDNINVKQTFERLVDIICDKMS	SLETD
PAITAAKQNTRLKETPPPPQPNCAC	
6318 1765 733 PWHPLRTLPLHHPHPRPPRAEGREGADSMSHLPGLELRI	
LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKA	SEAPPL
LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQI	
VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIO	AGRMNI
	agrmni Ehrtgt
ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAII	AGRMNI EHRTGT SVDFEM
DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTP	AGRMNI EHRTGT EVDFEM IVFNLN
EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALTF	AGRMNI EHRTGT EVDFEM IVFNLN AQYALM
ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP	AGRMNI EHRTGT EVDFEM IVFNLN AQYALM
6319 88 717 AATMRLNQNTLLLGKKVVLVPYTSEHVPSRYHEWMKSE	AGRMNI EHRTGT SVDFEM IVFNLN AQYALM EANVLA
ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPO	AGRMNI EHRTGT SVDFEM IVFNLN AQYALM EANVLA
CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTE	AGRMNI EHRTGT GVDFEM IVFNLN AQYALM EANVLA ELQRLT GATEES
SYGVTTLGLTKFEAKIGQGNEPSIRMFQKLHFEQVATS	AGRMNI EHRTGT GVDFEM IVFNLN AQYALM EANVLA ELQRLT GATEES

SEQ	Predicted	Predicted end	Amino acid segment contains
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	,,	\=possible nucleotide insertion)
			TLRLTVSESEHOWLLEQTSHVEEKPYRDGSAEPC
6320	90	1111	RPRTGREKVAMAAVDSFYLLYREIARSCNCYMEALALVGAWYTA
	1		RKSITVICDFYSLIRLHFIPRLGSRADLIKQYGRWAVVSGATDG
ł	ŀ	!	IGKAYABELASRGLNIILISRNEEKLQVVAKDIADTYKVETDII
1			VADFSSGREIYLPIREALKDKDVGILVNNVGVFYPYPQYFTQLS
			BDKLWDIINVNIAAASLMVHVVLPGMVERKKGAIVTISSGSCCK
	İ		PTPQLAAFSASKAYLDHFSRALQYEYASKGIFVQSLIPFYVATS
ł	ł	1	MTAPSNFLHRCSWLVPSPKVYAHHAVSTLGISKRTTGYWSHSIQ
1	ļ		FLFAQYMPEWLWVWGANILNRSLRKEALSCTA
6321	1418	341	HRKAALGALMAGRLLGKALAAVSLSLALASVTIRSSRCRGIQAF
	•		RNSFSSSWFHLNTNVMSGSNGSKENSHNKARTSPYPGSKVERSQ
1	1		VPNEKVGWLVEWQDYKPVEYTAVSVLAGPRWADPQISESNFSPK
1	j		FNEKDGHVERKSKNGLYEIENGRPRNPAGRTGLVGRGLLGRWGP
1	ł		NHAADPIITRWKRDSSGNKIMHPVSGKHILQFVAIKRKDCGEWA
]			IPGGMVDPGEKISATLKREFGEBALNSLOKTSAEKREIEEKLHK
1			LFSQDHLVIYKGYVDDPRNTDNAWMETEAVNYHDETGEIMDNLM
]			LEAGDDAGKVKWVDINDKLKLYASHSQFIKLVAEKRDAHWSEDS
L			EADCHAL
6322	2017	1083	NQEILKNVESSRTVQPHFLEFLLSLGWSVDVGRHPGWTGHVSTS
			WSINCCDDGEGSQQEEVISSEDIGASIFNGQKKVLYYADALTEI
			AFVVPSPVESLTDSLESNISDQDSDSNMDLMPGILKQPSLTLEL
			FPNHTDNLNSSQRLSPSSRMRKLPQGRPVPPLGPETRVSVVWVE
1			RYDDIENFPLSELMTEISTGVETTANSSTSLRSTTLEKEVPVIF
			IHPLNTGLFRIKIQGATGKFNMVIPLVDGMIVSRRALGFLVROT
1			VINICRRKRLESDSYSPPHVRRKQKITDIVNKYRNKQLEPEFYT
			SLFQEVGLKNCSS
6323	1	656	PASTTDGAQEARVPLDGAFWIPRPPAGSPKGCFACVSKPPALQA
			PAAPAPEPSASPPMAPTLFPMESKSSKTDSVRAAGAPPACKHLA
			EKKTMTNPTTVIEVYPDTTEVNDYYLWSIFNFVYLNFCCLGFIA
			LAYSLKVRDKKLLNDLNGAVEDAKTDRLINITRSGLAASCIMLW
6324	1	200	MALSVIATHRGLRSSASILVAEPHDWNTERPQVTFRERCPAL
0324	–	2061	EGAGMRRCPCRGSLNEAEAGALPAAARMGLEAPRGGRRRQPGQQ
			RPGPGAGAPAGRPEGGGPWARTEGSSLHSEPERAGLGPAPGTES
1			PQAEFWTDGQTEPAAAGLGVETERPKQKTEPDRSSLRTHLEWSW
1	ļ		SELGTTCLWTETGTDGLWTDPHRSDLQFQPEEASPWTQPGVHGP
			WTELETHGSQTQPERVKSWADNLWTHQNSSSLQTHPEGACPSKE
1	i		PSADGSWKELYTDGSRTQQDIEGPWTEPYTDGSQKKQDTEAARK
			QPGTGGFQIQQDTDGSWTQPSTDGSQTAPGTDCLLGBPEDGPLE
1			EPEPGELLTHLYSHLKCSPLCPVPRLIITPETPEPEAQPVGPPS RVEGGSGGPSSASSEDESEDDINACCGGASDPEDEGGANNING
			RVEGGSGGFSSASSFDESEDDVVAGGGGASDPEDRSGSKPWKKL KTVLKYSPFVVSFRKHYPWVQLSGHAGNFQAGEDGRILKRFCQC
1 1	,		EQRSLEQLMKDPLRPFVPAYYGMVLQDGQTFNQMEDLLADFEGP
) [SIMDCKMGSRTYLEEELVKARERPRPRKDMYEKMVAVDPGAPTP
[[ľ		EEHAQGAVTKPRYMQWRETMSSTSTLGFRIEGIKKADGTCNTNF
1			KKTQALEQVTKVLEDFVDGDHVILQKYVACLEELREALEISPFF
] [}	KTHEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPDHQTLSHRLP
			WAEGNREDGYLWGLDNMICLLQGLAQS
6325	165	944	GLRDPFRRKRRLKPQVKMSNYVNDMWPGSPOEKDSPSTSRSGGS
j 1	i	·	SRLSSRSRSFSRSSRSHSRVSSRFSSRSRRSKSRSRRRRHQ
			RKYRRYSRSYSRSRSRSRSRRYRERRYGFTRRYYRSPSRYRSRS
, l	į		RSRSRSRGRSYCGRAYAIARGQRYYGFGRTVYPBEHSRWRDRSR
1	1		TRSRSRTPFRLSEKDRMELLEIAKTNAAKALGTTNIDLPASLRT
1	l		VPSAKETSRGIGVSSNGAKPEVSILGLSEQNFQKANCQI
6326	238	680	GEPSPATQQKPSATGAGVLHQHFSSGHIYVLMGLLPPPWTISFT
[[1	VQTTLQPPGGLPAAPVSGRMAFEPVGRDLARRMVPRAGKRTQTL
j !	İ	l	GARRVAAQGARPLPEDRRPKSGERLHVTVAPCWEFVLPSVSLTA
		<u>-</u>	THE TOURS TOUR TOUR TOUR TOURS OF THE SUBSTITUTE

	T 3 - 5 - 5 - 5 - 5 - 5 - 5 - 5 - 5 - 5 -	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	H=Histidine, i=isoledcine, k=hysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of		Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		
			QAWGGVGQEASSGVP
6327	1	1337	SLARLAPAGGSVVMPTQQPAAPSTRAPKPSRSLSGSLCALFSDA
6321	. -		DSGSGMKAELPPGPGAVGREMTKEEKLQLRKEKKQQKKKRKEEK
]	GAEPETGSAVSAAQCQGPTRELPESGIQLGTPREKVPAGRSKAE
		i	LRAERRAKQEAERALKQARKGEQGGPPPKASPSTAGETPSGVKR
	1	1	LRAERRARQEAERALRQARROEQUOFFFRADESTAODIT DOVICE
		į	LPEYPQVDDLLLRRLVKKPERQQVPTRKDYGSKVSLFSHLPQYS
	ļ.		RQNSLTQFMSIPSSVIHPAMVRLGLQYSQGLVRGSNARCIALLR
	1	ĺ	ALQQVIQDYTTPPNEELSRDLVNKLKPYMSFLTQCRPLSASMHN
	1	1	AIKFLNKEITSVGSSKREEEAKSELRAAIDRYVQEKIVLAAQAI
	1	}	SRFAYQKISNGDVILVYGCSSLVSRILQEAWTEGRRFRVVVVDS
	1	ļ	RPWLEGRHTLRSLVHAGVPASYLLIPAASYVLPEVSTEEKDSKV
Ì	1	1	1
	1		GGEKV
6328	1030	276	HASAEVTTAAARGLGAMEEEMHTDAKIRAENGTGSSPRGPGCSL
0320	1 1000	1	RHFACEONLLSRPDGSASFLQGDTSVLAGVYGPAEVKVSKEIFN
i	}	1	KATLEVILRPKIGLPGVAEKSRERLIRNTCEAVVLGTLHPRTSI
l	1	1	TVVLQVVSDAGSLLACCLNAACMALVDAGVPMRALFCGVACALD
1	1		TVVIQVVSDAGSDIMCCIMARCIMAD DAG FING DEFECT VCDT
l .	1	1	SDGTLVLDPTSKQEKEARAVLTFALDSVERKLLMSSTKGLYSDT
ļ			ELQQCLAAAQAASQHVFRFYRESLQRRYSKS
6329	3	2016	SSEVAAGGGTRSAMAEGSGEVVTVSATGAANGLNNGAGGTSATT
0323	1		SNPLSRKLHKILETRLDNDKEMLEALKALSTFFVENSLRTRRNL
!	}	1	RGDIERKSLAINEEFVSIFKEVKEELESISEDVQAMSNCCQDMT
l.	Į.	ı	SRLQAAKEQTQDLIVKTTKLQSESQKLEIRAQVADAYLSKFQLT
1			SDEMSLLRGTREGPITEDFFKALGRVKQIHNDVKVLLRTNQQTA
1	ì	}	SDEMSLLRGTREGPTTEDFFRALGRANGIANDARABHRINGGIA
i	i		GLEIMEQMALLQETAYERLYRWAQSECRTLTQESCDVSPVLTQA
i	Į.	i	MEALQDRPVLYKYTLDEFGTARRSTVVRGFIDALTRGGPGGTPR
1	1	1	PIEMHSHDPLRYVGDMLAWLHQATASEKEHLEALLKHVTTQGVE
1			ENIQEVVGHITEGVCRPLKVRIEQVIVAEPGAVLLYKISNLLKF
i .	1		YHHTISGIVGNSATALLTTIEEMHLLSKKIFFNSLSLHASKLMD
i	1		KVELPPPDLGPSSALNQTLMLLREVLASHDSSVVPLDARQADFV
1			KVELPPPDLGPSSPLINQ I INIDERS V DROMBOS V V Z DESTANDA I ALE
i	1		QVLSCVLDPLLQMCTVSASNLGTADMATFMVNSLYMMKTTLALF
1	1	1	EFTDRRLEMLQFQIEAHLDTLINEQASYVLTRVGLSYIYNTVQQ
1			HKPEOGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL
1			HKPEOGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL
			HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR
			HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPOOVOTLLS
6330	1151	333	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL
6330	1151	333	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHOPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR
6330	1151	333	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC
6330	1151	333	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVOTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN
6330	1151	333	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN ROVICVTLKVLOHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV
6330	1151	333	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN ROVICVTLKVLOHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV
6330	1151	333	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVOTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQFL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP
6330	1151		HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKMMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLLN
6330	1151	333	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLLN OGGORVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL
			HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAPINIKYVVP TYESCLLN QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY
			HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAPINIKYVVP TYESCLLN QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY
			HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVOTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQFL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLLN QGGQRVRTGGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV
6331	3	495	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVOTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQFL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLLN QGGQRVRTGGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV
			HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVOTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLLN QGGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDT
6331	3	495	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVOTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLLN QGGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLIASIVAASKSYNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS
6331	3	495	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTELVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVOTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLIPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLLN QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVITCISWPLSELLHYLIGTLLLLIASIVASKSYNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY
6331	3	495	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAPINIKYVVP TYESCLLN QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDT NLLDYLPEILDGLFQILGDNGKEIKKCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD
6331	3	495	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAPINIKYVVP TYESCLLN QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDT NLLDYLPEILDGLFQILGDNGKEIKKCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD
6331	3	495	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAPINIKYVVP TYESCLLN QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVITCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD ELRPGOROAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD
6331	3	495	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAPINIKYVVP TYESCLLN QQQQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAPICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVITCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD ELRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG
6331	3	495	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQOVOTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQFL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLLN QGGQRVRTGGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD BLRPGQRQAEPTPDDALFKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KISTMATHSOLVKTGTGLEPRQAVSSSH
6331	1	495	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQOVOTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQFL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLLN QGGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD ELRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH TRTPSEAEAGGESPOSCVSAAHSDWTAGKFVSLLAPLIPPRSAG
6331	1	495 878	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVOTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLLN QGGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD ELRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSH TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG
6331	1	495 878	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQQVQTLLS FYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLIN QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY SGGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD ELRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG GLMMCHPGMHYAPMGMHPMGCRANMPPVPHGMMPQMMPPMGGPP
6331	1	495 878	HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL LSATVKEQIVKQSTBLVCRAYGEVYAAVMNPINEYKDPENILHR SPQOVOTLLS FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQFL PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP TYESCLLN QGGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNQSGLVAGA IFGFMATFLCMASIWLSYKISCVTQSTDAAV VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS SVKFAEMANILVIHCQTTDDLIQLTAMCMMREFIQLAGRVMLPY SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD ELRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG KLSTMATHSQLVKTGTGLEPRQAVSSSH TRTPSEAEAGGESPOSCVSAAHSDWTAGKFVSLLAPLIPPRSAG

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-ch
-	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1		·	GAKSMWTEHKSPDGRTYYYNTETKOSTWEKPDDLKTPAFOLLSK
1			CPWKEYKSDSGKPYYYNSQTKBSRWAKPKELEDLEGYONTTVAG
1	1		SLITKSNLHAMIKAEESSKOEECTTTSTAPVPTTEIPTTMSTMA
1		:	AAEAAAAVVAAAAAAAAAAAAAANANASTSASNTVSGTVPVVDRP
1	i		EVTSIVATVVDNENTVTISTEEOAOLTSTPAIODOSVEVSSNTG
1			EETSKQETVADFTPKKEEEESOPAKKTYTWNTKEEAKOAFKELL
1			KEKRVPSNASWEQAMKMI INDPRYSALAKLSEKKOAFNAYKVOT
6334	. 17		EKK
0331	1 - 1	644	GGNPSGRAAGFAAAAMPSSPLRVAVVCSSNQNRSMEAHN1LSKR
	j .		GFSVRSFGTGTHVKLPGPAPDKPNVYDFKTTYDQMYNDLLRKDK
			ELYTQNGILHMLDRNKRIKPRPERFQNCKDLFDLILTCEERVYD
}			QVVEDLNSREQETCQPVHVVNVDIQDNHERATLGAFLICELCQC
6335	82	529	IQHTEDMENBIDELLQEFEEKSGRTFLHTVCFY
1	_		AARARPGVLCCRLLGAALGDQSRVEMSYIPGQPVTAVVQRVEIH KLRQGENLILGFSIGGGIDQDPSQNPFSEDKTDKGIYVTRVSEG
			GPAELAGLQIGDKIMQVNGWDMTMVTHDQARKRLTKRSEEVVRL
L	1		LVTRQSLQKAVQQSMLS
6336	1003	438	HEPASKGRAEVGNMRLSVAAAISHGRVFRRMGLGPESRIHLLRN
1.	ł		LLTGLVRHERIEAPWARVDEMRGYAEKLIDYGKLGDTNERAMRM
			ADFWLTEKDLIPKLFQVLAPRYKDQTGGYTRMLQIPNRSLDRAK
ł	! !		MAVIEYKGNCLPPLPLPRRDSHLTLLNQLLQGLRQDLRQSQEAS
- 6339			NHSSHTAQTPGI
6337	76	524	EGIQMLSVQPDTKPKGCAGCNRKIKDRYLLKALDKYWHEDCLKC
1			ACCDCRLGEVGSTLYTKANLILCRRDYLRLFGVTGNCAACSKLT
			PAFEMVMRAKDNVYHLDCFACOLCNORFCVGDKFFLKNNMTLCO
6338	66	1349	TDYREGLMKEGYAPQVR
		1349	APNSESGTQGPLPTPANLFWTRRANPDPTTSMSATDRMGPKAVP
	1		GLRLALLLLIGLGTPKSGVQGQEGLDFPEYDGVDRVINVNAKNY
			KNVFKKYEVLALLYHEPPEDDKASQRQFEMEBLILELAAQVLED
1			KGVGFGLVDSEKDAAVAKKLGLTEVDSMYVFKGDEVIEYDGEFS ADTIVEFLLDVLEDPVELIEGERELQAFENIEDEIKLIGYFKSK
			DSEHYKAFEDAAEEFHPYIPFFATFDSKGAKKLTLKLNEIDFYE
			AFMEEPVTIPDKPNSEEEIVNFVEEHRRSTLRKLKPESMYETWE
			DDMDGIHIVAFAEEADPDGFEFLETLKAVAQDNTENPDLSIIWI
1			DPDDFPLLVPYWEKTFDIDLSAPQIGVVNVTDADRLWMEMDDEE
			DLPSAEELEDWLEDVLEGEINTEDDDDDDDDD
6339	246	1823	NRCDRGGGGQAERQAGQGCRTOGAGPGFGFGHSFFSOGAMKARU
, 1		i	TFCVVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDS
] [[VTESPORVIITEDDEDETTVELEGODENOEGDFEDADTOEGDTE
1 1	1		SEPYDDEEFEGYEDKPDTSSSKNKDPITIVDVPAHLQNSWESYY
	l		LEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNTHRELLESNFTL
]			VGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFL
	. [KRODLLNVLARMMRPVSDQVQIKVTMNDEDMDTYVFAVGTRKAL
1 1		ļ	VRLQKEMQDLSEFCSDKPKSGAKYGLPDSLAILSEMGEVTDGMM
]]		DTKMVHFLTHYADKIESVHFSDQFSGPKIMQEEGQPLKLPDTKR
1 1	1		TLLLTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNRE GKQKADKNRARVBENFLKLTHVQRQEAAQSRREEKKRAEKBRIM
			NEEDPEKQRRLEBAALRREOKKLEKKOMKMKÖIKVKAM
6340	2	583	EACAHTLSCPAFARLGRARRRPWMSHRTSSTFRAERSFHSSSS
, l	İ		SSSTSSSASRALPAQDPPMEKALSMFSDDFGSFMRPHSEPLAF
[PARPGGAGNIKTLGDAYEFAVDVRDFSPEDIIVTTSNNHIEVRA
			EKLAADGTVMNNFAHKCQLPBDVDPTSVTSALREDGSLTIRARR
			HPHTEHVQQTFRTEIKI
6341	2	645	KMAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSTO
		}	PALPKARAVAPKPSSRGEYVVAKLDDLVNWARRSSLWPMTFGLA
			CCAVEMMHMAAPRYDMDRFGVVFRASPRQSDVMIVAGTLTNKMA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
WO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	sequence	\=possible nucleotide insertion)
	sequence		PALRKVYDOMPEPRYVVSMGSCANGGGYYHYSYSVVRGCDRIVP
ļ	1	1	VDIYIPGCPPTAEALLYGILQLQRKIKRERRLQIWYRR
6342	2	1191	DPRVRAMLATLARVAALRKTCLFSGRGGRGLWTGRPOSDMNNI
6342	2	1191	KPLEGVKILDLTRVLAGPFATMNLGDLGAEVIKVERPGAGDDTR
]	1	j .	TWGPPFVGTESTYYLSVNRNKKSIAVNIKDPKGVKIIKELAAVC
1	1		DVFVENYVPGKLSAMGLGYEDIDEIAPHIIYCSITGYGQTGPIS
1	1	i	ORAGYDAVASAVSGLMHITGPEVACLSHIAANYLIGQKEAKRWG
1	}	Į.	TAHGSIVPYQAFKTKDGYIVVGAGNNQQFATVCKILDLPELIDN
ļ	1	1	SKYKTNHLRVHNRKELIKILSERFEEELTSKWLYLFEGSGVPYG
1	1	i	PINNMKNVFAEPOVLHNGLVMEMEHPTVGKISVPGPAVRYSKFK
	ł	1	1 · · · · · · · · · · · · · · · · · · ·
			MSEARPFPLLGQHTTHILKEVLRYDDRAIGELLSAGVVDQHETH
6343	2	936	GTAMVSDEDELNLLVIVVDANPIWWGKQALKESQFTLSKCIDAV
İ			MVLGNSHLFMNRSNKLAVIASHIQESRFLYPGKNGRLGDFFGCP
1	1		GNPPEFNPSGSKDGKYELLTSANEVIVEEIKDLMTKSDIKGQHT
	İ	İ	ETLLAGSLAKALCYIHRMNKEVKDNQEMKSRILVIKAAEDSALQ
			YMNFMNVIFAAQKQNILIDACVLDSDSGLLQQACDITGGLYLKV
1	ļ.	j	POMPSLLQYLLWVFLPDQDQRSQLILPPPVHVDYRAACFCHRNL
1	}	ł	IBIGYVCSVCLSIFCNFSPICTTCETAFKISLPPVLKAKKKLK
			VSA TMPTATLGNLRGYGMASPGLAAPSLTPPQLATPNLQQFFPQATR
6344	2508	147	1
1	1	į.	QSLLGPPPVGVPMNPSQFNLSGRNPQKQARTSSSTTPNRKDSSS OTMPVEDKSDPPEGSEEAAEPRMDTPEDQDLPPCPEDIAKEKRT
ł	ł		PAPEPEPCEASELPAKRLRSSEEPTEKEPPGQLQVKAQPQARMT
1			VPKOTOTPDLLPEALEAOVLPRFQPRVLQVQAQVQSQTQPRIPS
[į	1	TDTQVQPKLQKQAQTQTSPEHLVLQQKQVQPQLQQEAEPQKQVQ
1	1	1	PQVQPQAHSQGPRQVQLQQEAEPLKQVQPQVQPQAHSQPPRQVQ
İ		1	LOLOKOVOTOTYPOVHTQAQPSVQPQEHPPAQVSVQPPEQTHEQ
1	1	į	PHTQPQVSLLAPEQTPVVVHVCGLEMPPDAVEAGGGMEKTLPEP
İ	ł		
ļ	ì	i	VGTQVSMEEIQNESACGLDVGECENRAREMPGVWGAGGSLKVTI LQSSDSRAFSTVPLTPVPRPSDSVSSTPAATSTPSKQALQFFCY
1	Ī	1	1 **
i	ł	l	ICKASCSSQQEPQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR
ì		i	DVLETEDEEPPPRRWCNTCQLYYMGDLIQHRRTQDHKIAKQSLR PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKELKSLEKEIAGQDE
1		1	
1	1		DHFITVDAVGCFEGDEEEEEDDEDEEEIEVEEBLCKQVRSRDIS REEWKGSETYSPNTAYGVDFLVPVMGYICRICHKFYHSNSGAQL
Į.	1		REEWKGSETYSPNTAYGVDFLVPVMGIICKICHKFIHSNSGAQL SHCKSLGHFENLQKYKAAKNPSPTTRPVSRRCAINARNALTALF
1	}		TSSGRPPSOPNTODKTPSKVTARPSQPPLPRRSTRLKT
	 	3483	PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMIEQLQEKV
6345	2	3183	PRVRTKLIGLVNDKKRYERVGGGPKRIGRDVEMEEMIEGLGEKV HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK
1	1	1	ANENAGLOECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE
	1	1	IRNLENVIOSORGOIEELEHLAEILKTQLRRKENEIELSLLQLR
1		1	
ļ	1		EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER
1	1		
1			RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ
1		!	QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNEKLVQENREL
1	1	1	QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE
		1	QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM
1	[LIMOHKINKDYOMEVEAVTRKMENLOODYELKVEQYVHLLDIRA
	1		ARIHKLEAQLKDIAYGTKQYKFKPEIMPDDSVDEFDETIHLERG
1			ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV
1		1	VRGLHPEYNFTSQYLVHVNDLFLQYIQKNTITLEVHQAYSTEYE
ļ	1	1	TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL
1			RVPMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL
1			SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA
1	1	1	DHDTAIIPSSNDPQFDDHMYFPVPMNMDLDRYLKSESLSFYVFD
L		<u></u>	DSDTQENIYIGKVNVPLISLAHDRCISGIFELTDHQKHPAGTIH

SEO	Predicted	Dyodiata	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
- 1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
- 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ī	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +=Stop
l l	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
			VILKWKFAYLPPSGSITTEDLGNFIRSEEPEVVORLPPASSVST
ł			LVLAPRPKPRQRLTPVDKKVSFVDIMPHQSDVSOEGSVDEVKEN
1			TEKMQQGKDDVSLLSEGQLAEQSLASSEDETEITEDLEPEVEED
1			MSASDSDDCIIPGPISKNIKQPSEKIRIEIIALSLNDSOVTMDD
Į			TIQRLFVECRFYSLPAEETPVSLPKPKSGQWVYYNYSNVIYVDK
[ENNKAKRDILKAILQKQEMPNRSLRFTVVSDPPEDEQDLECEDI
	İ		GVAHVDLADMFQEGRDLIEQNIDVFDARADGEGIGKLRVTVEAL
6346	2921	533	HALQSVYKQYRDDLEA
ĺ		223	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
1			AKYTQKEESAEQPEFYYDEFGFRVYKEEGDEPGSSLLANSPLME
1			DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
			QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
1			QGTGMVAACLLLFLEBEDAFWMMSAI IEDLLPASYFSTTLLGVQ
1			TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
			DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIOSENSAST
1			FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETORRKHLAVI.
			IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
1			KAKNI KQTELVADLREAILRVARHFQCTDPKNCSVVSROLPGLL
			PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
1			RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
			ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL
			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSPLRSPGWVQIKC
1			ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW
62.0			l nade
6347	2921	533	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
1			AKYTOKEESAEQPEFYYDEFGFRVYKEEGDEPGSSLIANSPIME
			DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKIRSI.VI.A
			GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
1	ŀ		QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
1 1			QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ
			TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
1 1			DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL
			IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
1 1			KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL
1 1			PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
] [ļ	RRRAKALLDFERHDDDELGFRKNDIITIVSOKDEHCWVGETNGT
1			RGWFPAKFVEVLDERSKEYSLAGDDSVTEGVTDLVRGTLCPALK
1 1			ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVVSRLVI.
	}		CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAOMDVKLRSI.
]]	-		ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC
	İ		ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW DVDG
6348	3	3679	_ : = =
	į	1	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
1	ì	!	KLAEQLKQAEELRQYKVLVHSOERELTQLREKLREGRDASRSLM EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
1		i	DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
			NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
}		ł	ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
-			EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
1	1		ERQFKEEKLAEQLKQAEELROYKVLVHSOERELTOLREKLREGR
1		1	DASRSLNEHLQALLTPDEPDKSOGODLOEOLAEGCRLAOHT.VOK
		<u> </u>	LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE

Deginning corresponding to first amin acid contion corresponding to first amin acid residue of amin acid residue of amin acid sequence residue residue of amin acid sequence residue resid	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO: location corresponding to first amino acid residue of seidue o				
corresponding to first amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence sequence	1			
to first amino acid residue of amino acid residue of amino acid sequence Ference F	140.			
To first amino acid residue of amino acid amino acid amino acid amino acid amino acid sequence ##TYPtOphan, Y=Tyxcoine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,				1 · · · · · · · · · · · · · · · · · · ·
mino acid residue of amino acid sequence solve of amino acid sequence (Codon, /-possible nucleotide deletion, /-possible nucleotide deservion) (Possible nucleotide nucleotide deservion) (Possible nucleotide deservion) (Possible nucleotide deservion) (Possible nucleotide deservion) (Possible nucleotide deservion) (Possible nucleotide deservion) (Possible nucleotide deservion) (Possible nucleotide deservion) (Possible nucleotide deservion) (Possible nucleotide deservion) (Possible nucleotide deservion) (Possible nucleotide deservion) (Possible nucleotide deservion) (Possible nucleotide deservion) (Possible nucleotide deservion) (Possible nucleotide deservion) (Pos				,
residue of amino acid sequence				
amino acid sequence Codon, /-possible nucleotide deletion, -possible nucleotide insertion) ECAITCSNSHGPYDSNOPHRKYKITFEEDKVDSTLIGSSSHVER EDANITIPENSBODEEEEKGPYDSPNIGESEEEKGPVGSNDEE ECAITCSNSHGPYDSNOPHRKYKITFEEDKVDSTLIGSSSHVER EDANITIPENSBODEEEEKGPYDSPNIGESEEKGPVGSNDEE COPYRSAFYVLEOGRVGLAVNHOEIEKYGSVEEDQDPSCPRISS ELDEKEPEVLQDSLGRCYTPSSCLELIDSSCPVISSTSCLELDTON COPYRSAFYVLEOGRVGLAVNHOEIEKYGSVEEDQDPSCPRISSAVISEE GYLGLALDVDRIKKDGEEEDQGPPCPFLISSRLLEGVVEPEVLQD SLDRCYSTPSSCLEDDSCCPYRSAFYLLEGGRVGATALD SLDRCYSTPSSCLEDDSCCPYRSAFYLLEGGRVGATALD DMDEIEKYGSVEEDQDPSCPPRISSFLLEGGRVGATAL DMDEIEKYGSVEEDQDPSCPPRISSFLLEGGRVGATAL DMDEIEKYGSVEEDQDPSCPPRISSFLLEGGRVGATAL DMDEIEKYGSVEEDQDPSCPRASFYLLEGGRVGATALDEKTEP DODPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGTLELDEGGRVGATALDEKTEPTALOGENCATAL DMDEIEKYGSVEEDQDPSCPRASFYLLEGGRVGATALDEKTEPTALOGENCATAL DMDEIEKYGSVEEDQDPSCPRASFYLLEGGRVGATALDEKTEPTALOGENCATAL DMDEIEKYGSVEEDQDPSCPRASFYLLEGGRVGATALDEKTEPTALOGENCATALDEKTERTALDEKTEPTALOGENCATALDEKTEPTALOGENCATALDEKTEPTALOGENCATALDEKTERTALDEKTEPTALOGENCATALDEKTERTALDEKTEPTALOGENCATALDEKTERTALDEKTEPTALOGENCATALDEKTERTALDEKTEPTALOGENCATALDEKTERTALDEKTEPTALOGENCATALDEKTERTALDEKTEPTALOGENCATALDEKTERTALDEKTEPTALOGENCATALDEKTERTALDEKTEPTALOGENCATALDEKTERTALDEKTEPTALOGENCATALDEKTERTALDEKTEPTALOGENCATALDEKTERTALDEKTEPTALOGENCATALDEKTERTALDEKTEPTALOGENCATALDEKTERTALDEKTERTALDEKTERTALDEKTERTALDEKTERTALDEKTERTALDEKTERTALDEKTERTALDEKTERTALDEKTERTALDEKTERTALDEKTERTALDEKTERTALDEKTERTALD				
Sequence Sequence				
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VGPSLDVGBIEKKGKGKKRRGRESKERRGRKEGEEDOMPPCP RINSMLMEVEEPEVLQDSLDICYSTPSMYFELDSFOHYRSVFY SFEEBHISRALVDNRFFILTVTSLHLVFQMGVIFPQ AGAEKCFVTLLACFLAKQONKYKYEECKDLIKSMLRNELQFKEE KLABQLKQABELRQYKVLVHSQEEKTDLIKSMLRNELQFKEE KLABQLKQABELRQYKVLVHSQEEKTDVLBEKLEGRDASRSLN EIILQALLTPDEPDKSQGQDLQBQLABGCRLAQHLVOKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEKEVEPEDSLMECAITCS NSKGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILLPVFGFTSSATNVSMVVSAGPLSGEKAANILEINEKLRFQLA EKKQQFRNLREKFFLTQLACFLANQONKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEBLRQYKVLVHSQERELTQLREKKLRFGR DASRSLMEHLQALLTDDEPDKSQGQDLQEQLABGCRLAQHLVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIJFNENSDDEEEEKGPVSFRNLQSSEEEEVQGESWDEG YSTLSIPPRMLASYKSYSSTFHSLEEQQVCMAVDIGRHRMDQVK KEDHRATGPRLSRELLDEKGPVSFRNLQSSEEEEVQGESWDEG YSTLSIPPRMLASYKSYSSTFHSLEEQQVCMAVDIGRHRMDQVK KEDHRATGPRLSRELLDEKGPVSFRNLQSSEEELVQESWDEG YSTLSIPPRMLASYKSYSSTFHSLEEQQVCMAVDIGRHRMDQVK KEDHRATGPRLSRELLDEKGPVSFRNLQSSLEGEVPGCENDEG YSTLSIPPRVLSQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR ELLDEKKPBVLQDSLGCRCYSTPSGVLELDLOGPYSSAVYSLEE QYLGLALDVDRIKKDQEBEEDQGPPCPRLSRELLEVE KKKKKRRGRRSKKERRGRKSKERRGFRALLEKHWGFSLDVGEIE KKKKKRRGRRSKKERRGRKSKERRGPLASELDLOGPYSSAVYSLEE QYLGLALDVDRIKKDQEBEEDQGPPCPLSRELLEVE KKKKKKRRGRRSKKERRGRKSKERRGPLASELDVEYEPVLQD SLDRCYSTPSGCLEUTDSCQPYGSSFYALEEKH KKKKKKRRGRRSKKERRGRKSKERRGNKSEPEDLORYS PEVLQDSLDRCYSTPSGCLELDDSCQPYGSSFYALEEKH VGPSLDVGLGLALDVDRIKKDQEBEDQOPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPPSCQPYGSSFYALEEKH VGPSLDVGLGLALDVDRIKKDQEBEDQOPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPPSCQPYGSSFYALEEKH VGPSLDVGLGLALDVDRIKKDQEBEDQOPPCPRLSREL LEVVEPEVLQDSLDLCYSTPSSCLEQPPSCQPYGSSFYALEEKH VGPSLDVGLGLALDVGRKKRRGRRSKKERRRRRKERBEDOMPCCP RLNSMLMEVEEPEVLQDSLDICYSTPSSCLERDPSCOPYGSSPYALEEKH VGPSLDVGLGLKLGKKKRKRRRRKKKRRRRRKERRERDNINGERHDN DDDEDVQFVARAEVTLACFLAKQONKYKYEECKDLIKSPENDN DDDEDVQFVARAEVTLACFLAKQONKYKPECKDLIKSPENDN DDDEDVQFVARAEVTLACGAKANILIUTDDEPDKSGAGDLAGHLOVKLRSPENDN DDDEDVQFVARAEVTNSWVASAGPLEKAGRANILIUEINNKLRPGDL EKKQQFRNLKEKCFLTQACFLANQONKYKYEECKDLIKFMGR				PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL
RIANSMIMBUEDEPULQDSLDICYSTPSMYFELPDSFOHYRSVFY SFEEHISPALYUDNRFFTLTVTSILLVFQMGVIFPQ 6349 3 3679 AGAEKCFVTLLACFLAKQONKYKYEECKDLIKSMIKNELQFKEE KLABQLKQABELRQYKVLVHSQERELTQLEKKLEGRDASRSLN DILLQALITPDEPDKSGQOLDGOLAGCGRLAQHLVOKLSPENIN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSKGPCDSNOPHKNIKITFEBDEVNSTLVDRESSHDECQDALD ILPVPGPTSSATINVSMVVSAGPLSGEKAANNILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ROFFKEKLABQLKOABELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQQOLDGULABGGRLAQHLVQX LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHGFYDSNOPHRKTKITFEBDKVDSTLIGSSSHVEW EDAWHIIPENESDDEEEEKGPVSPRNLOBSEEEVPQESWDEG YSTLSIPPRMLASYKSYSSTHFISLEQQVCMAVDICRHRHROVE ECAHTCSNSHGFYDSNOPHRKTKITFEBDKVDSTLIGSSSHVEW EDAWHIIPENESDDEEEEKGPVSPRNLOBSEEEVPQESWDEG YSTLSIPPRMLASYKSYSSTHFISLEQQVCMAVDICRHRHROVE ELDEKRPEVLQDSLGRCYSTPSGCVEEDQDPSCPRLSR GELEKFEVELQDSLGRCYSTPSGCVEEDQDPSCPRLSR GLEKFREVELQBSLGRCYSTPSGCVEEDQDPSCPRLSR GLEKFREVELQBSLGRCYSTPSGCVEEDQDPSSPAVSLEE QYLGLALDVDRIKKDQEEEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYSSSFYALEEKHVFSLDVGEIE EKKGKKRRGRRSKKERRRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSSCLEUTDSCQPYRSAFYILEQGRVGLAV DMBEIEKYGSVEEDQDPSCCPHLSGELLDEKEPEVLQSELDRCYS TPSGCLELTDSCQPYRSAFYILEQGRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSSCLEDLDSCQPYLGSEDRCYS TPSGCLELTDSCQPYRSAFYILEQGRVGLAVDMDEIEKYQEVEE DQPSSPRYSEEDQILGRLALDVUR KKDGEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYSSFYALEEKH VGFSLDVGEIEKKKGKKRRGRKSKKERRGRKSEEDDONPPC RLNSMLMEVEEPEVLQDSLDICYSTPSNYFELPDSPQHYRSVFY SPEEHISFALYVDNRFFTLTVTSLHUFFOMGVIFPQ CRLNSMLMEVEEPEVLQDSLDICYSTPSNYFELPDSPQHYRSVFY SPEEHISFALVDNRFFTLTVTSLHUFFOMGVIFPQ CRLNSMLMEVEEPEVLQDSLDICYSTPSNYFELPDSPQHYRSVFY SPEEHISFALVDNRFFTLTVTSLHUFVOMGVIFPQ CRLNSMLMEVEEPEVLQDSLDGCAAINLIEBELQFKEE NSHGPCDSNOPHKNIKITFEEDEVNSTLVVRESSHEEGADARSLN EHLQALLTPDEPDKSQGQDLQEGLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQRAEEKEVPEDSLEECAITCS NSHGPCDSNOPHKNIKITFEEDEVNSTLVVRESSHEDCQDALN ILPVPGGTSSATNYSMVVSAGFLSGEKANNILEINEKLRPGL EKKQQFRNLKEKCFLTQLACFLARGKRLREGR DARSKNEHLGLALTTDEPDENSGQGDLQEGLAEGCRL	ţ			LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH
SPEERHISPALYVDNRFFTLTVTSLHLUVFDMGVIFPO AGAEKCFVTLLACFLAKQONKYKYEECKDLIKSMLRNELQFKEE KLABQLKQABELRQYKVUHYGERELTQLREKLREGRDASRSLM EILQALLTPDEPDKSQQQDLQEQLABCCLAGCHLOVKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEKKEVPEDSLBECAITCS NSHGPCDSNOPHKNIKITFEDEWNSTLVVDRESSHDECQDALM ILPVPGPTSSATNVSMVVSAGPLSGEKAANINLEINEKLRPQLA EKKQQFKNLKEKCFLTQLAGCHLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLABQLKQABELRQYKVUHYGGRELTQLREKLREGR DASRSLNEHLQALLTDDEPDKSQQQDLQEQLABGCHLAGHIVQK LSPENDNDDDBDVQVEVAEKVQKSSAPREMPKAEKEVPEDSLE ECAITCSNSHGPYDSNQPHRKTKITFEDEWOSTLIGSSHVEW EDAVHIIPENESDDEEEEKGFVSPRNLOESEEBEVPQESWBEG YSTLSIPPENLASYKSYSSTFHSLERQVMANDICHRRHRDQVK KEDHRATGPRLSKELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVCLAVMMDEIRKYGEVEEDQDPSCPRLSR ELLDEKBPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDGEBEEDQGPPCPRLSRELLEVVEEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSTYALEEKHVGFSLDVGEIE KKGKKRRGRRSKEERRGKSGEDQNFPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSREPLLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSREPLLDEKG PSSCLELTDSCQPYRSAFYILEQQRVGLAVBMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLDRCYSTPSGYLELPDLGQ PYSSAVYSLEEQXIGLALDVDRIKKDQEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSGCLEDDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRKKERRGRKEGEEDQNPPCP RLMSMLMEVEEPEVLQDSLDCYSTPSGYLELPDLGQ PYSSAVYSLEGXIGLALDVDRIKKDQEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSGCLEOPSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRKKERRGRKEGEEDQNPPCP RLMSMLMEVEEPEVLQDSLDCYSTPSGYLEDPDLGQ PYSSAVYSLEGXIGLADVDRIKKDQEEEDQFPCPRLSREL LEVVEPEVLQDSLDRCYSTPSGCLEQDFCQFCCPRLSREDL FULGALLTPDEPDRSGCQDLGQLAEGCRLAQHLVQKLSPENDIN DDDEDVQVEVAERVQKSSSPREMQKAEEKEVPEDSLECCAITCS NSHGPCDSNOPHKNIKTFFEDEWNSTLVVDRESSBIDCCDDALN ILPPPGPTSSATNVSMVVSAGPLSGEKAANILBINEKLREPULA EKKQQFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLNN ERGFKEEKLAEQLKQAEELRQYKULVHSGERELTQLREKLREGR BKKQQFRNLKEKCFLTQLACFLANOONKYKYEECKDLIKFMLNN ERGFKEEKLAEQLKQAEELRQYKULVHSGERELTQLREKLREGR BKKQGFRNLKEKCFLTQLACFLANOONKYKYEECKDLIKFMLNN ERGFKEEKLAEQLKQAEELRQYKULVHSGERELTGLREKLREGR	}			VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP
3 3679 AGARKEPVILLACELAKQONKYKYEEKKÜLIKSMILNELQFKEE KLAEQIKQAEELRQYKVIVINSQERELTQIREKLREGRDASRSIN EIILQALLTPDEPPKSQGQDLQEQLABGCRLAGHIVOKLSPENDN DDDEDVQVEVAEKVQKSSSPREMOKAEKKVPEDSLEECAITCS NSKGPCDSNOPHNIKITTEEDEVSTSTLVVDRESSHDECQDALM ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQOKKKYEECKDLIKFMENN ERGFKEEKLAEGLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALITDEPPKSQGQDLQEQLABGCRLAGHIVOK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHGPVDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEEERGFVSPRNLOESEEBEVPQESWDEG YSTLSIPPENLASYSSYSSTYHSLEEQQVVGMAVDIGRHRMOVK KEDHRATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELIDS CQPYRSAFYVLEQQRVGLAVMMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEEDQCPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEOPDSCOPYGSSTYALEERHVGFSLUDGEIE KKGKGKKRRGRRSKKERRGRKSGEEDONPPCPRLSRELLEVVEPEVLQD DEDESCPRLSRELLDEKGPESPLQESPLLDEKGPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKGPSPLOPSGRVLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKGPSTPSGLELDBLKGPSLVQEVEE DQDPSCPRLSRELLDEKGPSPLOPSGRVLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKGPSPLOPSGRVLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKGPSPLOPSGVPTSGSYLLEDLOG PYSSAVYSLEEQYIGLALDVDRIKKDQEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSGLLDEKGPSVLQESEDLOG PYSSAVYSLEEQYIGLALDVDRIKKDQEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEGDPSCQPYGSSFYALEEHN VGFSLDVGGTEKKGKGKKRGRRSKKERRGRKEGEEDOMPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELDBCOMPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELDBCOPYTSYFY SFEERHISPALYVDNFFFTLTVYSLHLVFOMGVIFFQ 6350 3 3679 AGAEKCFVTLLACFLAKQOKKYKYEECKDLIKSMLENELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSIN EHLQALLTPDEPDKSQGQDLOGQLAEGCRLAGHLVOKLSPENDN DDDEDVQVEVAEKVQKSSFRENQKAEEKEVPEDSLEECAITCS NSHGPCDSNOPHNIKTTFEDEDVNSTLVVDRESSBIDECQDALN ILEVPGFTSSATNVSMVVSAGPLSGEKAATNILENTEKLREPGIA EKKQQFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLEN ERGFKEEKLAEQLKQAEELRQYKVLVHSGERELTQLREKLREGG DASRSINSHHUAGALLTTDEPDKNSGGODLOGOLAEGCRLAGHLVOKL				RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY
KLAEQLKQAEELRQYKVI.VHSQERELTQLREKLREGRDASRSI.N EIILQALLTPDEPDKSQQDLQEQLAEGCRLAQHLVOKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLÆCCAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVUDRESSHDECQDALN ILPVPGPTSATNVSMVVSAGGLSGEKAAINILEINEKLRPQLA EKKQQFKNI.KEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERGFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSI.MEHLQALLTPDEPDKSQGDLQBQCHALQGHLVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHGPYDSNOPHRKTKITFEEDKVDSTLIGSSSHYEW EDAVHIIPENSDDEEEEEREGFVSFRNLQESEEREVPQESWDEG YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK KEDHRATGPRILSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVMMDEIEKYQEVEEDQDPSCPRLSR ELLDEKRPEVLQDSLGRCYSTPSGYLELPDLGQPYSAAVYSLEE QYYGLALDVDRIKKDQEBEEDQGPPCPRLSRELLEVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGKKRRGRRSKKERRGRKEGEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLEUTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEBDDDPSCPRLSGELLDEKGPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKERPULQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGJALDVDRIKKQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKRRGRRSKKERRGKEGEEDONPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSNYFELPDSFQHYRSVFY SPEECHISPALLYUNNRFTFLTVTSLHLVPGMVIFPO FLNSMLMEVEEPEVLQDSLDICYSTPSNYFELPDSFQHYRSVFY SPEECHISPALYUNNRFTFLTTVTSLHLVPGMVIFPO FLNSMLMEVEEPEVLQDSLDICYSTPSNYFELPDSFQHYRSVFY SPEECHISPALYDNNRFTFLTTVTSLHLVPGMVIFPO FLAGALLTPDEPDKSQGODLQBCLAGGCRAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLECAITCS NSHGPCDSNGPHKNIKTTFEEDEVSTLVVDRESSHDECQDALN LLEVPGPTSSATNVSMVVSAGFLSGEKAAINILEINEKLRPGLA EKKQOFRNLKEKCFITQLACFLANGONKYKYEECKDLIKFMLRNE EKKQOFRNLKEKCFITQLACFLANGONKYKYEECKDLIKFMLRNE EKKQOFRNLKEKCFITQLACFLANGONKYKYEECKDLIKFMLRNE EKKQOFRNLKEKCFITQLACFLANGONKYKYEECKDLIKFMLRNE EKKQOFRNLKEKCFITQLACFLANGONKYKYEECKDLIKFMLRNE EKKQOFRNLKEKCFITQLACFLANGONKYKYEECKDLIKFMLRNE EKKQOFRNLKEKCFITQLACFLANGONKYKYEECKDLIKFMLRNE EKKQOFRNLKEKCFITQLACFLANGONKYKYEECKDLIKFMLRNE EKKQOFRNLKEKCFITQLACFLANGONKYKYEECKDLIKFMLRNE EKKQOFRNLKEKCFITQLACFLANGONKYKYEECKDLIKFMLRNE EKKQOFRNLKEKCFITQLACFLANGONKYKYEECKDLIKERG			ļ	SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
EIILQALITPDEPDKSQGQDLQEQLABGCRLAQHLUVGKLSPENDN DDDEDVQVEVABKVQKSSSPREMQKABEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVASTLVVDRESSHDECQDALM ILPVPGFTSSATNVSMVVSAGFLSGEKAATNILEINEKURPQLA EKKQOPRILKEKCEITQLAGFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLABQLKQABELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGGQLQEQLABEGCRLAQHLVQK LSPENDNDDDEDVQVEVVAEKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPENLASYKSYSSTPHSLEEQQVCMAVDIGRHEWDGVK KEDHBATGPRIJSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS QYERSAFYVLEQQRVCLAVMDETEKYGEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGVLEIDDLGQPYSSAVYSLEE QYIGLALDVDRIKKQEEEEDQGPPCPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS QYIGLALDVDRIKKQEEEEDQGPPCPRLSRELLDEKGP EVLQDSLDRCYSTPSSCLEDPDSCQPYGSSFYALEEKHVGPSLDVGEIE KKGKGKKRGRGRSKKERRGKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSSCLEDTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEBDQDPSCPRLSGELLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE QDQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGVLELDFLGQ PYSSAVYSLEEQYIGLALDVDRIKKDQEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEDPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKKGKKRRGRSKKERRGREGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDRCYSTPSGVEEDDNPCCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEDPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKKGKKRRGRSKKERRGREGEEDDNPCCP RLNSMLMEVEEPEVLQDSLDRCYSTPSSVFELDPDGFQHKRSVFY SFEEHLISFALYVDNRFFTLTVTSLHLVFOMGVIFPO RLNSMLMEVEEPEVLQDSLDRCYSTPSSVFELDSFQNKXSVFY SFEEHLISFALYVDNRFFTLTVTSLHLVFOMGVIFPO GAGAEKCFVTLLACFLAKQQNKXKYEECKDLIKSMLRNELQFKEE KLAGQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSGQGDLQEOLABGCRLAGHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLECAITCS NSHGPCDSNQPHKNIKTTFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGFLSGEKAANILIENTEKLRPQTA EKKQOFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRNE EKKQFRSKKLAEGUKQAEELRQYKVLVHSQERELTQLREKLREGR EKKQFRSKKLEEGLKGAEELRGALGAELRGYKVLUHSQERELTQLREKLREGR EKKQFRSKLKECGLETQALLTPDEPDKSGQODLQBOLAEGCRLAQHLVGK	6349	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
DDDEDVQVEVARKVOKSSSPREMOKAEEKEVPEDSLEECAITCS NSHGPCDSNOPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILEVPGPTSSATNVSMVSAGPLSGEKAANILEINEKLRPQLA EKKQOFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERQFKEEKLAFQLKQAEELRQYKVLVHSGERELTQLREKLREGR DASRSLHEHQALITPDEPDKSQGQDLQEQLABGCRLAQHLVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHGPYDSMOPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEEKGPVSPRNLQESEEEEVPQESWDEG YSTLSIPPEMLASYKSYSSTFHELEKQQVCMAVDIGRHRWDQVK KEDHBATTSPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVMMDEIEKYGEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEEEDQSPPCPRLSRELLEVVSPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGKKRRGRRSKKERRGKKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIBKYQEVEBDQDPSCPRLSGBLLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIBKYQEVEBDQDPSCPRLSGBLLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEDQGPPCPRLSREL LEUVEPEVLQDSLDRCYSTPSSCLEQPDSCOPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRGRKEGEEDQNPPCP RLMSMLMEVEBPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SPEEMLISFALLYVDMFTTLTVTSLHLVFOMGVIFPQ 6350 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNBLQFKEE KLABQLKQAEELRQYKVLVHNSGERELTQLREKREGRDASRSLM EHLQALLTPDEPDKSGQODLQEQLAEGCRAAGHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLBECAITCS NSHGPCDSNOPHKNIKITFEEDEVNSTLVVDKLSSHDECQDALN ILPVPGFTSSATNVSMYVSAGPLSGEKAANNILEINEKLRPQLA EKKQOFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERGFKEEKLAEQLKQAEELRQYKVLVHSGERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSGQODLQELAEGCRLAQHLVQKLSFENDN LEKKQOFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERGFKEEKLAEQLKQAEELRQYKVLVHSGERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSGGODLQEGLAEGCRLAGHLVQKL	1			KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN
NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILEVPGFTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFKNLKEKCFLTQLACFLANQOKYKYEECKDLIKFMIRN ERQFKEEKLABQLKQAEBLRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQQGDLQEQLAEGCRLAQHLVQK LSPENDNDDDBDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPENBSDDEEEEKGPVSPRNLQESEEEEVPQESWDEG YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK KEDHRATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVMMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYIGIALDVDRIKKDQEBEDQGPPCPRLSRELLEVVSPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEKHVGFSLDVGEIE KKCKGKKRRGRRSKERRRGRKSGEEDQNPPCPRLSRELLDKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSRELLDEKGPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEQYLGLALDVDRIKKDQEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRSKKERRRGKSGEEDDNPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSGCLEDPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRSKKERRRGREGEEDDNPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEHLSFALVVDNRFFTLTVTSLHLVFOMGVIFPQ 6350 3679 AGABCCFVTLLACFLAKQONKYKYEECKDLIKSMLRNELGFKEE EHLQALLTPDEPDRSQGQDLQECLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILEVPGFTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERGFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR BKKQCFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERGFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR	1	1		EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
ILPVPGPTSSATNVSMVVSAGPLSGEKAATNILEINEKLRPQLA EKKQFKNLEKKCFITQLACFLANQOMKYKYEECKDLIKFMLRN ERGFKEEKLABQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSIMEHLQALITPDEPDKSGGQDLQEQLAEGCRLAQHLVQK LSPENDNDDDDDDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHGPYDSNQPHRKTKITTEEDKVDSTLIGSSSHVEW EDAWHIIPENSDDEEEEKGPVSPRNLQSSEEREVPQESWDEG YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK KEDHBATGPRLSRELLDEKGPEVJOPSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVNMEIEKYQEVEEDQDPSCPRLSR ELLDEKSPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYIGLALDVDRIKKDQEEEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGFIE KKGKGKKRGRRSKKERRGRKSGEEDDNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPYSGSPYALEEKHVGFSLDVGFIE KKGKGKKRGRRSKKERRRGKSGEEDDNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELDBKEPEVLQBSLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMBEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYIGLALDVDRIKKNQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEERH VGFSLDVGGIEKKGKGKKRGRRSKKERRGRKEGEEDDNPCP RINSMLMEVEREPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SPEEHLISFALVYDNRFFTLTVTSLHLVFOMGVIFPQ 6350 3 3679 AGAEKCFVTLLACPLAKQQNKYXYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRARSLIN EHLQALLTPDEPDMSGQODLQEQLAEGCRLAQHLVQKLSPEEND DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILEVPGFTSSATNVSMYVSAGPLSGEKAANILLEINEKLRPQLA EKKQOFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERGFKEEKLAEQLKQAEELLQVKVLVHSQERELTQLREKLREGR DASRSLMEHLQALLTPDEPDKSGQODLQELAECRLACHLVQKLSPEEND EKKQOFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERGFKEEKLAEQLKQAEELLRQYKVLVHSQERELTQLREKLREGR DASRSLMEHLQALLTPDEPDKSGQODLQELAECRLACHLVQK	}		•	DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLARQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLMEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK LSPENDNDDDBDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE ECATTCSNSHGFYDSNQPHRKTKITTEEDKVDSTLIGSSSHVEM EDAYHI IPENESDDEEEEKGPVSPRNLQESEEBEVPQESWBEG YSTLS IPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK KEDHBATGPRLSRELLDEKGFPVTQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVMMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPPVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYIGLALDVDRIKKDQEBEEDGPPPCPRLSRELLEVVEFEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHWGFSLDVGEIE KKGKGKKRRGRRSKKERRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPPVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPBVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEBQYLGLALDVDRIKKQDEEEDQFPCPRLSREL LEVVEPEVLQDSLDRCYSTPSGCLEQPPCCRLSREL LEVVEPEVLQDSLDRCYSTPSGCLEQPPCCRLSREH VGFSLDVGEIEKKGKGKKRRGRSKKERRRGRKEGEEDQNPCP RLMSMLMBVESPEVLDSLDLTCYSTSMYFELPDSFQHYRSVFY SFEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ RLMSMLMBVESPEVLDSDLDICTSTSMYFELPDSFGHYRSVFY SFEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ 6350 3 3679 AGAEKCFVTLLACFLAKQGNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSGGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVABKVQKSSSPREMQKAEEKEVPEDSLEECATTCS NSHGPCDSNQPHKNIKITFFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSNVVSAGPLSGEKAAINILEINEKLREPGLA EKKQQFRRILKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRD EKKQGFRRILKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERGFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRD DASRSLMBHLQALLTPDEPDKSGGGDLOEQLAEGCRAAQHLVQK			1	NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLMEHLQALLTDEPPDKSQGQDLQEQLAEGCRLAQHLVQK LSPENDNDDBBDVQVEVAEKVQKSSAPRMPKAEEKEVPEDSLE ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEERKGPVSRNLQSEEEEVPQESWDEG YSTLSIPPENLASYKSYSSTHSLEEQQVCMAVDIGRHRWDQVK KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVMMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEKHVGFSLDVGEIE KKGKKKRRGRRSKKERRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSRELLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKKRRGRRSKKERRGREGEEDONPPCP RLNSMLMEVEEPEVLQDSLDRCYSTPSMYFELPDSFQHYRSVFY SFEEBHISFALVVDNRFFTLTVTSLHLVPOMGVIFPQ 6350 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQEERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDDDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNOPHKIN KITFEEDEVMSTLVVDRESSHDECODALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAECHQYKVJUVHSQERELTQLREKLREGR DASRSLMBHLQALLTPDEPDKSQGQDLOEQLAEGCRLAQHLVQK	İ	l		ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE ECATTCSNSHGFYDYDSNQPHKKTKITFEDKVDSTLIGSSSHVEW EDAVHIIPENESDDEEEEKGPVSPRNLQESEEBEVPQESWDEG YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK KEDHRATGPRLSRELLDEKGPEVLQDSLDGCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYTGLALDVDRIKQDEEEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGKKRRGRRSKKERRRGRKSGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEEDQDPSCPRLSGELLDEKSPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQXIGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGKEGEEDQNPPCP RLMSMLMMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SPEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ 6350 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSOGERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLBECATTCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVNRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQONKYKYEECKOLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNRHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	1			EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
LSPENDNDDDBDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHGPYDSNGPHRKTKITTEEDKUDSTLIGSSSHVEW EDAWHIIPENESDDEEEERKGPVSPRNLOESEEEEVPQESWDEG YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK KEDHRATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVMMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGKKRRGRRSKKERRGGKEGEEDQNPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCOPYGSSFYALEEKHVGFSLDVGEIE KKGKKKRGRRSKKERRGKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEBDQDPSCPRLSGELLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRGKEGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEHISFALYVDNRFFTLTVTSLHLVFOMGVIFPQ KLASQLKQAEELRQYKVLVHSQERELTQLREKLREGGEDASRSLN BHLQALLTPDEPDKSQGQDLQQLABGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS MSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNHHLQALLTPDDEPDKSQGQDLQEQLAEGCRLAQHLVVK	j	1	ļ	EROFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW EDAVHIIPSNSDDEEEEERGPVSPRNLQSEEBEVPQESKDEG YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK KEDHEATGPRLSTRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVMMDEIEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDSLGRCYSTPSGTLELPDLGQPYSSAVYSLEE QYLGALDUDVRIKKDQEEBEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGKKRRGRRSKKERRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQSVEEDDQDPSCPRLSGELLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYILGALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRGRKEGEEDQNPPCP RLMSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SPEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ 6350 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQGLABGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLBECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR			·	DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
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KEDHRATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS CQPYRSAFYVLEQQRVGLAVNMDETEKYQEVEEDQDPSCPRLSR ELLDEKEPEVLQDLGRCYSTPSGYLELPDLGQPYSSAVYSLEE QYLGLALDVDRIKKDQEEBEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGKKRRGRRSKKERRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEBDQDPSCPRLSGELLDEKEPEVLQDSLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKKRKRGRRSKKERRGRKEGEEDQNPPCP RLMSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SPEEBHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ 6350 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLBECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLERKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	}	ł	1	EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG
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QYLGLALDVDRIKKDQEEBEDQGPPCPRLSRELLEVVEPEVLQD SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE KKGKGKKRRGRSKKERRGRKEGEEDQNPPCPRLSRELLDEKG PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV DMDEIEKYQEVEBDQDPSCPRLSGELLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRGREGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ 6350 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVFGFTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERGFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	İ	1	i	COPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
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DMDEIEKYQEVEBDQDPSCPRLSGELLDEKEPEVLQESLDRCYS TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRGRKEGEEDQNPPCP RLMSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEEHISPALYVDNRFFTLTVTSLHLVFQMGVIFPQ 6350 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNOPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	[į		PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV
TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDRIKKDQEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRGRKEGEEDQNPPCP RLINSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEEHISPALYVDNRFFTLTVTSLHLVFQMGVIFPQ 6350 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	1.]
DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGLALDVDR1KKDQEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ 6350 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	1	•		
PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGF5LDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SPEEBHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ 6350 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQIKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNBHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	Į.	ļ	ļ	1 · · · · · · · · · · · · · · · ·
LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP RLMSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SPEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	l			
VGFSLDVGEIEKKGKGKKRRGRRSKKEGREGEDQNPPCP RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SFEEBHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ 6350 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLECCAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	ļ	1	[
RLMSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY SPEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFBEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK]	1		
SFEEBHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ 6350 3 3679 AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEBLRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLBECAITCS NSHGPCDSNQPHKNIKITFBEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNBHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	1	}	Í	
AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	l			
KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	6350	 	3679	
EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTIVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	1 0000		33,3	
DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	!	1		
NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNBHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	1	i	1	
ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	ţ	}		
EKKQQFRNIKEKCFLTQLACFLANQONKYKYEECKDLIKFMLRN ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	l	1	İ	
ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK)	1	1	
DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK	[
		ł	1	
	i		i	
LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE	L	<u> </u>		LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE

)

SEQ	Predicted	Predicted end	Amino acid
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, O=Glutamine, D=Arginine
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine
Į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown *-Ston
İ	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
1			ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEN
1			EDAVHIIPENESDDEEEEEKGPVSPRNLOESEEEEVDOESWDEG
1	1		YSTLS I PPEMLASYKSYSSTFHSLEEOOVCMAVDIGRHPWDOVK
			KEDHEATGPRLSRELLDEKGPEVLODSLDRCYSTPSGCLRLTDS
İ			CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
}			ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
			QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD
1			SLDRCYSTPSSCLEOPDSCOPYGSSFYALEEKHVGFSLDVGEIE
1	İ		KKGKGKKRGRRSKKERRRGRKEGEEDONPPCPRLSRELLDEKG
			PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV
1			DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS
]			TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
]			PYSSAVYSLEEQYLGLALDVDRIKKDQBEEEDQGPPCPRLSREL
			LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH
			VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP
			RENSMEMEVEEPEVEODSEDICYSTPSMYFFLDDSFORVDCVCV
6351			SFEEEHISFALYVDNRFFTLTVTSLHLVFOMGVIFPO
6351	1291	319	REARRITERSQLGRMLVVEVANGRSLVWGAEAVOALBERLGVGG
			RTVGALPRGPRQNSRLGLPLLLMPEEARLLAEIGAVTI.VSADDD
			DSRHHSLALTSFKROOEESFOEOSALAAEARETROOF.I.EVITE
			GQAAKKQKLEQASGASSSOEAGSSOAAKEDETSDGOASGEOVER
			GPSSSQAGPSNGVAPLPRSALLVOLATARPRPVKARPI.DWDVOC
			KDWPHAGRPAHELRYSIYRDLWERGFFLSAAGKFGGDFLVVDGD
			PLRFHAHYIAQCWAPEDTIPLQDLVAAGRLGTSVRKTLLLCSPQ
6352	235	923	PDGKVVYTSLQWASLQ
1		523	WSEWLSPCHAAKCKGLSMLRITMKTRAISLAADATEFVQGRSAP
- 1			AMARSLVHDTVFYCLSVYQVKISPTPQLGAASSAEGHVGQGAPG
1			LMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPROOPQPPPEE PAQAAMEGPQPENMQPRTRRTKFTLLQVEELESVFRHTQYPDVP
ļ			TRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLANELRADP
			DDCVYIVVD
6353	65	672	RFAGAGAIPEARARPPDVQAAEEEKEMDLPDSASRVFCGRILSM
ĺ	ĺ		VNTDDVNAIILAQKNMLDRFEKTNEMLLNFNNLSSARLQQMSER
			FLHHIRTLVEMKRDLDSIFRRIRTLKGKLAROHPEAFSHIDEAG
	i		FLEEEDEDPIPPSTTTTIATSEOSTGSCDTSPDTVSPSLSPGFF
6354			DLSHVQPGSPAINGRSQTDDEEMTGE
0354	965	510	PSLRPMEPTRDCPLFGGAFSAILPMGAIDVSDLRPVPDNOEVEC
			HPVTDQSLIVELLELQAHVRGEAAARYHFEDVGGVOGAPAVHVE
- 1			SVQPLSLENLALRGRCQEAWVLSGKOOIAKENOOVAKDUTT.HOA
6355	150		LLRLPQYQTDLLLTFNQPP
3333	158	1662	RGSSAAFRGSGLRGAMIRRVLPHGMGRGLLTRRPGTRRGGFSLD
		ļ	WDGKVSEIKKKIKSILPGRSCDLLODTSHLPPEHSDVVIVCCCV
			LGLSVAYWLKKLESRRGAIRVLVVERDHTYSOASTGLSVGGICO
ļ	i		QFSLPENIQLSLFSASFLRNINEYLAVVDAPPLDLRFNPSGYLL
1	i		LASEKDAAAMESNVKVQRQEGAKVSLMSPDQLRNKFPWINTEGV
ľ	1	I	ALASYGMEDEGWFDPWCLLQGLRRKVQSLGVLFCQGEVTRFVSS
ļ	ļ	ļ	SQRMLTTDDKAVVLKRIHEVHVKMDRSLEYOPVECAIVINAACA
ĺ			WSAQIAALAGVGEGPPGTLQGTKLPVEPRKRYVYVWHCPQGPGL
[1	1	ETPLVADTSGAYFREGLGSNYLGGRSPTEQEEPDPANLEVDHD
1	1	1	FFQDKVWPHLALRVPAFETLKVQSAWAGYYDYNTFDQNGVVGPH
ı		į	PLVVNMYFATGFSGHGLQQAPGIGRAVAEMVLKGRFQTIDLSPF
	1	1	I.PTDEVI.CEVIODANITI
6356	354	633	LFTRFYLGEKIQENNII
6356	354	633	LFTRFYLGEKIQENNII TGLTSSCLPLQVMMTKRTKDMGKFSSVTVSTIDEBEBEIEAREV ADSYAQNAKVIEKQLERKGMSKRRLQBLABLEAKKAKMKGTLID

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide .	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
•1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
6357	2	915	GLLRNMALLVRVLRNQTSISQWVPVCSRLIPVSPTQGQGDRALS
1	!		RTSQWPQMSQSQACGGSEQIPGIDIQLNRKYHTTRKLSTTKDSP
1	1		QPVEEKVGAFTKIIBAMGFTGPLKYSKWKIKIAALRMYTSCVEK
1	1	}	TDFEEFFLRCQMPDTFNSWFLITLLHVWMCLVRMKQEGRSGKYM
1		Ì	CRIIVHFMWEDVQQRGRVMGVNPYILKKNMILMTNHFYAAILGY
1	ſ	ĺ	DEGILSDDHGLAAALWRTFFNRKCEDPRHLELLVEYVRKQIQYL
į	!		DSMNGEDLLLTGEVSWRPLVEKNPQSILKPHSPTYNDEGL
6358	2009	1040	ASDALHSLSAPVLRLSSRSAARPATMTEQAISFAKDFLAGGIAA
	İ		AISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPK
1	1	1	EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHT
1	1		QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKSGTE
	1	1	REFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRAAYFGVY
l	1 .		DTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
I	1		MQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMG
	1		GAFVLVLYDELKKVI
6359	98	1086	VCRQEEEKMKEDCLPSSHVPISDSKSIQKSELLGLLKTYNCYHE
1		i	GKSFQLRHREEEGTLIIEGLLNIAWGLRRPIRLQMQDDREQVHL
Ì	· ·		PSTSWMPRRPSCPLKEPSPQNGNITAQGPSIQPVHKAESSTDSS
	1		GPLEEAEEAPQLMRTKSDASCMSQRRPKCRAPGEAQRIRRHRFS
1	1		INGHFYNHKTSVFTPAYGSVTNVRVNSTMTTLQVLTLLLNKFRV
l	1		EDGPSEFALYIVHESGERTKLKDCEYPLISRILHGPCEKIARIF
ļ	İ		LMEADLGVEVPHEVAQYIKFEMPVLDSFVEKLKEEEEREIIKLT
			MKFQALRLTMLQRLEQLVEAK
6360	1	345	GTRGAVPSTLEEVVLPPRSCRVFWIHSGTTMSKVSFKITLTSDP
[į.		RLPYKVLSVPESTPFTAVLKFAAEEFKVPAATSAIITNDGIGIN
			PAQTAGNVFLKHGSELRIIPRDRVGSC
6361	615	158	RPGLGQLQHCALAPQAGNRRCRFHGRLHALTRSTHRGKPMSIMQ
}	1		FKDTLNTPLPDSSPVAVPLGAPIAVASTLSVEHNDGVETGIWAC
	}		APGRWRRQITSQEFCHFIQGRCTFTPDDGETLHIQAGDALMLPA
6362	350		NSTGIWDIQETVRKTYVLIL
6362	350	1576	TTMDGSHSAALKLQQLPPTSSSSAVSEASFSYKENLIGALLAIF
1			GHLVVSIALNLQKYCHIRLAGSKDPRAYFKTKTWWLGLFLMLLG
	į		ELGVFASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKWKPKDF
1		•	LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW
1			PFLLYMLVEIILFCLLLYFYKEKNANNIVVILLLVALLGSMTVV
			TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ ASOMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF
1			ALGCLIAFLGVFLITRNRKKPIPFEPYISMDAMPGMONMHDKGM
1			TVQPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG
ſ			VPYRVLEHTKKE
6363	21	1201	RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG
1			DQIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI
1			RYPMBHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL
1	ļ		NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD
1			SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY
i			DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS
1			TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIOKSDMDLR
			RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPOE
1			RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF
6364	21	1201	RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG
[=	DOIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI
1			RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL
]		NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD
			SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY
Į i			DFHSSSEFEIVKAIKERACYLSINPOKDETLETEKAOYYLPDGS
			TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Clutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	1	sequence	\=possible nucleotide insertion)
	sequence		1 · •
	· .	1	RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE
	i	İ	RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF
6365	234	1989	KHKSRASCAARAQAFGPSREREVHSRFRSGLRRLGESNSGCCTM
	İ	ł	ASMGTLAFDEYGRPFLIIKDQDRKSRLMGLEALKSHIMAAKAVA
	ł	1	NTMRTSLGPNGLDKYMVDKDGDVTVTNDGATILSMMDVDHQIAK
ĺ		}	LMVELSKSODDEIGDGTTGVVVLAGALLEEAEQLLDRGIHPIRI
	1	1	ADGYEQAARVAIEHLDKISDSVLVDIKDTEPLIQTAKTTLGSKV
		1	VNSCHROMAEIAVNAVLTVADMERRDVDFELIKVEGKVGGRLED
	1		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
l			TKLIKGVIVDKDFSHPQMPKKVEDAKIAILTCPFEPPKPKTKHK
l			LDVTSVEDYKALQKYFKEKFEEMIQQIKETGANLAICQWGFDDE
	}]	ANHLLLQNNLPAVRWVGGPEIELIAIATGGRIVPRFSELTAEKL
1]		GFAGLVQEISFGTTKDKMLVIEQCKNSRAVTIFIRGGNKMIIEE
ĺ			AKRSLHDALCVIRNLIRDNRVVYGGGAAEISCALAVSQEADKCP
	Ì		TLEQYAMRAFADALEVIPMALSENSGMNPIQTMTEVRARQVKEM
İ	1	1	NPALGIDCLHKGTNDMKQQHVIETLIGKKQQISLATQMVRMILK
1	i	ļ	IDDIRKPGESEE
6366	257	1898	GNKEGAHSSTFWVLLS1FLGAVAMLCKEQGITVLGLNAVFDILV
1 0300	23/	1055	IGKFNVLEIVOKVLHKDKSLENLGMLRNGGLLFRMTLLTSGGAG
	Ì	i	MLYVRWRIMGTGPPAFTEVDNPASFADSMLVRAVNYNYYYSLNA
1	1	l .	WLLLCPWWLCFDWSMGCIPLIKSISDWRVIALAALWFCLIGLIC
1	1	1	
i i	1	l	QALCSEDGHKRRILTLGLGFLVIPFLPASNLFFRVGFVVAERVL
ŀ	1	1	YLPSVGYCVLLTFGFGALSKHTKKKKLIAAVVLGILFINTLRCV
J	j.	}	LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTAAI
			RYYREAVRLNPKYVHAMNNLGNILKERNELQEAEELLSLAVQIQ
1		1	PDFAAAWMNLGIVQNSLKRFEAAEQSYRTAIKHRRKYPDCYYNL
Į.			GRLYADLNRHVDALNAWRNATVLKPEHSLAWNNMIILLDNTGNL
	Į.		AQAEAVGREALELIPNDHSLMFSLANVLGKSQKYKESEALFLKA
1		ł	IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT
	}		KENYGLLRRKLELMQKKAV
6367	287	1934	SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS
5507	1 -0.	1	OKNLYRDVMOETFKNLTSVGKTWKVQNIEDEYKNPRRNLSLMRE
1		i	KLCESKESHHCGESFNQIADDMLNRKTLPGITPCESSVCGEVGT
1	1	1	GHSSLNTHIRADTGHKSSEYQEYGENPYRNKECKKAPSYLDSFQ
1	ļ	1	•
ŀ		1	SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF
1			CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER
1		1	THTGVNADECKECGNAFSFPSEIRRHKRSHTGEKPYECKQCGKV
1			FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG
1			EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA
1		1	SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH
1		1	ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR
I		}	YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC
	1		GKAFIRASSCREHERTHTINR
6368	1	327	RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE
5366	_	1	DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK
1	i		DOFVCGETVPAPSANKELVKC
L		 	
6369	1	1745	AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT
1			PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMQET
1			FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG
İ	j	İ	ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD
			TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY
i		1	DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL
1			IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE
1			CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM
1			THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA
i .		1	FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG
1		1	FRCTSDEQRHEKTHIEDKYIGGKQCGKGFKCWSQDQTHEKIMSG
L	<u> </u>	1	EKPHECKECGKVFKYFSSLRIHERTHTGEKPHECKQCGKAFRYF

C 050	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	1	- '	Codon, /=possible nucleotide deletion,
l	amino acid	sequence	\=possible nucleotide insertion)
	sequence		SSLHIHERTHTGDKPYECKVCGKAFTCSSSIRYHERTHTGEKPY
		1	ECKHCGKAFISNYIRYHERTHTGEKPYOCKOCGKAFIRASSCRE
l	1		HERTHTINR
L			FVLSEORLRTERTWPRSPGLGRGAAAAGARTAGAGLLRLLLGCG
6370	1711	329	ALVGGLRPVTMTTPANAONASKTWELSLYELHRTPQEAIMDGTE
ì		1	IAVSPRSLHSELMCPICLDMLKNTMTTKECLHRFCSDCIVTALR
Ì	1		SGNKECPTCRKKLVSKRSLRPDPNFDALISKIYPSRBEYEAHQD
ł	ì	1	RVLIRLSRLHNQQALSSSIEEGLRMQAMHRAQRVRRPIPGSDQT
f .	ł	1	
1	1	į.	TTMSGGEGEPGEGEGDGEDVSSDSAPDSAPGPAPKRPRGGGAGG
1			SSVGTGGGGTGGVGGGAGSEDSGDRGGTLGGGTLGPPSPPGAPS
		1	PPEPGGEIELVFRPHPLLVEKGEYCQTRYVKTTGNATVDHLSKY
1			LALRIALERRQQQEAGEPGGPGGGASDTGGPDGCGGEGGGAGGG
1			DGPEEPALPSLEGVSEKQYTIYIAPGGGAFTTLNGSLTLELVNE
	1	<u> </u>	KFWKVSRPLELCYAPTKDPK
6371	3	288	GVANMSTAMNFGTKSFQPRPPDKGSFPLDHLGECKSFKEKFMKC
1		}	LHNNNFÉNALCRKESKEYLECRMERKLMLQEPLEKLGFGDLTSG
		l	KSEAKK
6372	2141	625	RVSAIASEGKAEERYKKLEDLLEKSFSLVKMPSLQPVVMCVMKH
ļ	1	1	LPKVPEKKLKLVMADKELYRACAVEVRRQIWQDNQALFGDEVSP
1	İ	1	LLKQYILEKESALFSTELSVLHNFFSPSPKTRRQGEVVQRLTRM
	1	ì	VGKNVKLYDMVLQFLRTLFLRTRNVHYCTLRAELLMSLHDLDVG
i	1	1	EICTVDPCHKFTWCLDACIRERFVDSKRARELQGFLDGVKKGQE
1	1	1	QVLGDLSMILCDPFAINTLALSTVRHLQELVGQETLPRDSPDLL
1	ì	1	LLLRLLALGQGAWDMIDSQVFKEPKMEVELITRFLPMLMSFLVD
ì	Ì	1	DYTFNVDQKLPAEEKAPVSYPNTLPESFTKFLQEQRMACEVGLY
	1		YVLHITKQRNKNALLRLLPGLVETFGDLAFGDIFLHLLTGNLAL
	1	1	LADEFALEDFCSSLFDGFFLTASPRKENVHRHALRLLIHLHPRV
	L	1	APSKLEALQKALEPTGQSGEAVKELYSQLGEKLEQLDHRKPSPA
			QAAETPALELPLPSVPAPAPL
6373	67	711	PSRAARASPARLPAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK
ì	ł		DIKEYVKWMMYWIIFALFTTAETFTDIFLCWFPFYYELKIAFVA
1	I		WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL
			VHFGKRGLNVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD
L	<u> </u>		GAPAPSGPPPPGSGRASGKHGQPKMSRSASESASSSGTA
6374	535	2105	HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS
1			CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD
			HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC
		1	CPAELQTEGSNGKKEVLSGFQVVLEDTVLFPEGGGQPDDRGTIN
			DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH
			SGQHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA
			IEQSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR
1	1		VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL
			SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKIQNSTKIL
			QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII
			ANEIGSESTLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL
1_			EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE
6375	1	1535	AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT
			CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK
1		1	PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAFYLYKLYQHYY
.	.	•	FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY
			SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER
		1	HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP
1	1		FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR
1	1		RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA
			SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP
1			GQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPETEQAGVLN

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine
ł	residue of amino acid	amino acid	W=Tryptophan, Y=Tvrosine, X=Unknown +-Stop
ŀ	sequence	sequence	Codon, /=possible nucleotide deletion
	bequence	 	\=possible nucleotide insertion)
İ			WFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAV
6376	380	1437	VGLFTVVRHDAELRVPSPTEEPYAPEL
1			ISSTDIDHYRFSFLVNSKMPSKESWSGRKTNRAAVHKSKQEGRQ QDLLIAALGMKLGSPKSSVTIWQPLKLFAYSQLTSLVRRATLKE
į			NEQIPKYEKIHNFKVHTFRGPHWCEYCANFMWGLIAQGVKCADC
			GLNVHKQCSKMVPNDCKPDLKHVKKVYSCDLTTLVKAHTTKRPM
1	ł		VVDMCIREIESRGLNSEGLYRVSGFSDLIEDVKMAFDRDGEKAD
i	1		ISVNMYEDINIITGALKLYFRDLPIPLITYDAYPKFIFSAKIMD
			PDEQLETLHEALKLLPPAHCETLRYLMAHLKRVTLHEKENLMNA
6377	2311		ENLGIVFGPTLMRSPELDAMAALNDIRYORLVVELLIKNEDILE
1 3377	2311	1845	SRIRRRSSRRPREPPGPSRRRRRRRPDPRTMPSEKTFKORPTFF
			QRVEDVRLIREQHPTKIPVIIERYKGEKQLPVLDKTKFLVPDHV
			NMSELIKIIRRRLQLNANQAFFLLVNGHSMVSVSTPISEVYESE KDEDGFLYMVYASQETFGMKLSV
6378	686	191	GAGPWEAFPDGIGRRSRRARLPQYKRPPGRVGGGDSGRRNMAVA
i i			DLALIPDVDIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYK
			WAEYHADIYDKVSGDMQKQGCDCECLGGGRISHQSQDKKIHVYG
			YSMAYGPAQHAISTEKIKAKYPDYEVTWANDGY
6379	35	378	BRAGSPSPSRAALRRCAPORSOAPRWPDRAACRRSFOGSOGPAV
			LFNSVVNVGCGPAEERVLLTGLHAVADIYCENCKTTLGWKVEHA
6380	1414	462	FESSQKYKEGKYIIELAHMIKDNGWD
	7474	462	PAVQGQRGAGPPTGRGSGNMARFALTVVRHGETRFNKEKIIQGQ
			GVDEPLSETGFKQAAAAGIFLNNVKFTHAFSSDLMRTKQTMHGI
			LERSKFCKDMTVKYDSRLRERKYGVVEGKALSELRAMAKAAREE CPVFTPPGGETLDQVKMRGIDPFEFLCQLILKEADQKEQFSQGS
			PSNCLETSLAEIFPLGKNHSSKVNSDSGIPGLAASVLVVSHGAY
1 1	ļ		MRSLFDYFLTDLKCSLPATLSRSELMSVTPNTGMSLFIINFEEG
1 1	Ī		REVKPTVQCICMNLQDHLNGLTENSLGLNLPSKSNHFEPLKGVP
6381	1668		LAUFTSLEC
0202	1000	218	AVVRAQGSRGFSGAGWRPRQAAAMNFSEVFKLSSLLCKFSPDGK
	j		YLASCVQYRLVVRDVNTLQILQLYTCLDQIQHIEWSADSLFILC
1	1		AMYKRGLVQVWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT
		·	TEFHLRITVWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER RDCKDYVSIFVCSDWQLLRHFDTDTQDLTGIEWAPNGCVLAVWD
1			TCLEYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG
1 1			SYDGKVRILNHVTWKMITEFGHPAAINDPKIVVYKEAFKSDOLG
1			LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLOTI.KPVTDPAND
1 1			KIGIGMLAFSPDSYFLATRNDNIPNAVWVWDIOKIRI.FAVI.FOI.
1 1	1		SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGEGDFA
6382	2	1062	VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACRQLGGHT
] [Í	-7772	FEEDEDRNLCLIAYPLKGDHGIVDIVDNSDCEPKSKLLRWTTNK KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEEFEWLKKSEVLYY
1 1		1	TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL
1 1	ĺ		LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS
	1	1	AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVOGFKEALFOFF
1		ł	HNGRYLRRELLGPVLKKLTELKAVLEROESYRFYSSSIJVIVDC
		1	KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSUDURM
]		!	IDFAHTTCRLYGEDTVVHRGQDAGYIFGLQSLIDIVTEISEESG
6383	3159	1061	E SPANCE DE CONTROL DE
ļ .		T. C. C. C. C. C. C. C. C. C. C. C. C. C.	SPAPGRPSPHGSQPAARAAAPAMPSAKQRGSKGGHGAASPSEK
[l	GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP AARAAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK
	1	1	PPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGKS
			SSSSASAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS
	ł	į.	GWCVHHVLEEVQQVRRSHODFSROREELGOGLOGVEOKVOSTOR
			TFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVLQKLQNEI

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	wallypcopian, larytosine, administry accept
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Į.	\=possible nucleotide insertion)
	 		LKDLSDGIHVVKDARERDFTSLENTVEERLTELTKSINDNIAIF
	i		TEVQKRSQKEINDMKAKVASLEESEGNKQDLKALKEAVKEIQTS
		Ì	AKSREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAFKEAAD
	ł	1	TERLALQALTEKLLRSEESVSRLPEEIRRLEEBLRQLKSDSHGP
	l e		
		1	KEDGGFRHSEAFEALQQKSQGLDSRLQHVEDGVLSMQVASARQT
	1	1	ESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLASTVRSL
	l .	l	GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLLSQDQA
	1	1	QAARLPPQDFLDRLSSLDNLKASVSQVEADLKMLRTAVDSLVAY
	1	1	SVKIETNENNLESAKGLLDDLRNDLDRLFVKVEKIHEKV
	<u> </u>	1000	IWEVPVCLTHLLHLQQANQPLPPPSSSINEEDADEANRAIGEKR
6384	738	1904	AAPDSGKKPKTPKTKQQKDPNEPQKPVSAYALFFRDTQAAIKGQ
1	1	I	WALDOUVLY INTO THE LAW AND THE TANK AND THE
1	J .	1	NPNATFGEVSQIVASMWDSLGEEQKQVYKRKTEAAKKEYLKALA
i	1	1	AYRASLVSKAAAESAEAQTIRSVQQTLASTNLTSSLLLNTPLSQ
1	l l	j	HGTVSASPQTLQQSLPRSIAPKPLTMRLPMNQIVTSVTIAANMP
1	1	1	SNIGAPLISSMGTTMVGSAPSTQVSPSVQTQQHQMQLQQQQQQQ
	1	l .	QQQMQQMQQQQLQQHQMHQQ1QQQMQQQHFQHHMQQHLQQQQQH
i	1		LQQQINQQQLQQQLQQRLQLQQLQHMQHQSQPSPRQHSPVASQI
1	1		TSPIPAIGSPQPASQQHQSQIQSQTQTQVLSQVSIF
		<u> </u>	TSPIPATGSPQPASQUQSQ1QSQ1Q1Q1Q1DADAACEC1CCTDEC
6385	2	1584	PRVRAADVAAGAQAVVSAGMAKSNGENGPRAPAAGESLSGTRES
	ì]	LAQGPDAATTDELSSLGSDSEANGFAERRIDKFGFIVGSQGAEG
		1	ALEEVPLEVLRQRESKWLDMLNNWDKWMAKKHKKIRLRCQKG1P
1		1	PSLRGRAWQYLSGGKVKLQQNPGKFDELDMSPGDPKWLDVIERD
]		1	LHROFPFHEMFVSRGGHGQQDLFRVLKAYTLYRPEEGYCQAQAP
i	ł .	1	IAAVLLMHMPAEQAFWCLVQICEKYLPGYYSEKLEAIQLDGEIL
	1	ł	FSLLQKVSPVAHKHLSRQKIDPLLYMTEWFMCAFSRTLPWSSVL
1		1	RVWDMFFCEGVKIIFRVGLVLLKHALGSPEKVKACQGQYETIER
}	1)	KAMPME CEGAKITEKAGUADUGUNDOL DKAMAGASA TATAT
1		1	LRSLSPKIMQEAFLVQEVVELPVTERQIEREHLIQLRRWQETRG
	1	}	ELQCRSPPRLHGAKAILDAEPGPRPALQPSPSIRLPLDAPLPGS
	1	1	KAKPKPPKQAQKEQRKQMKGRGQLEKPPAPNQAMVVAAAGDACP
İ	1		PQHVPPKDSAPKDSAPQDLAPQVSAHHRSQESLTSQESEDTYL
6386	819	195	TVCGSFYLGIMQRASRLKRELHMLATEPPPGITCWQDKDQMDDL
0200	913	1 233	RAQILGGANTPYEKGVFKLEVIIPERYPFEPPQIRFLTPIYHPN
ļ	1	1	IDSAGRICLDVLKLPPKGAWRPSLNIATVLTSIQLLMSEPNPDD
1	1	!	PLMADISSEFKYNKPAFLKNARQWTEKHARQKQKADEEEMLDNL
1	\	Į.	PEMANT SEEK INK PARTICIAN TO VINNE TO V
1			PEAGDSRVHNSTQKRKASQLVGIEKKFHPDV
6387	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
1	-		KQELAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYLTNQK
I	1	1	NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
1	1		REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
1	1	1	STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
L		_L	SISSENIAS TRANSPORTED TO THE BEAUTY AND THE BEAUTY
6388	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
1	1	ļ	KQELAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYLTNQK
Į.	1	1	NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
Į	ł	1	REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
1	1	ì	STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
		400	AEPGDRMAGHRLVLVLGDLHIPHRCNSLPAKFKKLLVPGKIQHI
6389	1074	497	LCTGNLCTKESYDYLKTLAGDVHIVRGDFDENLNYPEQKVVTVG
1	1	l	PCIGNFCLKERADITYLTAGDANTAKODEDENTIALE TOOLOGIA
1	j'	į.	QFKIGLIHGHQVIPWGDMASLALLQRQFDVDILISGHTHKFEAF
1		1	EHENKFYINPGSATGAYNALETNIIPSFVLMDIQASTVVTYVYQ
1		1	LIGDDVKVERIEYKKP
6390	158	535	GEERKEGRAPGKAFAPERNPAKMEKEETTRELLLPNWQGSGSHG
1 0330	120	333	LTIAQRDDGVFVQEVTQNSPAARTGVVKEGDQIVGATIYFDNLQ
1	Í	1	SGEVTQLLNTMGHHTVGLKLHRKGDRFFPSLGQTWDP
L_			SGEVIQUENTMENHI VOLKERRKGUKE FEBROXINDI
6391	5386	2897	VRWNSKTECYLSIQTQENFPANLNELVNCIVISSLVTTQRKLKA
- (]		MSLLGSRNQLARAVLNPNPMDFCTKDLLTTTSERIIAYLRDFNE
Į	ı		DOKKAIETAYAMVKHSPSVAKICLIHGPPGTGKSKTIVGLLYRL
1			

SEQ	Predicted	150	
ID	beginning	Predicted end	
NO:	nucleotide	nucleotide location	\n-n-quille, C=CVSteine
	location	corresponding	Olucamic Mcia, Fernenvialanine C.Cl
}	corresponding	to first	nentstiding, leisolencing V_fireing
1	to first	amino acid	L=Leucine, M=Methionine N=Acparacine
1	amino acid	residue of	P=PIOLINE, O=Glutamine D-Arginine
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
j	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion
		 	\=possible nucleotide insertion)
ŀ]	1	LTENORKGHSDENSNAKIKONRVLVCAPSNAAVDELMKKIILEF
ł		1	LEACADAMPLONCODINLVRI.GPEKSTNSFIT.FEGI.DCOMMIN
			MKKELPSHVQAMHKRKEFLDYQLDELSRQRALCRGGREIQRQEL
			DENISKVSKERQELASKIKEVQGRPQKTQSIIILESHIICCTLS
J	1	(TSGGLLESAFRGQGGVPFSCVIVDEAGQSCEIETLTPLIHRCN
1	1		KLILVGDPKQLPPTVISMKAQEYGYDQSMMARFCRLLEENVEHN
			MISRLPILQLTVQYRMHPDICLFPSNYVYNRNLKTNRQTEAIRC
	1		SSDWPFQPYLVFDVGDGSERRDNDSYINVQEIKLVMEIIKLIKD
1	i i		KRKDVSFRNIGIITHYKAQKTMIQKDLDKEFDRKGPAEVDTVDA FQGRQKDCVIVTCVRANSIQGSIGFLASLQRLNVTITRAKYSLF
- [1 .		ILGHLRTLMENQHWNQLIQDAQKRGAIIKTCDKNYRHDAVKILK
1			LKPVLQRSLTHPPTIAPEGSRPQGGLPSSKLDSGFAKTSVAASL
1			YHTPSDSKEITLTVTSKDPERPPVHDQLQDPRLLKRMGIEVKGG
]]		IFLWDPQPSSPQHPGATPPTGEPGFPVVHQDLSHVQQPAAVVAA
1	1		LSSHKPPVRGEPPAASPEASTCQSKCDDPEEELCHRREARAFSE
6392			GEQEKCGSETHHTRRNSRWDKRTLEOEDSSSKKPWLL
0392	972	186	GRTGVDLASSMAHRLOIRLLTWDVKDTI.I.RI.PHDI.GEAVAMVAD
	1		ANGLEVEPSALEOGFROAYRAOSHSFPNYGI, SHGI, TSPOURI DV
i			VLQTFHLAGVQDAQAVAPIAEOLYKDFSHPCTWOM DGAEDWID
1	1 1		ECRTRGLRLAVISNFDRRLEGILGGI.GLREHEDEVI.TERRACTUR
1	i		KPDPKIFQEALRLAHMEPVVAAHVGDNYI,CDVOGDDAVGMUGEI
6393	2017	730	VVGPQALDPVVRDSVPKEHILPSLAHT.T.PAT.DCT.ECCTDCT
1		/30	TGGSKMAAVATCGSVAASTGSAVATASKSNVTSROPPGPPASUM
1	i i		NDSGPREVSIAGTRPSVRNGOLLVSTGLPALDOLLGCGLAVGTV
1	1		LLIEEDKYNIYSPLLFKYFLAEGIVNGHTLLVASAKEDPANILO
1	1		ELPAPLLDDKCKKEFDEDVYNHKTPESNIKMKIAWRYQLLPKME
1 1			IGPVSSSRFGHYYDASKRMPQELIEASNWHGFFLPEKISSTLKV
1			EPCSLTPGYTKLLQFIQNIIYEEGFDGSNPQKKQRNILRIGIQN LGSPLWGDDICCAENGGNSHSLTKFLYVLRGLLRTSLSACIITM
1			PTHLIQNKAIIARVTTLSDVVVGLESFIGSERETNPLYKDYHGL
1 1	į.		IHIRQIPRLNNLICDESDVKDLAFKLKRKLFTIERLHLPPDLSD
			TVSRSSKMDLAESAKRLGPGCGMMAGGKKHLDF
6394	1418	511	GAAAGGEGARRPAAMATVMAATAAERAVLEEEFRWLLHDEVHA
! !	1		VLKQLQDILKEASLRFTLPGSGTEGPAKQENFILGSCGTDQVKG
]			VLTLQGDALSQADVNLKMPRNNOLLHFAFREDKOWKLOOLODAD
	1		NHVSQALYLLTSRDQSYOFKTGAEVI.KI.MDAVMI.OI.TDADNDI T
		ĺ	TPATETEPETAASGETRMFAPALPSDELVNVYTNINKIGITUVO
] [DHALQPNSTKNFRPAGGAVLHSPGAMFEWGSORI.EVSPNJUVJEC
6395	13		VIPWLNDALVYFTVSLOLCOOLKDKISVFSSYWSVPDF
	13	658	PSGRPTRPLCCAARRGAARHGGSVSGWDAGPTPTTTCNDGGGIA
	1		ESVTFEDVAVEFIOEWALLDSARRSI.CKVPMI.DOCPTI ACROTT
]]		•	PCAPSCVSQLGQRAEPKATERGILRATGVAWESOLUDER DEMO
	1	[DLLEEASSRDMQMGPGLFLRMOLVPSIEERETPITPEDPRALOR
6396	1	1223	PPWSLGCTGLKAAMQIQRVVIPVPTLGHRNPWVARDSGF
	- 1	1221	ANILSSPSKRGQKGTLIGYSPEGTPLYNFMGDAFOHSSOSIDDE
1	j	ĺ	TRESURGILEESDSRQIFYFLCLNLLFTFVELFYGVI.TMCI.CI.
	1	Į.	SUGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGPIFTISGE
!	1	ļ	INGLFLIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGLIVNL
1		ļ	IGICAFSHAHSHAHGASQGSCHSSDHSHSHHMHGHSDHGHGHSH
J	ļ		GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIAD
ļ	1	ſ	PLCSLFIAILIFLSVVPLIKDACQVLLLRLPPEYEKELHIALEK
į		ļ	IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV
		1	TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES MKYCKDGTYIM
6397	391		
			GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK
			KLIAAQTGTRWNKIVLKKWYTIFKDHVSLGDYEIHDGMNLELYY

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide		
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ſ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	1	\=possible nucleotide insertion)
	<u> </u>	 	O TOTAL TOTA
6398	353	1306	HKQMGPLINRCKKILLPTTVPPATMRIWLLGGLLPFLLLLSGLQ
			RPTEGSEVAIKIDFDFAPGSFDDQYQGCSKQVMEKLTQGDYFTK
1	1		DIEAQKNYFRMWQKAHLAWLNQGKVLPQNMTTTHAVAILFYTLN
i		j	SNVHSDFTRAMASVARTPOQYERSFHFKYLHYYLTSAIOLLRKD
1	}	l	SIMENGTLCYEVHYRTKDVHFNAYTGATIRFGQFLSTSLLKEEA
1			<u> </u>
1	1		QEFGNQTLFTIFTCLGAPVQYFSLKKEVLIPPYELFKVINMSYH
1	· ·	§	PRGDWLQLRSTGNLSTYNCQLLKASSKKCIPDPIAIASLSFLTS
			VIIFSKSRV
6399	75	1245	PNLETYFGRRCEKDSMNFTPTHTPVCRKRTVVSKRGVAVSGPTK
		1	RRGMADSLESTPLPSPEDRLAKLHPSKELLEYYQKKMAECEAEN
Ì		1	EDLLKKLELYKEACEGQHKLECDLQQREEEIAELQKALSDMQVC
		1	LFQEREHVLRLYSENDRLRIRELEDKKKIQNLLALVGTDAGEVT
		1	YFCKEPPHKVTILQKTIQAVGECEQSESSAFKADPKISKRRPSR
1	1	1	ERKESSEHYQRDIQTLILQVEALQAQLGEQTKLSREQIEGLIED
i		ŧ	RRIHLEEIOVOHORNONKIKELTKNLHHTQELLYESTKDFLOLR
ł	1		SENQNKEKSWMLEKDNLMSKIKQYRVQCKKKEDKIGKVLPVMHE
1			SHHAQSEYIKVMSLCRNEVVYFSGRVEGIPKNLQFVM
6400	2520	1053	KTMKCDEVVYEVOSAILRHNCGYAMKTGKFFHNLMERKDFETWL
0 200	2320	1 2000	DNISVTFLSLTDLOKNETLDHLISLSGAVOLRHLSNNLETLLKR
1			DFLKLLPLELSFYLLKWLDPQTLLTCCLVSKQWNKVISACTEVW
ļ	Ì		
1			QTACKNLGWQIDDSVQDALHWKKVYLKAILRMKQLEDHEAFETS
1		1	SLIGHSARVYALYYKDGLLCTGSDDLSAKLWDVSTGQCVYGIQT
1		ļ.	HTCAAVKFDEQKLVTGSFDNTVACWEWSSGARTQHFRGHTGAVF
1		į.	SVDYNDELDILVSGSADFTVKVWALSAGTCLNTLTGHTEWVTKV
1	1	•	VLQKCKVKSLLHSPGDYILLSADKYEIKIWPIGREINCKCLKTL
	1	<u> </u>	SVSEDRSICLQPRLHFDGKYIVCSSALGLYQWDFASYDILRVIK
j		l	TPEIANLALLGFGDIFALLFDNRYLYIMDLRTESLISRWPLPEY
ŀ			RKSKRGSSFLAGEASWLNGLDGHNDTGLVFATSMPDHSIHLVLW
			KEHG
6401	109	766	PGAAWSRPDLRGCCTGPQPALRMLVLPSPCPQPLAFSSVETMEG
1		1	PPRRTCRSPEPGPSSSIGSPQASSPPRPNHYLLIDTQGVPYTVL
1	{		VDEESQREPGASGAPGQKKCYSCPVCSRVFEYMSYLQRHSITHS
i		1	EVKPFECDICGKAFKRASHLARHHSIHLAGGGRPHGCPLCPRRF
		1	RDAGELAQHSRVHSGERPFQCPHCPRRFMEQNTLQKHTRWKHP
6402	1196	279	TTSQCGGIRQSSAIPVASMEFAAICLRNALLLLPEEQODPKQEN
1			GAKNSNOLGGNTESSESSETCSSKSHDGDKFIPAPPSSPLRKOE
i		Ì	LENLKCSILACSAYVALALGDNLMALNHADKLLQQPKLSGSLKF
1	1		LGHLYAAEALISLDRISDAITHLNPENVTDVSLGISSNEQDQGS
ł			DKGENEAMESSGKRAPOCYPSSVNSARTVMLFNLGSAYCLRSEY
1	†	Ì	DKARKCLHQAASMIHPKEVPPEAILLAVYLELQNGNTQLALQII
}	1	ł	KRNQLLPAVKTHSEVRKKPVFQPVHPIQPIQMPAFTTVQRK
6403	2	3600	
1 0.403	1	1690	RGIHTSVLQGNLQNQMYSHNVVIMNLNNLNLTQVQQRNLITNLQ
1			RSVDDTSQAIQRIKNDFQNLQQVFLQAKKDTDWLKEKVQSLQTL
!		ĺ	AANNSALAKANNDTLEDMNSQLNSFTGQMENITTISQANEQNLK
1		1	DLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIISNISYTAHH
1			LRTLTSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLR
1		1	MQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIKNFTILQGP
J			PGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGERGPIG
1	1	1	PAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPP
ĺ	[GKEGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGP
1			KGPPGPPGPSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY
1	i		FSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH
	1		WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC
Ī	i		AGLIYAGOWNDFOCEDVNNFICEKDRETVLSSAL
6404	1012	222	AAALAMAAPAPGLISVFSSSOELGAALAQLVAQRAACCLAGARA
	1 1012		WWITHT-WELLER TO A ED DO NO TOWN THAT AND A STATE OF THE OWNER.

SEQ	Predicted	Predicted end	Amino acid segment
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
i i	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			RFALGLSGGSLVSMLARELPAAVAPAGPASLARWTLGFCDERLV
1	}		PFDHAESTYGLYRTHLLSRLPIPESQVITINPELPVEEAAEDYA
- 1	1	1	KKLRQAFQGDSIPVFDLLILGVGPDGHTCSLFPDHPLLOERKKI
·]	į	VAPISDSPKPPPQRVTLTLPVLNAARTVIFVATGEGKAAVLKRI
			LEDQEENPLPAALVQPHTGKLCNFLDEAAARLLTVPFEKHSPL
6405	1	1456	AALPRPTPRAPLGREGTGSDSEMAASMFYGRLVAVATLRNHRPR
			TAQRAAAQVLGSSGLFNNHGLQVQQQQQORNLSLHEYMSMELLQE
	!		AGVSVPKGYVAKSPDEAYAIAKKLGSKDVVIKAOVLAGGRGKGT
	i		FESGLKGGVKIVFSPEEAKAVSSQMIGKKLFTKQTGEKGRICNQ
	į		VLVCERKYPRREYYFAITMERSFQGPVLIGSSHGGVNIEDVAAE
			TPEAIIKEPIDIEEGIKKEQALQLAQKMGFPPNIVESAAENMVK
			LYSLFLKYDATMIEINPMVEDSDGAVLCMDAKINFDSNSAYRQK
1]		KIFDLQDWTQEDERDKDAAKANLNYIGLDGNIGCLVNGAGLAMA
1			TMDIIKLHGGTPANFLDVGGGATVHQVTEAFKLITSDKKVLAIL
i .	i		VNIFGGIMRCDVIAQGIVMAVKDLEIKIPVVVRLQGTRVDDAKA
Ī			LIADSGLKILACDDLDEAARMVVKLSEIVTLAKQAHVDVKFQLP
			I
6406	1036	167	HPRQMRGEDTPEAPPYSSGRYDSIKTEVSGCPEDLTVGRAPTAD
j .			DDDDDDHDDHEDNDKMNDSEGMDPERLKAFNMFVRLFVDENLDRM
1 :			VPISKQPKEKIQAIIESCSRQFPEFQERARKRIRTYLKSCRRMK
1			KNGMEMTRPTPPHLTSAMAENILAAACESETRKAAKRMRLEIYO
i	1		SSQDEPIALDKQHSRDSAAITHSTYSLPASSYSQDPVYANGGLN
Į.			YSYRGYGALSSNLQPPASLQTGNHSNGESGEARALASRPAPSWV
			CRAALGSGMGRGKQRPVMERGCLTA
6407	492	150	VGLCLAVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGV
i i	ļ		SWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNAC
			VLTISPVQPEDDADYYCSVGYGFSP
6408	1458	903	RGCITSSQAWRLFGGVTRGFNMRIEKCYFCSGPIYPGHGMMFVR
1 1	1		NDCKVFRFCKSKCHKNFKKKRNPRKVRWTKAFRKAAGKELTVDN
1 1	i		SFEFEKRRNEPIKYQRELWNKTIDAMKRVEBIKQKRQAKFIMNR
1 1			LKKNKELQKVQDIKEVKQNIHLIRAPLAGKGKQLEEKMVQQLQE
1 1	1		DVDMEDAP
6409	150	446	NTALANLLRCFTCDRLCGGCTAPAPPAHQGIVLQPVMPSCDPGP
			GPACLPTKTFRSYLPRCHRTYSCVHCRAHLAKHDELISKSFQGS
1 1		•	HGRAYLFNSV
6410	85	607	RGGTAGCVACLGCWGQSSSPKAAFPAGSACLPADSCPCLLFQAC
1	ļ		AISGLFNCITIHPLNIAAGVWMIMNAFILLLCEAPFCCQFIEFA
1	ł	İ	NTVAEKVDRLRSWQKAVFYCGMAVVPIVISLTLTTLLGNAIAFA
1		ļ	TGVLYGLSALGKKCDATCVADTCCCDCCADDDVX
6411	302	772	TGVLYGLSALGKKGDAISYARIQQQRQQADEEKLAETLEGEL RLSIMASSLNEDPEGSRITYVKGDLFACPKTDSLAHCISEDCRM
1 1	_	7.12	GAGIAVI. EKKKEGGUCELI MOONYGGONYA
1			GAGIAVLFKKKFGGVQELLNQQKKSGEVAVLKRDGRYIYYLITK
] {			KRASHKPTYENLQKSLEAMKSHCLKNGVTDLSMPRIGCGLDRLQ
6412	61	1709	WENVSAMIEEVFEATDIKITVYTL
	-	1,03	RPVTSFSPLPGSCGGRLGTRTMLGRSLREVSAALKQGQITPTEL
1 1		1	CQKCLSLIKKTKFLNAYITVSEEVALKQAEESEKRYKNGQSLGD
] [ĺ	1	LDGIPIAVKDNFSTSGIETTCASNMLKGYIPPYNATVVQKLLDQ
1 1	ļ	ł	GALLMGKTNLDEFAMGSGSTDGVFGPVKNPWSYSKQYREKRKQN
1	!	. [PHSENEDSDWLITGGSSGGSAAAVSAFTCYAALGSDTGGSTRNP
j [j	• 1	AAHCGLVGFKPSYGLVSRHGLIPLVNSMDVPGILTRCVDDAAIV
1 1			LGALAGPDPRDSTTVHEPINKPFMLPSLADVSKLCIGIPKEYLV
1 1	ļ	}	PELSSEVQSLWSKAADLFESEGAKVIEVSLPHTSYSIVCYHVLC
1	i	ì	TSEVASNMARFDGLQYGHRCDIDVSTEAMYAATRREGFNDVVRG
1			RILSGNFFLLKENYENYFVKAQKVRRLIANDFVNAFNSGVDVLT.
] !			TPTTLSEAVPYLEFIKEDNRTRSAQDDIFTQAVNMAGLPAVSIP
1	}	J	VALSNOGLPIGLOFIGRAFCDQQLLTVAKWFEKQVQFPVIQLQE
L			LMDDCSAVLENEKLASVSLKQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Í		ş	Codon, /=possible nucleotide deletion,
ļ	amino acid	sequence	
	sequence	000	\=possible nucleotide insertion)
6413	2	885	HEPRCAGMAASLWMGDLEPYMDENFISRAFATMGETVMSVKIIR
ĺ		į	NRLTGIPAGYCFVEFADLATAEKCLHKINGKPLPGATPAKRFKL
		į	NYATYGKQPDNSPEYSLFVGDLTPDVDDGMLYEFFVKVYPSCRG
			GKVVLDQTGVSKGYGFVKFTDELEQKRALTECQGAVGLGSKPVR
ļ			LSVAIPKASRVKPVEYSQMYSYSYNQYYQQYQNYYAQWGYDQNT
1	1		GSYSYSYPQYGYTQSTMQTYEEVGDDALEDPMPQLDVTEANKEF
	<u> </u>		MEQSEELYDALMDCHWQPLDTVSSEIPAMM
6414	1	538	RGGRAALLPWRRFPCCRPRPQPARPSSRATPGPRSPGMATSIGV
		}	SFSVGDGVPEAEKNAGEPENTYILRPVFQQRFRPSVVKDCIHAV
	[LKEELANAEYSPEEMPQLTKHLSENIKDKLKEMGFDRYKMVVQV
1	1	ĺ	VIGEQRGEGVFMASRCFWDADTDNYTHDVFMNDSLFCVVAAFGC
L	L		FYY
6415	2	1168	FVRQWQSSHRRACGLGCEARAGGGEEPRGRASSVAGWVGAFRAP
1	1		FIEAAVAGLGAGSGKRRRGWKMPVHSRGDKKETNHHDEMEVDYA
1		1	ENEGSSSEDEDTESSSVSEDGDSSEMDDEDCERRRMECLDEMSN
1	ł		LEKQFTDLKDQLYKERLSQVDAKLQEVIAGKAPEYLEPLATLQE
į		1	NMQIRTKVAGIYRELCLESVKNKYECEIQASRQHCESEKLLLYD
1	1	1	TVQSELEEKIRRLEEDRHSIDITSELWNDELQSRKKRKDPFWPD
ł	1		KKKPGVVSGPYIVYMLQDLDILEDWTTIRKAMATLGPHRVKTEP
	1	1	PVKLEKHLHSARSEEGRLYYDGEWYIRGQTICIDKKDECPTSAV
L			ITTINHDEVWFKRPDGSKSKLYISQLQKGKYSIKHS
6416	410	1519	EIAPADLEIPACAPVLLSRATSSTMSVTGGKMAPSLTQEILSHL
1	1	}	GLASKTAAWGTLGTLRTFLNFSVDKDAQRLLRAITGQGVDRSAI
ļ	1		VDVLTNRSREQRQLISRNFQERTQQDLMKSLQAALSGNLERIVM
1	1]	ALLQPTAQFDAQELRTALKASDSAVDVAIEILATRTPPQLQECL
1		<u> </u>	AVYKHNFQVEAVDGITSETSGILQDLLLALAKGGRDSYSGIIDY
1	1		NLAEQDVQALQRAEGPSREETWVPVFTQRNPEHLIRVFDQYQRS
ł		ł.	TGQELEEAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHQALQ
1		1	ETEPNYQVLIRILISRCETDLLSIRAEFRKKFGKSLYSSLQDAV
			KGDCQSALLALCRAEDM
6417	1	845	RGESRVLWSELEGEAGGAGGWASSLNARMDNRFATAFVIACVLS
1	1	1	LISTIYMAASIGTDFWYEYRSPVQENSSDLNKSIWDEFISDEAD
			EKTYNDALFRYNGTVGLWRRCITIPKNMHWYSPPERTESFDVVT
		1	KCVSFTLTEQFMEKFVDPGNHNSGIDLLRTYLWRCQFLLPFVSL
Į.	1		GLMCFGALIGLCACICRSLYPTIATGILHLLAGLCTLGSVSCYV
1		1	AGIELLHQKLELPDNVSGEFGWSFCLACVSAPLQFMASALFIWA
-			AHTNRKEYTLMKAYRVA
6418	2	662	TRTRPRRPPGLGAAVGKAGARSTSTPAGASPAAAYQADPPPPAH
1	1	1	TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQPIFTTQQEAELVQ
1			YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRRGRQ
1	1		TYSRFQTLELEKEFLFNPYLTRKRRIEVSHALALTERQVKIWFQ
			NRRMKWKKENNKDKFPVSRQEVKDGETKKEAQELEEDRAEGLTN
6419	1	973	PGRPRVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP
!	1		MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL
		1	PSPDPVTVPYLSPLVVWKELESLLENEGDHAITVADFVDHHPIV
1	1		FWNLVWYFRRLDLPSNLPGLILSSBHCNKYSKIPRHCMSEDSKY
		1	VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF
1	1		NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYREI
1			LFLSLVALGRENIDIDAFDKEYKMAYDRLTPSQVKSTHNCDRPP
	1		STGVMECRKTFGEPYL
6420	207	1187	RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN
]			YLLWVFTPLILLILPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH
			NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPEDGPALIIFYH
1	1		GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC
			ALHGPREKCVEILRSGHLLAISPGGVREALISDETYNIVWGHRR
	1	1 '	GFAQVAIDAKVPIIPMFTQNIREGFRSLGGTRLFRWLYEKFRYP
			<u> </u>

SEO	Predicted	Predicted end	I Amino poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine
ı	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
1			FAPMYGGFPVKLRTYLGDPIPYDPQITAEELAEKTKNAVQALID
6421	1044		KHQRIPGNIMSALLERFH
6421	1844	362	WALSLRROPERMSNKLLSPHPHSVVLRSEFKMASSPAVLRASRL
ļ	1		YQWSLKSSAQFLGSPQLRQVGQIIRVPARMAATLILEPAGRCCW
1	1		DEPVRIAVRGLAPEQPVTLRASLRDEKGALFQAHARYRADTLGE
			LDLERAPALGGSFAGLEPMGLLWALEPEKPLVRLVKRDVRTPLA
1			VELEVLDGHDPDPGRLLCQTRHERYFLPPGVRREPVRVGRVRGT
			LFLPPEPGPFPGIVDMFGTGGGLLEYRASLLAGKGFAVMALAYY
l			NYEDLPKTMETLHLEYFEEAMNYLLSHPEVKGPGVGLLGISKGG ELCLSMASFLKGITAAVVINGSVANVGGTLRYKGETLPPVGVNR
			NRIKUTKDGYADIVDVLNSPLEGPDQKSFIPVERAESTFLFLVG
1			QDDHNWKSEFYANEACKRLQAHGRRKPQIICYPETGHYIEPPYF
1	·		PLCRASLHALVGSPIIWGGEPRAHAMAQVDAWKQLQTFFHKHLG
			GREGTIPSKV
6422	181	2133	EGENLSWFQEFWGDIAKEFYWKTPCPGPFLRYNFDVTKGKIFIE
}	j		WMKGATTNICYNVLDRNVHEKKLGDKVAFYWEGNEPGETTOITY
1			HQLLVQVCQFSNVLRKQGIHKGDRVAIYMPMIPELVVAMLACAR
			IGALHSIVFAGFSSESLCERILDSSCSLLITTDAFYRGEKLVNI.
			KELADEALQKCQEKGFPVRCCIVVKHLGRAELGMGDSTSQSPPI
			KRSCPDVQISWNQGIDLWWHELMQEAGDECEPEWCDAEDPLFIL
			YTSGSTGKPKGVVHTVGGYMLYVATTFKYVFDFHAEDVFWCTAD
	•		IGWITGHSYVTYGPLANGATSVLFEGIPTYPDVNRLWSIVDKYK
			VTKFYTAPTAIRLLMKFGDEPVTKHSRASLQVLGTVGEPINPEA
1			WLWYHRVVGAQRCPIVDTFWQTETGGHMLTPLPGATPMKPGSAT FPFFGVAPAILNESGEELEGEAEGYLVFKQPWPGIMRTVYGNHE
1 1			RFETTYFKKPPGYYVTGDGCQRDQDGYYWITGRIDDMLNVSGHL
1			LSTAEVESALVEHEAVAEAAVVGHPHPVKGECLYCFVTLCDGHT
			FSPKLTEELKKQIREKIGPIATPDYIQNAPGLPKTRSGKIMRRV
			LRKIAQNDHDLGDMSTVADPSVISHLFSHRCLTIQ
6423	614	1237	ANLKEIPRDLPPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLS
j j			KNGIEFIDEHAFKGVAETLQTLDLSDNRIQSVHKNAFNNLKARA
1 1			RIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRP
1			FLNAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRON
6424			QEDARRHLEYLKSLPSRQKKADEPDDISTVV
0424	1	1188	KKVSWPVAAMVHCSCVLFRKYGNFIDKLRLFTRGGSGGMGYPRL
			GGEGGKGGDVWVVAHNRMTLKQLKDRYPRKRFVAGVGANSKISA
1 1			LKGSKGKDWEIPVPVGISVTDENGKIIGELNKENDRILVAQGGL
1 1			GGKLLTNFLPLKGQKRIIHLDLKLIADVGLVGFPNAGKSSLLSC
1 1			VSHAKPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH MNKGMGHKFLKHIERTRQLLFVVDISGFQLSSHTQYRTAFETII
i i			LLTKELELYKEELQTKPALLAVNKMDLPDAQDKFHELMSQLQNP
l 1	ļ		KDFLHLFEKNMIPERTVEFQHIIPISAVTGEGIEELKNCIRKSL
	1		DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII
6425	1850	1144	LAMEGGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG
ļ i		-	LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR
]			CRRGSLVDIGSGDGRIVIAAAKKGFTAVGYELNPWLVWYSRYRA
			WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE
1			RELEDDARVIACREPPPHWTPDHVTGEGIDTVWAYDASTERGRE
		i	KRPCTSMHFQLPIQA
6426	30	565	SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR
		1	LHAEFAAERDWEQFHQPRNLLLALVGEVGELAELFOWKTDGEPG
1	}	Ì	PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI
	1		NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT
6427	145		ST
/	143	959	AASWGPPHVPKAGKMVSWMICRLVVLVFGMLCPAYASYKAVKTK
			NIREYVRWMMYWIVFALFMAAEIVTDIFISWFPFYYEIKMAFVL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion.
1	sequence		\=possible nucleotide insertion)
			WLLSPYTKGASLLYRKFVHPSLSRHEKEIDAYIVQAKERSYETV
1			LSFGKRGLNIAASAAVQAATKSQGALAGRLRSFSMODLRSISDA
1			PAPAYHDPLYLEDQVSHRRPPIGYRAGGLQDSDTEDECWSDTEA
1		Ì	VPRAPARPREKPLIRSQSLRVVKRKPPVREGTSRSLKVRTRKKT
	1		VPSDVDS
6428	1982	444	SGSGGKMEDHQHVPIDIQTSKLLDWLVDRRHCSLKWOSLVLTIR
		· · ·	EKINAAIQDMPESEEIAQLLSGSYIHYFHCLRILDLLKGTEAST
1			KNIFGRYSSQRMKDWQEIIALYEKDNTYLVELSSLLVRNVNYEI
1			PSLKKQIAKCQQLQQEYSRKEEECQAGAAEMREQFYHSCKOYGI
1	·	Į	TGENVRGELLALVKDLPSQLAEIGAAAQQSLGEAIDVYQASVGF
1	1		VCESPTEQVLPMLRFVQKRGNSTVYEWRTGTEPSVVERPHLEEL
1			PEQVAEDAIDWGDFGVEAVSEGTDSGISAEAAGIDWGIFPESDS
			KDPGGDGIDWGDDAVALQITVLEAGTQAPEGVARGPDALTLLEY
	Í		TETRNOFLDELMELEIFLAORAVELSEEADVLSVSOFOLAPAIL
1			OGOTKEKMVTMVSVLEDLIGKLTSLOLOHLFMILASPRYVDRVT
			EFLQQKLKQSQLLALKKELMVQKQQEALEEQAALEPKLDLLLEK
ł			TKELQKLIEADISKRYSGRPVNLMGTSL
6429	3413	3442	EPSSWTAAPRGPLAAHPLEAAVQEDDRRALSFDSRIKVFANGTL
1	1		VVKSVTDKDAGDYLCVARNKVGDDYVVLKVDVVMKPAKIEHKEE
1	}		NDHKVFYGGDLKVDCVATGLPNPEISWSLPDGSLVNSFMOSDDS
1	1		GGRTKRYVVFNNGTLYFNEVGMREEGDYTCFAENOVGKDEMRVR
			VKVVTAPATIRNKTCLAVQVPYGDVVTVACEAKGEPMPKVTWLS
1	}	•	PTNKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGE
			DRKTVWIHVNVQPPKINGNPNPITTVREIAAGGSRKLIDCKAEG
			IPTPRVLWAFPEGVVLPAPYYGNRITVHGNGSLDIRSLRKSDSV
	·		QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGH
			TISLNCSAAGTPTPSLVWVLPNGTDLQSGQQLQRFYHKADGMLH
1	i		ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL
			VSIINGETLKLPCTPPGAGQGRFSWTLPNGMHLEGPQTLGRVSL
			LDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPR
1			ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG
1			VQARLYGNRFLHFQGSLTIQHATQRDAGFYKCMAKNILGSDSKT
		1	TYIHVF
6430	1946	602	RTRVSTGLRRTLLWSEAVGASSTRGDTG1PGSGEGGAGPGGGEG
			AMLEAMAEPSPEDPPPTLKPETQPPEKRRRTIEDFNKFCSFVLA
			YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI
1			QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM
1			KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS
1			HPPRKKDRKNRKLGPGAGAGFGVLRRPRPTPGDGEKRSRIKKSK
]]		KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEEEEEEEEEEMA
			TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE
			TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR
			PMIECSLCGTWIHLSCAKIKKTNVPDFFYCOKCKELRPEARRLG
			GPPKSGEP
6431	. 3	605	WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR
1	i	- -	LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH
]			RELRLRNYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV
			IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER
1			LKGQEDSLASAVDAATEQKTCDSD
6432	56	1692	GGLGTMGSRIKONPETTFEVYVEVAYPRTGGTLSDPEVOROFPE
			DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR
j i			FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ
1 1			WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN
]			LTEYFVAVDVNNMLHLYASMLYERRILIICSKLSTLTACIHGSA
1 1			AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGIHLSLMEKVRN
, !			MALDDVVILNVDTNTLETPFDDLQSLPNDVISSLKNRLKKVSTT
<u></u>			A A THEA DITE LE DONGO DE MONTA A STRUKTUR A 211

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
		· · · · · · · · · · · · · · · · · · ·	TGDGVARAFLKAQAAFFGSYRNALKIEPEBPITFCERAFVSHYR
1	1		SGAMRQFLQNATQLQLFKQFIDGRLDLLNSGEGFSDVPEEEINM
İ			GBYAGSDKLYHQWLSTVRKGSGAILNTVKTKANPAMKTVYKFDI
1	ì		AENGCAPTPEEQLPKTAPSPLVEAKDPKLREDRRPITVHFGQVR
Ì			PPRPHVVKRPKSNIAVEGRRTSVPSPEQNTIATPATLHILQKSI
1			THFAAKFPTRGWTSSSH
6433	1524	484	APVTKRKEVFAKDSKGSALDAGRDPKRPALPETLCESGWASNTA
l .	1		PTTPPQPGWCLCGKDFKSSCQTPGREKERRLATMHGSCSFLMLL
1	1		LPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDML
l	i ·		HMRWDEELAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDV
İ	1		PLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCG
	[SHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP
1			SGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMG
L	1		AEGPDKPSVVSGLNSGPGHVWGPLLGLLLLPPLVLAGIF
6434	40	2002	MPQLNFGMADPTQMGGLSMLLLAGEHALGTPEVFSGTCRPDVSE
			SPELRQKSPLFQFAEISSSTSHSDASTKQCQTSALFQFAEISSN
	l		TSQLGGAEPVKRCGKSALFQLAEMCLASEGMKMEESKLIKAKES
			DGGRIKELEKGKEEKEIKMEKTDETRLOKEAEFEKSAKENLRDS
1			KELRNFEALQIDDIMAIKMEDPKEIRKEELEEDHKCSHFPDFSY
1		:	SASSKIIISDVPSRKDHMCHPHGIMIIEDPAALNKPEKLKKKKK
1	[KSKMDRHGNDKSTPKKTCKKRQSSESDIESVIYTIEAVAKGDWG
}	Į į		IEKLGDTPRKKVRTSSSGKGSILDAKPPKKKVKSREKKMSKEKS
ļ	1		SDTTKESRPPDFISISASKNISGETPEGIKAEPLTPMEDALPPS
1			LSGQAKPEDSDCHRKIETCGSRKSERSCKGALYKTLVSEGMLTS
]	1		LRANVDRGKRSSGKGNSSDHEGCWNBESWTFSQSGTSGSKKFKK
[[TKPKEDCLLGSAKLDEEFEKKFNSLPQYSPVTFDRKCVPVPRKK
]	}	•	KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT
	1		MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ
6435	2227	657	DTQRAGYHHEEVLWMTNIMNNCGGVYLKQLRHTAMTNA
1		657	ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE
l	i		VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA
1			VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD
1			PTRESVLQPSPQVPATTVAHTATQQPAAPAPPAVSPREALMEAM
i !			HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEBEDDIRNVI
			GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY
1 1			GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR
			AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA
			VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG
			LRRNFYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR
			LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY
6436	1295	341	GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVM
ļ J			YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL
			NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC
	1		VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG
			AFYRSYTTQLTMNVPFQAIHFMTYEFLQEHFNPQRRYNPSSHVL
]		SGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS
ĺ	į į		AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT
		. 	KRQEEWRAGK
6437	1828	360 .	PPAPAPPASPARHVTRTARGHLEGGSRAPPLLQAVFLQIKNMVK
	j		LIHTLADHGDDVNCCAFSFSLLATCSLDKTIRLYSLRDFTELPH
ļ	į		SPLKFHTYAVHCCCFSPSGHILASCSTDGTTVLWNTENGQMLAV
			MEQPSGSPVRVCQFSPDSTCLASGAADGTVVLWNAQSYKLYRCG
	į	ľ	SVKDGSLAACAFSPNGSFFVTGSSCGDLTVWDDKMRCLHSEKAH
·	Į.		DLGITCCDFSSQPVSDGEQGLQFFRLASCGQDCQVKIWIVSFTH
			ILGFELKYKSTLSGHCAPVLACAFSHDGQMLVSGSVDKSVIVYD

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	554-5	\=possible nucleotide insertion)
 	Doguesion		TNTENILHTLTOHTRYVTTCAFAPNTLLLATGSMDKTVNIWOFD
i			LETLCQARSTEHQLKQFTEDWSEEDVSTWLCAQDLKDLVGIFKM
i	,		NNIDGKELLNLTKESLADDLKIESLGLRSKVLRKIEELRTKVKS
1	1	İ	LSSGIPDEFICPITRELMKDPVIASDGYSYEKEAMENWDPAKRN
		Ì	RTSPP
6438	109	901	EVQILRAKMFOTGGLIVFYGLLAOTMAOFGGLPVPLDOTLPLNV
	1	1	NPALPLSPTGLAGSLTNALSNGLLSGGLLGILENLPLLDILKPG
Į.			GGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGLVQSP
[ĺ	[DGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRD
		1	KQERIHLVLGDCTHSPGSLQISLLDGLGPLPIQGLLDSLTGILN
			KVLPELVQGNVCPLVNEVLRGLDITLVHDIVNMLIHGLQFVIKV
6439	23	412	SIQTASAITTEMASQSQGIQQLLQAEKRAAEKVADARKRKARRL
1	1	1	KQAKEEAQMEVEQYRREREHEFQSKQQAAMGSQGNLSAEVEQAT
1			RRQVQGMQSSQQRNRERVLAQLLGMVCDVRPQVHPNYRISA
6440	3	517	RARWNSDMGDLPGLVRLSIALRIQPNDGPVFYKVDGQRPGONRT
			IKLLTGSSYKVEVKIKPSTLQVENISIGGVLVPLELKSKEPDGD
	1		RVVYTGTYDTEGVTPTKSGERQPIQITMPFTDIGTFETVWQVKF
i		ţ	YNYHKRDHCQWGSPFSVIEYECKPNETRSLMWVNKESFL
6441	234	1373	KSGGLRRRQRPGRSAAVGEEELPPGMEKFKAAMLLGSVGDALGY
i	Ì	Ì	RNVCKENSTVGMKIQEELQRSGGLDHLVLSPGEWPVSDNTIMHI
1	Į.	į	ATAKALTTDYWCLDDLYREMVRCYVEIVEKLPERRPDPATIEGC
1			AQLKPNNYLLAWHTPFNEKGSGFGAATKAMCIGLRYWKPERLET
}	ì]	LIEVSVECGRMTHNHPTGFLGSLCTALFVSFAAQGKPLVQWGRD
			MLRAVPLAEEYCRKTIRHTAEYQEHWFYFEAKWQFYLEERKISK
1]		DSENKAIFPDNYDAEEREKTYRKWSSEGRGGRRGHDAPMIAYDA
1	i	1	LLAAGNSWTELCHRAMFHGGESAATGTIAGCLFGLLYGLDLVPK
			GLYQDLEDKEKLEDLGAALYRLSTEEK
6442	34	796	AEDPAGGLAGQDTMFARGLKRKCVGHEEDVEGALAGLKTVSSYS
1			LQRQSLLDMSLVKLQLCHMLVEPNLCRSVLIANTVRQIQEEMTQ
1	1		DGTWRTVAPQAAERAPLDRLVSTEILCRAAWGQEGAHPASGLGD
1	(GHTQGPVSDLCPVTSAQAPRHLQSSAWEMDGPRENRGSFHKSLD
ŀ]		QIFETLETKNPSCMEELFSDVDSPYYDLDTVLTGMMGGARPGPC
6443	ļ		EGLEGLAPATPGPSSSCKSDLGELDHVVEILVET
6443	2	555	MASPAASSVRPPRPKKEPOTLVIPKNAAEEOKLKLERLMKNPDK
1	1	[AVPIPEKMSEWAPRPPPEFVRDVMGSSAGAGSGEFHVYRHLRRR
1			EYQRQDYMDAMAEKQKLDAEFQKRLEKNKIAAEEQTAKRRKKRQ
1	1		KLKEKKLLAKKMKLEQKKQEGPGQPKEQGSSSSAEASGTEEEEE VPSFTMGR
6444	390	899	GSTPRGKMRAPIPEPKPGDLIEIFRPFYRHWAIYVGDGYVVHLA
"""	330	677	PPSEVAGAGAASVMSALTDKAIVKKELLYDVAGSDKYQVNNKHD
1	1		DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNELRYGVA
1			RSDOVRDVIIAASVAGMGLAAMSLIGVMFSRNKROKO
6445	2	753	AGAAGAAGAARSPRPQAHTKGVRGLPSRRRSPDCGRMELAAGSF
1		, 55	SEEQFWEACAELQQPALAGADWQLLVETSGISIYRLLDKKTGLY
1	1		EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQYVKELYEQECNGE
1]		TVVYWEVKYPFPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM
	[•	PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYFDNPGGQIP
1			SWLINWAAKNGVPNFLKDMARACQNYLKKT
6446	1	1651	RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS
			DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAEETFSHCKS
{			EHOPNIDSMYHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV
1	ł	•	PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS
1			VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT
			CSSSTSVIADLOEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD
ì			FIYQNPHIFKDKVVLDVGCGTGILSMFAAKAGAKKVLGVDQSEI
L	<u> </u>		

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	-	\=possible nucleotide insertion)
			LYQAMDIIRLNKLEDTITLIKGKIEEVHLPVEKVDVIISEWMGY
			FLLFESMLDSVLYAKNKYLAKGGSVYPDICTISLVAVSDVNKHA
			DRIAFWDDVYGFKMSCMKKAVIPEAVVEVLDPKTLISEPCGIKH
	ŀ		IDCHTTSISDLEFSSDFTLKITRTSMCTAIAGYFDIYFEKNCHN
1			RVVFSTGPQSTKTHWKQTVFLLEKPFSVKAGEALKGKVTVHKNK
			KDPRSLTVTLTLNNSTQTYGLQ
6447	1554	1068	RLGPAEWHLSGPCHATLGAANRGRALGVRAAWRGAPLCORVMMP
1	1		SRTNLATGIPSSKVKYSRLSSTDDGYIDLOFKKTPPKIPYKATA
1]		LATVLFLIGAFLIIIGSLLLSGYISKGGADRAVPVLIIGILVFL
-			PGFYHLRIAYYASKGYRGYSYDDIPDFDD
6448	74	559	GQVLSHCYHYRSSRWRRGGLSRGRGAGVMALVPYEETTEFGLQK
ļ			FHKPLATFSFANHTIQIRQDWRHLGVAAVVWDAAIVLSTYLEMG
i	}		AVELRGRSAVELGAGTGLVGIVAALLACRIRYERDNNFLAMLER
6449	597	1006	QFIVRKVHYDPEKDVHIYEAQKRNQKEDL
0	391	1876	EYGVCENLRKLEITGVSCRDVYAKLLHRYRHILGLWQPDIGPYG
			GLLNVVVDGLFIIGWMYLPPHDPHVDDPMRFKPLFRIHLMERKA
	1 1		ATVECMYGHKGPHHGHIQIVKKDEFSTKCNQTDHHRMSGGRQEE
ļ	1		FRTWLREEWGRTLEDIFHEHMQELILMKFIYTSQYDNCLTYRRI
1			YLPPSRPDDLIKPGLFKGTYGSHGLEIVMLSFHGRRARGTKITG
}	i i		DPNIPAGQQTVEIDLRHRIQLPDLENQRNFNELSRIVLEVRERV RQEQQEGGHEAGEGRGRQGPRESQPSPAQPRAEAPSKGPDGTPG
1			EDGGEPGDAVAAAEQPAQCGQGQPFVLPVGVSSRNEDYPRTCRM
1		•	CFYGTGLIAGHGFTSPERTPGVFILFDEDRFGFVWLELKSFSLY
	ĺ		SRVQATFRNADAPSPQAFDEMLKNIQSLTS
6450	848	269	FVPAPRTVSGKRSLPGEWEERGEGEQRTGREFSGNGGRAVEAAR
			MRLLCGLWLWLSLLKVLQAQTPTPLPLPPPMQSFQGNQFQGEWF
ł .			VLGLAGNSFRPEHRALLNAFTATFELSDDGRFEVWNAMTRGOHC
			DTWSYVLIPAAQPGQFTVDHRVWTHEQAGRPQDQPAGQELVAAS
6451			RDAGPVHLPGQSSGPLG
045L	232	939	HSPTPPTSPRASTMEDVKLEFPSLPQCKEDAEEWTYPMRREMQE
1			ILPGLFLGPYSSAMKSKLPVLQKHGITHIICIRQNIEANFIKPN
			FQQLFRYLVLDIADNPVENIIRFFPMTKEFIDGSLQMGGKVLVH
1	1		GNAGISRSAAFVIAYIMETFGMKYRDAFAYVQERRFCINPNAGF
1			VHQLQEYEAIYLAKLTIQMMSPLQIERSLSVHSGTTGSLKRTHE
6452	1	652	EEDDFGTMQVATAQNG
1 1	- 1	032	RTRGESSNMEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQ
1			LKFLKPKINSFYAFEVKDAKGRTVSLEKYKGKVSLVVNVASDCQ LTDRNYLGLKELHKEPGPSHFSVLAFPCNQFGESEPRPSKEVES
1		•	FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWK
			YLVNPEGQVVKFWRPEEPIEVIRPDIAALVRQVIIKKKEDL
6453	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC
] }	!		RDKKNCKVVFSQQELRKRLTPLQYHVTQEKGTESAFEGEYTHHK
1 1	1		DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD
1 [FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT
<u> </u>			PADSSGTAEGGSGVASPAQADKAEL
6454	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC
] [ļ	RDKKNCKVVFSQQELRKRLTPLQYHVTQEKGTESAFEGEYTHHK
!!	Į		DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD
	1		FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT
EART -			PADSSGTAEGGSGVASPAQADKAEL
6455	1042	173	RVHLATVSASAAWDALGLPVRSHMQGSTRRMGVMTDVHRRFLOL
1	i		LMTHGVLEEWDVKRLQTHCYKVHDRNATVDKLEDFINNINSVLE
j .		1	SLYIEIKRGVTEDDGRPIYALVNLATTSISKMATDFAENELDLF
1		1	RKALELIIDSETGFASSTNILNLVDQLKGKKMRKKEAEQVLOKF
<u> </u>			VQNKWLIEKEGEFTLHGRAILEMEQYIRETYPDAVKICNICHSL

		·	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	location		L=Leucine, M=Methionine, N=Asparagine,
i	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
1	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
1	amino acid	sequence	Codon, /=possible nucleotide delection,
1	sequence		\=possible nucleotide insertion)
			LIQGQSCETCGIRMHLPCVAKYFQSNAEPRCPHCNDYWPHEIPK
1	i		VFDPEKERESGVLKSNKKSLRSRQH
6456	2	555	RPQSRSISMWRNSLLQVSSGLRWLRVCAMVDILGERHLVTCKGA
1	1	Ì	TVEAEAALQNKVVALYFAAARCAPSRDFTPLLCDFYTALVAEAR
1	i		RPAPFEVVFVSADGSSQEMLDFMRELHGAWLALPFHDPYRHELR
1	i	j	KRYNVTAIPKLVIVKQNGEVITNKGRKQIRERGLACFQDWVEAA
4	1		DIFQNFSV
6457	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
1		1	KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
i		}	IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
1			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
1	•	1	TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
1		•	SFLTLSSQLKPKPVGEENICLDLKS
6458	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
"""			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
i	ł		IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
l .	1		IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
1	1		DLOOATEFNOWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
ſ	j		TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
1	1		SFLTLSSQLKPKPVGBENICLDLKS
6459	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
0133	1 22		KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
1	1	1	IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
1		1	IFTAANGVYTKOKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
1			DLOOATEFNOWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
	1		TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
	1		SFLTLSSOLKPKPVGEENICLDLKS
6460	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
0400	1 23		KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
ł			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
ļ			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
1	1	1	DLOOATEFNOWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
1			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
1			SFLTLSSOLKPKPVGEENICLDLKS
6461	1653	360	LQQRTLRITAVGQTHPIAWMAWEPSLGAFYGPASFITFVNCMYF
0401	1033	300	LSIFIQLKRHPERKYELKEPTEEQQRLAANENGEINHQDSMSLS
1			LISTSALENEHTFHSQLLGASLTLLLYVALWMFGALAVSLYYPL
1			DLVFSFVFGATSLSFSAFFVVHHCVNREDVRLAWIMTCCPGRSS
1	1		YSVQVNVQPPNSNGTNGEAPKCPNSSAESSCTNKSASSFKNSSQ
1			GCKLTNLOAAAAOCHANSLPLNSTPQLDNSLTEHSMDNDIKMHV
l			APLEVQFRTNVHSSRHHKNRSKGHRASRLTVLREYAYDVPTSVE
1			GSVQNGLPKSRLGNNEGHSRSRRAYLAYRERQYNPPQQDSSDAC
		1	STLPKSSRNFEKPVSTTSKKDALRKPAVVELENQQKSYGLNLAI
1	1	Ī	QNGPIKSNGQEGPLLGTDSTGNVRTGLWKHETTV
		J	QNGFIKSNGQEGFILGIDSIGNVKIGLWKREITV SEELDREKKLKEDSPRKTPNKESGVPSLPVSLTSIKEEPKEAKH
6462	3	773	PDSQSMEESKLKNDDRKTPVNWKDSRGTRVAVSSPMSQHQSYIQ
1	1		FDSG2WEESKPKWDDKYTLAMMYD2KGTKAWA22LH26WG2TTG
[YLHAYPYPQMYDPSHPAYRAVSPVLMHSYPGAYLSPGFHYPVYG
1	· ' '		KMSGREETEKVNTSPSVNTKTTTESKALDLLQQHANQYRSKSPA
1	1	i	PVEKATAEREREAERERDRHSPFGQRHLHTHHHTHVGMGYPLIP
			GQYDPFQGLTSAALVASQQVAAQASASGMFPGQRRE
6463	2	350	VILCILGGWIFKNADRSMEKKKGEPRTRAEARPWVDEDLKDSSD
1			LHQAEEDADEWQESEENVEHIPPSHNHYPEKEMVKRSQEFYELL
1			NKRRSVRFISNEQVPMEVIDNVIRTAGL
6464	12	1154	GILROKEREERNRIHKKEILFLEHLLVVPSEMSSLSGKVQTVLG
	,		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
- 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ľ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	_	\=possible nucleotide insertion)
			LVEPSKLGRTLTHEHLAMTFDCCYCPPPPCQEAISKEPIVMKNL
-			YWIQKNAYSHKENLQLNQETEAIKEELLYFKANGGGALVENTTT
İ	į	1	GISRDTQTLKRLABETGVHIISGAGFYVDATHSSETRAMSVEQL
İ	ļ		TDVLMNEILHGADGTSIKCGIIGEIGCSWPLTESERKVLQATAH
i i		j	AQAQLGCPVIIHPGRSSRAPFQIIRILQEAGADISKTVMSHLDR
l l		Į.	TILDKKELLEFAQLGCYLEYDLFGTELLHYQLGPDIDMPDDNKR
	1	ł	IRRVRLLVEEGCEDRILVAHDIHTKTRLMKYGGHGYSHILTNVV
	ļ		PKMLLRGITENVLDKILIENPKQWLTFK
6465	126	1396	KMTVFFKTLRNHWKKTTAGLCLLTWGGHWLYGKHCDNLLRRAAC
1			ORAQVEGNOL TERMACITY ACTION AND A CHARGE TO THE CONTRACT OF
	İ	1	QEAQVFGNQLIPPNAQVKKATVFLNPAACKGKARTLFEKNAAPI LHLSGMDVTIVKTDYEGQAKKLLELMENTDVIIVAGGDGTLQEV
ı	1	1	VTGVLRRTDEATFSKIPIGFIPLGETSSLSHTLFAESGNKVQHI
1	}	l	TDATLAIVKGETVPLDVLQIKGEKEQPVFAMTGLRWGSFRDAGV
	1		KVSKYWYLEPLKIKAAHFFSTLKEWPQTHQASISYTGPTERPPN
	ł		EPETTENOPESI VERIL DEL ACUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DEL CUELO DEL CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DE LA CUELO DEL CUELO DE LA CUELO DE LA CUELO DEL CUELO DE LA LA CUELO DEL LA CU
	1		EPEETPVQRPSLYRRILRRLASYWAQPQDALSQEVSPEVWKDVQ LSTIELSITTRNNQLDPTSKEDFLNICIEPDTISKGDFITIGSR
1			KVRNPKLHVEGTECLQASQCTLLIPEGAGGSFSIDSEEYEAMPV
1	İ	[EVKLLPRKLQFFCDPRKREQMLTSPTQ
6466	1134	828	VARGTELSQLEKAHPPADMGRRKSKRKPPPKKKMTGTLETQFTC
-			PPCNHEKSCDVKMDRARNTGVISCTVCLEEFQTPITYLSEPVDV
			YSDWIDACEAANQ
6467	301	2571	GBLRVLALAHGELACHAVLTASLLSLRSRLMDSDMDYERPNVET
	l i		IKCVVVGDNAVGKTRLICARACNATLTQYQLLATHVPTVWAIDQ
1	[YRVCQEVLERSRDVVDDVSVSLRLWDTFGDHHKDRRFAYGRSDV
ł			VVLCFSIANPNSLHHVKTMWYPEIKHFCPRAPVILVGCQLDLRY
-			ADLEAVNRARRPLARPIKPNEILPPEKGREVAKELGIPYYETSV
i			VAQFGIKDVFDNAIRAALISRRHLQFWKSHLRNVQRPLLQAPFL
			PPKPPPPIIVVPDPPSSSEECPAHLLEDPLCADVILVLQERVRI
1	·		FAHKIYLSTSSSKFYDLFLMDLSEGELGGPSEPGGTHPEDHQGH
		1	SDQHHHHHHHHHGRDFLLRAASFDVCESVDEAGGSGPAGLRAST
ł			SDGILRGNGTGYLPGRGRVLSSWSRAFVSIQEEMAEDPLTYKSR
			LMVVVKMDSSIQPGPFRAVLKYLYTGELDENERDLMHIAHIAEL
			LEVFDLRMMVANILNNEAFMNQEITKAFHVRRTNRVKECLAKGT
1 1	1		FSDVTFILDDGTISAHKPLLISSCDWMAAMFGGPFVESSTREVV
			FPYTSKSCMRAVLEYLYTGMFTSSPDLDDMKLIILANRLCLPHL
1 1	1		VALTEQYTVTGLMEATQMMVDIDGDVLVFLELAQFHCAYQLADW
	İ		CLHHICTNYNNVCRKFPRDMKAMSPENQEYFEKHRWPPVWYLKE
1 1	İ	l	EDHYQRARKEREKEDYLHLKRQPKRRWLFWNSPSSPSSSAASSS
<u> </u>			SPSSSSAVV
6468	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
		[LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEPED
1			KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
1	.		SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN
1 1			QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS
į l		1	TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA
] [•	GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWLMAAL
1		1	PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYYITHLLKGALLF
, ,		ļ	ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYITIES
	1	í	TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD
	1	į	GKGKFSRAHFVLLSLL
6469	3	1374	
]		4.7.3	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
1	1		LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEPED
(l	1		KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
1 1	1		SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN
1 1	İ		QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS
			TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA

Deginning nucleotide location corresponding corresponding cofirst amino acid residue of amino acid residue of amino acid sequence	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Solidation Costation Costation Goltanic Acid, F-Phenylalanine, G-Glycine, corresponding to first amino acid residue of amino acid residue of amino acid sequence Section, F-Phenylalanine, S-Asparagine, P-Proline, O-Goltutanine, R-Asparagine, S-Serine, T-Threonine, V-Valine, W-Tirytophan, Y-Tyrosine, M-Turk, Winknown, V-Turk, W-Turk, V-	_	l		(A=Alanine C-Cysteins D-Assartis Asid
Coration Corresponding Coffiest Coff				Glutamic Acid E-Dhom-1-1-mine C clark
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence se		l .		W-Wietidine T. Terlandine, G-Glycine,
to first amino acid residue of amino acid sequence (amino acid sequence) sequence (amino acid				Laborate, Isisoleucine, Kabysine,
amino acid residue of amino acid sequence surveyables, X-Dixtonine, X-	1		† ·	B-Broline, Manetatonine, Nasparagine,
residue of amino acid sequence ##Tryptophan, X=Tyrosine, X=Duknown, *=stop codon, /=possible nucleotide delation ### deciding sequence ##	1		1	r-rioithe, Q=Glucamine, K≈Arginine,
amino acid sequence Codon, /-possible nucleotide insertion) GETPLPKIJISMAFFFFLSSTIWHILERERENDVEKIBULARIA PFTESISLVERAL INSERTION OF STREET AND STREET A		I '	1	S=Seline, Tainreonine, Vavaline,
Sequence N=possible nuclectide insertion	1	1		w=iryptopnan, r=ryrosine, x=Unknown, *=Stop
GETPLPKLYTSHAFFFLSGTIVHILLKRERNDVEKTHEWIMANL PPTKSISLIVFHAIDTHYLSGSGPFLEGMAVTIALLKGALLP PTTKSISLIVFHAIDTHYLSGSGPFLEGMAVTIALLKGALLP TITALIGTGWAFIKHLISDKOKKITMIVIPRRVLANVAYITIES TEEGTTEYGLWKOSLFLVULGCGATLPPVWNSTHLOGRASHO GKGFSRAHFULISLL 6470 2726 1437 AAASGUSSBAADVLAGSBAAGNGRESTEVVGSRRHPSARRS GPLEREDGGTTPGPOLLPLGGALLAPRTULSSABTGRSHPTO GHPSGGGRGGTSS SSAAGRAPBAADVASSSNILNRPGCARG SLOKTSADTIKKKOROAKEEKARPLKIAKVEEGARG SLOKTSADTIKKKOROAKEEKARPLKIAKVEEGARG SLOKTSADTIKKKOROAKEEKARPLKIAKVEEGARG SLOKTSADTIKKKOROAKEEKARPLKIAKVEEGARG SLOKTSADTIKKKOROAKEEKARPLKIAKVEEGARG SLOKTSADTIKKKOROAKEEKARPLKIAKVEEGARG SLOKTSADTIKKKOROAKEEKARPLKIAKVEEGARG SLOKTSADTIKKKOROAKEEKARPLKIAKVEEGARG SLOKTSADTIKKKOROAKEEKARPLKIAKVEEGARG SLOKTSADTIKKKOROAKEEKARPLKIAKVEEGARGALVEERAR PYTTYSTERMENDERPOVEPFOOVISKTYTIKGGGSLDGFYRAM VEYYRVIRFPDGHVWMILTTEEPOSTVPELURI PYTTYSWEMEMILERPOVEPFOOVISKTYTIKGGGSLDGFYRAM VEYYRVIRFPDGHVWMILTTEEPOSTVPELURI GPRKKKGWRELAGEBPOLGKUODILERPSUDPALURERPORT GPRKKKGWRELAGEBPOLGKUODILERPSUDPALURERPORT GPRKKKGWRELAGEBPOLGKUONICKEETSGGLLGEADN KELPPUTOSKKKILKKYCHVOKKSLLLKKAGGBLPERVERDLILBOT GTKKKGWREPARLHTEPSQAPAVEVAPAGASNINPSPEDHOTILG AAHEVELGORGKEEKKLIKKYCHVOKKSLLLKKAGGBLPERVERDLILBOT GTKKKGWREPARLHTEPSQAPAVEVAPAGASNINPSPEDHOTILG AAHEVELGORGKEEKKLIKKYCHVOKKSLLLKKAGGBLPERVERDLILG GTKKKGWREPARLHTEPSQAPAVEVAPAGASNINPSPEDHOTILG AAHEVELGORGKEEKKLIKKYCHADERLAGTBANGGARTHYT GTKKKGWREPARLHTEPSQAPAVEVAPAGASNINPSPEDHOTILG AAHEVELGORGKEEKKLIKKYCHADERLAGTBANGGARTHYT GTKHTYLLTOONINPSTELGGGLAGEARPTTP ARVOLOQUINTI IDELIGIAARAGNILGATTERLAGTAGGAR GARRABABAUFTURUTI IDELIGIAARAGNILGATTERLAGTAGARG KURKERCEARGAGARTHYTOONINPSTERFERTYNKACTGAGARG LINKHYLLGTTVOVNNTVI FEGEFAHORRPAPASLANTRIKEDA AVOPTPAAPARATUPATHYDHILDHISTSTILDSWINWFO LIKHHILGTTVOVNNTVI FEGEFAHORRPAPASLANTRIKEDAA AVOPTPAAPARATUPATHYDHILDHISTSTILDSWINWFO LIKHHILGTTVOVNNTVI FEGEFAHORRPAPASLANTRIKERDA LORGORGHPAARATUPATATATATATATATATATATATATATATATATATAT	İ	B .	sequence	Codon, /=possible nucleotide deletion,
PPTKSISLYFHAIDYHYISSOGPPIEGRAVVYYITHLIKGALIP ITIALIGITUMPA IHAILSINGKHITMYLUFRAINAVAITIES TEGGTTEYGLWKDSLPIVÜLLCGALIPPVVWSIRHQGASATO CKGKFSRAHPVLISLU AAASGVSRADAFVLAGSBASAGNGRPSTFRVPGGSRHPSARG GPLPREDGGTPGGQLLPPGGALIPPVTUSSAATTGRSHPDT OHPSSGGRCRGGTESPSAAGRASMABAEEDCHSDTVRADDDE ENESPARTIJOAGLOWFFAGAGALIPPTLIKSSAASTGRSHPDT OHPSSGGRCRGGTESPSAAGRASMABAEEDCHSDTVRADDDE ENESPARTIJOAGLOWFFAGAGALIPPTLIKSSAASTGRSHPDT OHPSSGGRCRGGTESPSAAGRASMABAEEDCHSDTVRADDDE ENESPARTIJOAGLOWFFAGAGALIPPTLIKSSAASTGRSHPDT OHPSSGGRCRGGTESPSAAGRASMABAEEDCHSDTVRADDDE ENESPARTIJOAGLOWFFAGAGALIPPTLIKSSAASTGRSHPDT FRAMOLVPDIP BY TITTHSPEGGVSWYSTLOMBYCKWGRGSTIKU PYTSHREMPLERPRVRPGOVIJSKTTYTIRGGRQSLDGFYRAWHQ VEYTYNIRPPDGHVMMLTTEPEPGSVVPHLAVWGRGSTIKU PYTSHREMPLERPRVRPGOVIJSKTTYTIRGGRQSLDGFYRAWHQ VEYTYNIRPPDGHVMMLTTEPEPGSVVPHLAVWGRGSTIKU PYTSHREMPLERPRVRPGOVIJSKTTYTIRGGRQSLDGFYRAWHQ VEYTYNIRPPDGHVMMLTTEPEPGSVVPHLAVGRGSTIKU PYTSHREMPLERPRVRPGOVIJSKTTYTIRGGRQSLDGFYRAWHQ EKLPFVDTGSKEKGLIKKRTKVOKKSLLLKKPLRVDLILBNISK VPAPKOVLAHQVORAKLERREQUHELAKGGELDEEVRAQAR EKLPFVDTGSKEKGLIKKRTKVOKKSLLLKKPLRVDLILBNISK VPAPKOVLAHQVORAKLERREQUHELAKGGELDEEVRAQAR LLMPSATRAKPGCQDTVERPFVDLWASDNPLDRPLWGQDFFLE GTKKKGVKRPARHLTNEPSGAAROVENPAGASTOSTFOELCEGILE ESDGEGEGGGEGEGABAEVGTVARVATAFBEHRTALDSTSLETLKEGE GTKKKGVKRPARHLTHESPAGAROVENPAGAATQSSTFOELCEGILE ESDGEGEGGGEGPEGADAEVGTPTABLATTEGGREKKA VHELRVQGAARAARHLTERFLETLESTERFUNGTSLERTLKEGE AAHEVELGROKEABKLERQLADATGGAATQSSTFOELCEGILE ESDGEGEGGGEGPEGADAEVCTPTABLATTEGGREKKA VHELRVQGAARAARHLTERFLETLESTERRYVEVELCIL DFYTHESVQRRGGGREFFOVMLVKRLEVLUDBEARRYVEVELCIL DFYTHESVQRRGGGREFFOVMLVKRLEVLUDBEARRYVEVELCIL DFYTHESVQRRGGGREFFOVMLVKRLEVLUDBEARRYVEVELCIL DFYTHESVQRRGGGREFFOVMLVKRLEVLUDBEARRYVEVELCIL DFYTHESVQRRGGGREFFOVMLVKRLEVLUDBEARRYVEVELCIL DFYTHESVQRRGGGREFTANGERHEVEVELCIL DFYTHESVQRRGGGREFTANGERHEVEVELCIL LRCMQVQGANAARATAFFRGHCCTANDANTKYNSRAGMYREKIRG LLGMQVQGANAARATAFFRGHCCTANDANTKYNSRAGMYREKIRG LLGMQVQGANAARATAFFRGHCCTANDANTKYNSRAGMYREKIRG KKKEKCEABAAVVSVGTFOTTOTIVHFKKRSPENTEGKOGS KVTKOEPTRISAALSAKAGLAKKGLGAKVKSOEPTTANGSFTANDAVTSRGGT	ļ	sequence		\=possible nucleotide insertion)
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OHPSSGGRCRGSTESPSSAAGRAENDERDCHSDTVRADDDE ENSSPARTDLQAQLOMPRAQMMELLSYSSMLENPECRANG SLOKTSADTKGKOGAKEEKARELFLKAVEEGONGALYEAIKPY RRAMGILUPDIEREITJYTSSPDGGGVUSTENDENDENGMADLLS YFQQQITFOESULKLCOPELESSOTHISVLDMDDENGMADLLS YFQQQITFOESULKLCOPELESSOTHISVLDMDENGMADLLS YFQQQITFOESULKLCOPELESSOTHISVLDMDENGMADLLS YFQQQITFOESULKLCOPELESSOTHISVLDMDENGMADLLS YFQQQITFOESULKLCOPELESSOTHISVLDMDENGMADLS SDLLARSLEQLSLUCGEFYICARDDEIWRLACKWGRSCIKLU PYTSWREMPLERPRVREPGVIJSKTTITGGGGSLOGFYRAWHO VEYTRYIRFFPDGHVMMITTPEEPGSLVFELRTR FFFDRWAAGGSGVGGKEKSSKSDADSEGFLGRPTSVDPALRERRE GPRNKKRGWRRIAAGGSGVGGKKESKSSGDADSFGLGRPTSVDPALRERRE KALFFVDTGSKEKGLTKKRTKVKKKKLKKLKLERULLLENTSK VPAPKDVLAHQVPNAKKLRKKGCLWEKLAKGGSLPEVKRAQAR LLDRSATRAKPGQPOTVERFFPDLWAMPSGEDHOTLLS AAHSVELGOKKEBABLERQLARPAGRATOESTFGELCEGLE ESDGGEGPGGGSPPEAGDAEVCTFARLATTEKKTEQORRESKA AHISVELGOKKEBABLERQLARPAGPATOESTFGELCEGLE ESDGGEGPGGGSPPEAGDAEVCTFARLATTEKKTEQORRESKA VHILRVOQAALRAARLHRINGSLFILISTUADHLARPGARRETTIP GARREADARFRIGHKVQAAPDIDVQLSSELTDGLPTLKPEG ROARREAEADKFRIGHKVQAAPDIDVQLSSELTDGLPTLKPEG ROARREAEADKFRIGHKVQAAPDIDVQLSSELTDGLPTLKPEG ROARREAEADKFRIGHKVQAAPDIDVQLSSELTDGLPTLKPEG ROARREAEADKFRIGHKVQAAPDIDVQLSSELTDGLPTLKPEG ROARREAEADKFRIGHKVQAAPDIDVQLSSELTDGLPTLKPEG ROARREAEADKFRIGHKVQAAPDIDVQLSSELTDGLPTLKPEG ROARREAEADKFRIGHKVQAAPDIDVQLSSELTDGLPTLKPEG ROARREAEADKFRIGHKVQAAPDIDVQLSSELTDGLPTLKPEG ROARREAEADKFRIGHKVQAAPDIDVQLSSELTDGLPTLKPEG ROARREAEADKFRIGHKVQAAPDIDVGLSSELTDGLPTLKPEG ROARREAEADKFRIGHTVALGOKARCHEVALLE ROARREACKVALVERVERPETICL DFYTHBSVQRHGHERFPPDVDALFPRRTTVLDQHLARPPARRFGTTTP ARVDLQQIMTII IDELGKASAARQANGASATKAQARCHEVLAVEPPUPLIN ARVDLQQIMTII IDELGKASAARQANGARSANQANGRINVVY LLDGSSARAARGARILTYVGLGFFAARGATUKALVELVERAPPPUPL ARVDLQQIMTII IDELGKASAAGANGARPAPSELGSKLUKAVEPPUPLIN ARVPRATTPAHPPPURSSLLOPPPUPLAFSTGGARGKKLAKVAPPPUPLENKAARGATARGAAAAAAVAPTATARGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	6470	2726	1437	AAASGVSSRADAPVLAQSPASAGNGRPSTPRVPGSRRHPSAPRS
ENESPABTDLOQALOMFRAGOMERADRILAPOVSSKILENPECRAARG SLOKTSADTYKGKOGAKEKARELIKAVEEGOMGALYBA IKFY RRAMOLVPDIEFKITYTRSPDGGGVGNSYIEDNDDGKMADILS YFQQOLTPGSVLKLOOPELESSOITLUMBEVLMYI PIWVUS SDLDLRSLEQLSLUCRGFYICARDPEIWRLACLKVWGRSCIKLV PYTSWREMPLERPRYREPGYVISKTYIRGGEGSLGGFYRAWHO OVYYRYIRFPDGHWMINTTEEPGSLUFBTYNDFALRERR 6471 1750 295 FFFDKMAAGGSGVGGKRSSKSDABGGFLGLEPTSVUDPALRERR GPRNKKRGWRLAGDFJGLEVOOPLENUCERTSGGLLSEAPN EKLFFUDTGSKEKGLTKKRFKKUVKSLLLKKPLRVUDLILENTSK VPAPKDULAHQVPNAKKLRKEGLEWAKGGSLPEVVUDPALRERRA EKLFFUDTGSKEKGLTKKRFKVOKKSLLLKKPLRVUDLILENTSK VPAPKDULAHQVPNAKKLRRKEGLEWAKGGSLPEVVDLILENTSK VPAPKDULAHQVPNAKKLRRKEGLEWAKGGSLPEVVDLOEFFLE CYKKKGVKRABLHITKPSQAPAVEVAPAGASYMPSFEDHOTLLS AAHSVELQROKKRABKLERGLAAPATGAATOESTFOELCEGLLE ESDGGEGFOGGSDPAGDASVCTTARLATGKGR ROARREAEADKRRRLGGLKYGAPATGOATOESTFOELCEGLLE ESDGGEGFOGGSDPAGDASVCTTARLATTEKKTEGORRREKA VHRLRVQOAALRAARLRHOELFRLGGIKGQVALRLAELARRORR ROARREAEADKRRRLGGIKKYGAPDIDVLSSEILTDSLETLKPEG GATZ 3 897 SCGSDRRQMAMFFFEDVALFPERTTVLDCHLEPPARREGTTF ARVDLOQQINTI IDELGKASAAQANLETSASRMOSRRHVY ILKDSSARPAGKGAIGFIKVGVKLVEKRAFEETQL DFYIHESVORGHHGREFFOYMLOKRFKVKVKLVEKRAFEETQL LNKHYNLETTVPONNFVIFEGFFAHORPPARSLEATHHSRAA AVDPTFAAPARLPPKRAEGDIKPYSSDREPLKVAVEPBPLL INKHYNLETTVPONNFVIFEGFFAHORPPARSLEATHHSRAA AVDPTFAAPARLPFKRAEGDIKPYSSDREPLKVAVEPBPLL RAPPRATTPPAHPPPRSSSLCINSPEEGPLRPPVD 6473 22 912 SSAVEFWGGEKMAAEPNTETQTLFKRLROPPTKACFDCGAK NPSMASITYGVFLCIDCSGVHRSLUVHLSIRISTBLDSINMWFQ LRCMQVGGNARAAFFFRQHGCTANDANTKNISRAAQMYREKIRG LGSAALARAGTAFFRQHGCTANDANTKNISRAAQMYREKIRG LGSAALARAGTAFFRGHGCTANDANTKNISRAAQMYREKIRG LGSAALARAGTAFFRGHGCTANDANTKNISRAGMYREKIRGD KSSIICKKKPAAAKKGJAKGJAKGLGARVSGSFSIERGAQVAB KLREQQAADAKKGPAFFRGARLSATVUPTJIMPKRKSPENTEGKDGS KVYKQBPTRRSARLSAKPAPPKPERKRTSAKKBPGAKLISRGG KGKKEKGPAGKGGARSACGARROFFREKKTSAKKBPGAKLISRGT KVYKQBPTRRSARLSAKPAPPKPERKRTSAKKBPGAKLISRGT KVYKQBPTRRSARLSAKPAPPKPERKRTSAKKBPGAKLISRGT KVYKQBPTRRSARLSAKAPPKPERFRRKTSAKKBPGAKLISRGT KSCVKKERKORACKGTAPPSKNGSTKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVVKYGTEN 6475 1060 ARAMAGYKGTHREAGKNULVKGRTAEETIL GGRGHFFAHADAVTVKTERN		İ		GPLPREDGCRTPGPQLLPLPGALLRPRTLLSSAAETGRSRHPDT
ENESPABTDLOQALOMFRAGOMERADRILAPOVSSKILENPECRAARG SLOKTSADTYKGKOGAKEKARELIKAVEEGOMGALYBA IKFY RRAMOLVPDIEFKITYTRSPDGGGVGNSYIEDNDDGKMADILS YFQQOLTPGSVLKLOOPELESSOITLUMBEVLMYI PIWVUS SDLDLRSLEQLSLUCRGFYICARDPEIWRLACLKVWGRSCIKLV PYTSWREMPLERPRYREPGYVISKTYIRGGEGSLGGFYRAWHO OVYYRYIRFPDGHWMINTTEEPGSLUFBTYNDFALRERR 6471 1750 295 FFFDKMAAGGSGVGGKRSSKSDABGGFLGLEPTSVUDPALRERR GPRNKKRGWRLAGDFJGLEVOOPLENUCERTSGGLLSEAPN EKLFFUDTGSKEKGLTKKRFKKUVKSLLLKKPLRVUDLILENTSK VPAPKDULAHQVPNAKKLRKEGLEWAKGGSLPEVVUDPALRERRA EKLFFUDTGSKEKGLTKKRFKVOKKSLLLKKPLRVUDLILENTSK VPAPKDULAHQVPNAKKLRRKEGLEWAKGGSLPEVVDLILENTSK VPAPKDULAHQVPNAKKLRRKEGLEWAKGGSLPEVVDLOEFFLE CYKKKGVKRABLHITKPSQAPAVEVAPAGASYMPSFEDHOTLLS AAHSVELQROKKRABKLERGLAAPATGAATOESTFOELCEGLLE ESDGGEGFOGGSDPAGDASVCTTARLATGKGR ROARREAEADKRRRLGGLKYGAPATGOATOESTFOELCEGLLE ESDGGEGFOGGSDPAGDASVCTTARLATTEKKTEGORRREKA VHRLRVQOAALRAARLRHOELFRLGGIKGQVALRLAELARRORR ROARREAEADKRRRLGGIKKYGAPDIDVLSSEILTDSLETLKPEG GATZ 3 897 SCGSDRRQMAMFFFEDVALFPERTTVLDCHLEPPARREGTTF ARVDLOQQINTI IDELGKASAAQANLETSASRMOSRRHVY ILKDSSARPAGKGAIGFIKVGVKLVEKRAFEETQL DFYIHESVORGHHGREFFOYMLOKRFKVKVKLVEKRAFEETQL LNKHYNLETTVPONNFVIFEGFFAHORPPARSLEATHHSRAA AVDPTFAAPARLPPKRAEGDIKPYSSDREPLKVAVEPBPLL INKHYNLETTVPONNFVIFEGFFAHORPPARSLEATHHSRAA AVDPTFAAPARLPFKRAEGDIKPYSSDREPLKVAVEPBPLL RAPPRATTPPAHPPPRSSSLCINSPEEGPLRPPVD 6473 22 912 SSAVEFWGGEKMAAEPNTETQTLFKRLROPPTKACFDCGAK NPSMASITYGVFLCIDCSGVHRSLUVHLSIRISTBLDSINMWFQ LRCMQVGGNARAAFFFRQHGCTANDANTKNISRAAQMYREKIRG LGSAALARAGTAFFRQHGCTANDANTKNISRAAQMYREKIRG LGSAALARAGTAFFRGHGCTANDANTKNISRAAQMYREKIRG LGSAALARAGTAFFRGHGCTANDANTKNISRAGMYREKIRGD KSSIICKKKPAAAKKGJAKGJAKGLGARVSGSFSIERGAQVAB KLREQQAADAKKGPAFFRGARLSATVUPTJIMPKRKSPENTEGKDGS KVYKQBPTRRSARLSAKPAPPKPERKRTSAKKBPGAKLISRGG KGKKEKGPAGKGGARSACGARROFFREKKTSAKKBPGAKLISRGT KVYKQBPTRRSARLSAKPAPPKPERKRTSAKKBPGAKLISRGT KVYKQBPTRRSARLSAKPAPPKPERKRTSAKKBPGAKLISRGT KVYKQBPTRRSARLSAKAPPKPERFRRKTSAKKBPGAKLISRGT KSCVKKERKORACKGTAPPSKNGSTKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVVKYGTEN 6475 1060 ARAMAGYKGTHREAGKNULVKGRTAEETIL GGRGHFFAHADAVTVKTERN	1			QHPSSGGRCRGGTESPSSAAGRPASMAEAEEDCHSDTVRADDDE
RRAMQLVPDIEFKITTTRSPEGDEVENSYIEDNDDDSKMADLLS YFQQQLTFQESVLKLQOPELSSQITSVLPWFTRWWYF1RWWS SDLDLRSLEGLSLVCRGFYTCARDPETWRLACLKVWGRSCTKLV PYTSWRPMPLERPREVPEDVOYISTYTRQGDGSLDGFYRAWHQ VEYYRYTRFPDCHTWMLTTPEDOSIVPRLRTR 6471 1750 299 FFFDKMARGGSGVGKRSKSGADSGFYLGHFSVDPALRRRRR GPRNKKRGWRLAGGELGLEUQPLEDVRLQERTSGGLLSEAPM EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLLLENTSK VPAPKDVLAHQVPNAKKLRRRGEVLAKKQGELDFEVBRADGR CFRNKKRGWRRLAGGELGLEUQPLADGRTSGGLLSEAPM EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLLLENTSK VPAPKDVLAHQVPNAKKLRRRGEVLAKKQGELDFEVBRADGR LLNDSATRAKPGFQDTVERPFYDLWASDNPLDRPLVGQDEFFLE QTKKKGVKRRARLHTHFSQAAPUSHAGSVNDSFEDHOTLLS AAHSVELQRQKEABKLERQLALPATGEKTGGORREKA VHALRVQQAALRARLHHGELFRLRGTKAQVALRLABELARPQRR RQARREABADKPRLGUKLKYQADJVOLSSELTDSLRTLKPEG NILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFREIQL FOLLESVAGAMEFPFDVDALFPERTIVLDQHLERFPARRFGTTTF ARVDLOQUIMTI IDELGKASKAMAJSTITSASRMGSNRHVVY ILKDSSARPAGKGAI IGFIKVGYKKLFVLLDGHERFPARRFGTTTF ARVDLOQUIMTI DELGKASKAMAJSTITSASRMGSNRHVVY ILKDSSARPAGKGAI IGFIKVGYKKLFVLLDGHERFPARRFGTTTF ARVDLOQUIMTI DELGKASKAMADSTITSASRMGSNRHVVY ILKDSSARPAGKGAI IGFIKVGYKKLFVLLDGHERFPARRFGTTTF ARVDLOQUIMTI DELGKASKAMADSTITSASRMOSNRHVVY ILKDSSARPAGKGAI IGFIKVGYKKLFVLLDGHERFPARRFGTTTF ARVDLOQUIMTI DELGKASKAMADSTITSASRMOSNRHVVY ILKDSSARPAGKGAI IGFIKVGYKKLFVLLDGHERFPARRFGTTTF ARVDLOQUIMTI DELGKASKAMADSTITSASRMONNRHVVY ILKDSSARPAGKGAI IGFIKVGYKKLFVLLDGHERFPARRFGTTTF ARVDLOQUIMTI DELGKASKAMADSTITSASRMONNRHVVY ILKDSSARPADRAKSPERFERDFTTARFARBAA NOPTPAPARAKLIPSVRHGHERFLOYMLGRERVEPHOLA INFSSKLIKBRA ANDFTAPAPARKLIP FRRADGELFOYHORFRUSDERGHENDSKLIKBRA ANDFTAPAPARKLIP FRRADGELFOYHORFRUSDERGHENDSKLIKBRA ANDFTAPAPARKLIP FRRADGRANTHEKTRADA NFSWASITYGVPLCIDCSGVHRSLGVHLSPIRSTELDSNMNWFQ LRCMQVCGRANATAFFRQHGCTANDANTCYNRRAQMYREFTRETH ARRATTPROHGCTANDANTCYNRRAGGRAMGENG LKKERQADADAVPKCPTFCFTDIVIMPKKSEPTTEGKDGS KVYKQBPTRSARLSAKPAPKPEPKPRKTAKKEPQAKISGGA KGKEEKGPGAGGGTAPSENGETKABEIHI SRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN ARMAQYKGTMEAGARAHHLLKKRROREOMEULKORILNEETIL KSCUGKPABHADAVPVRCTYFTYWGTEN LGQARKVKDEMEVTFSYWGGSGRERKRKISCLSFALDDLDD QAAARARAGAALSK	ł	i	ł	ENESPAETDLQAQLQMFRAQWMFELAPGVSSSNLENRPCRAARG
RRAMQLVPDIEFKITTTRSPEGDEVENSYIEDNDDDSKMADLLS YFQQQLTFQESVLKLQOPELSSQITSVLPWFTRWWYF1RWWS SDLDLRSLEGLSLVCRGFYTCARDPETWRLACLKVWGRSCTKLV PYTSWRPMPLERPREVPEDVOYISTYTRQGDGSLDGFYRAWHQ VEYYRYTRFPDCHTWMLTTPEDOSIVPRLRTR 6471 1750 299 FFFDKMARGGSGVGKRSKSGADSGFYLGHFSVDPALRRRRR GPRNKKRGWRLAGGELGLEUQPLEDVRLQERTSGGLLSEAPM EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLLLENTSK VPAPKDVLAHQVPNAKKLRRRGEVLAKKQGELDFEVBRADGR CFRNKKRGWRRLAGGELGLEUQPLADGRTSGGLLSEAPM EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLLLENTSK VPAPKDVLAHQVPNAKKLRRRGEVLAKKQGELDFEVBRADGR LLNDSATRAKPGFQDTVERPFYDLWASDNPLDRPLVGQDEFFLE QTKKKGVKRRARLHTHFSQAAPUSHAGSVNDSFEDHOTLLS AAHSVELQRQKEABKLERQLALPATGEKTGGORREKA VHALRVQQAALRARLHHGELFRLRGTKAQVALRLABELARPQRR RQARREABADKPRLGUKLKYQADJVOLSSELTDSLRTLKPEG NILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFREIQL FOLLESVAGAMEFPFDVDALFPERTIVLDQHLERFPARRFGTTTF ARVDLOQUIMTI IDELGKASKAMAJSTITSASRMGSNRHVVY ILKDSSARPAGKGAI IGFIKVGYKKLFVLLDGHERFPARRFGTTTF ARVDLOQUIMTI DELGKASKAMAJSTITSASRMGSNRHVVY ILKDSSARPAGKGAI IGFIKVGYKKLFVLLDGHERFPARRFGTTTF ARVDLOQUIMTI DELGKASKAMADSTITSASRMGSNRHVVY ILKDSSARPAGKGAI IGFIKVGYKKLFVLLDGHERFPARRFGTTTF ARVDLOQUIMTI DELGKASKAMADSTITSASRMOSNRHVVY ILKDSSARPAGKGAI IGFIKVGYKKLFVLLDGHERFPARRFGTTTF ARVDLOQUIMTI DELGKASKAMADSTITSASRMOSNRHVVY ILKDSSARPAGKGAI IGFIKVGYKKLFVLLDGHERFPARRFGTTTF ARVDLOQUIMTI DELGKASKAMADSTITSASRMONNRHVVY ILKDSSARPAGKGAI IGFIKVGYKKLFVLLDGHERFPARRFGTTTF ARVDLOQUIMTI DELGKASKAMADSTITSASRMONNRHVVY ILKDSSARPADRAKSPERFERDFTTARFARBAA NOPTPAPARAKLIPSVRHGHERFLOYMLGRERVEPHOLA INFSSKLIKBRA ANDFTAPAPARKLIP FRRADGELFOYHORFRUSDERGHENDSKLIKBRA ANDFTAPAPARKLIP FRRADGELFOYHORFRUSDERGHENDSKLIKBRA ANDFTAPAPARKLIP FRRADGRANTHEKTRADA NFSWASITYGVPLCIDCSGVHRSLGVHLSPIRSTELDSNMNWFQ LRCMQVCGRANATAFFRQHGCTANDANTCYNRRAQMYREFTRETH ARRATTPROHGCTANDANTCYNRRAGGRAMGENG LKKERQADADAVPKCPTFCFTDIVIMPKKSEPTTEGKDGS KVYKQBPTRSARLSAKPAPKPEPKPRKTAKKEPQAKISGGA KGKEEKGPGAGGGTAPSENGETKABEIHI SRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN ARMAQYKGTMEAGARAHHLLKKRROREOMEULKORILNEETIL KSCUGKPABHADAVPVRCTYFTYWGTEN LGQARKVKDEMEVTFSYWGGSGRERKRKISCLSFALDDLDD QAAARARAGAALSK		ł.		SLOKTSADTKGKQEQAKEEKARELFLKAVEEEQNGALYEAIKFY
SPILDIRSIEGISLVCKGFYTCARPENLACHERMISCITHUS SPILDIRSIEGISLVCKGFYTCARPENLACHERMISCITHUS PYTSWREMPLERBRUKPDGVVISKTTYIRGGGOSLDGFYRAWHO VEYTRYIRFPPOHYWMLTTPEPOSIVPRLRTR 6471 1750 299 FFFDKMAAGGSUGGKRSKSDADSGFIGLRPTSUDPALRRRRR GPRIKKRSGWRILAGELIGLEVDGFLEDVELIGETSGGLISEAPIN EKLFFVUTGSKEEGITKKRTKVCKKSLLKKPLRVDLILENTISK VPAPKDVLAHQVENAKKLRREGUMERLARGGELPREVRRAGAR LLNPSATRARDFGODTVERPFYDLADDFELDVLLIENTISK VPAPKDVLAHQVENAKKLRREGUMERLARGGELPREVRRAGAR LLNPSATRARDFGODTVERPFYDLADDFELDVLLIENTISK VPAPKDVLAHQVENAKKLRREGUMERLARGGELPREVRRAGAR LLNPSATRARDFGODTVERPFYDLADDFELTSKATEVGODEFFLE GTKKKGVKRRARLHTKPSGAPAVEVAPAGASYNPGFEDHOTILS AAHEVELQRKKEABEKLERQLALPRAGATOSSTPOFLCEGILE ESDGEGFPGGGEPAGDAVCYTPARLATTEKKTEQURREKA VHRLRVQQAALRAARLRRIGELFRIKGIKAQVALRLABELARRORR ROARREAEADKPRIKGIKKYQADPUJGSSELITSLETLLPREG NILRDRYKSFQRRAMMIEPREAKKRKKVKUKLVEKRAFREIQL 6472 3 897 SCSSDRAQMAMEPFFDVOLPFPEILTUDGHLEPPARFGTTTF ARVDLQQQIMTIIDELGKASKAQNISJAPITSASRMQSNRHVVY ILKDSSAPPAGKGAI LIGIFIKUGYKHJDDREAINEVPEDLCILL DFYTHESVORHGHGRELFCVWLLOKERVEPHOLAIDRPSOKLLKF LINKYNLETTVPOVNITVIFGFFAHQHRPPAPSLRATRHSRAA AVDPTPAAPARKLP PKRAEGDIKYSSSDREPLKVAVEDPWPLIN RAPRRATPPAHPPPRSSSLONSPERGPLRPFVD 6473 22 912 SSAVEFVWESEKMAREPRKTEIGTHATRHSKACH AVDPTPAAPARKLP PKRAEGDIKTSSSDREPLKVAVEDPWPLIN RAPRRATPFRHOFTDANTKYNSRAAOMYREEIRG LIGHKVGGNANTATFRGHGCTANDKYNSRAAOMYREEIRG LIGHKVGGNANTATFRGHGCTANDKYNSRAAOMYREEIRG LIGHKVGGNANTATFRGHGCTANDKYNSRAAOMYREEIRG LIGHKVGGNANTATFRGHGCTANDFRONTULLGTSVKALELL KSSIIGKKRAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE KLREQQAADAKQAESMVASMELAYQELJUIR 6474 3 462 LQRCRGHPAAAPAVVRCFTFCTIDLVIMPRKSSPENTEGKDGS KVYKGEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKEEKQEAGEGTAPSENDETKAAELHIISRSTVNYSTSRGTP PSTLSVKGGIETVRVKGTEN 6475 106 1090 ARAMAQYKGTWEEAGARAHHLLKKRERQREGMEVLKORIAEETTL KSSUOGRAPAADAVVRCFTRCTIDLVIMPRKSSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPKTSAKKEPGAKISRGA KGKEEKQEAGEGTAPSENDETKAELHIISRSTVNYSTSRGTP PSTLSVKGGIETVRVKGTEN 6476 1090 ARAMAQYKGTWEEAGARAHHLLKKRERQREGMEVLKORIAEETTL KSSUORFSAHTADVABALKSSTULDDRDEEERSTVLNSTGRTD PSTLSVKGGIETVRVKGTEN 6476 1090 ARAMAG	1			RRAMQLVPDIEFKITYTRSPDGDGVGNSYIEDNDDDSKMADLLS
SDLDLRSLEGLSIJVCRGFYTCARDPEIWRIACLKVWGRSCIKLV PYTSWRMFLERPRVRPDGVYISTIRGGGSCLGFYRAWHO VEYYRYTRFPPDGHVMMLTTBEDQGSTUPFLERR 6471 1750 299 FFFDKMAAGGSGVGGKRSKSDADSGFLGIRFTSVDDFALRRRRR GPRNKKRGWRIAGGELGLEUQFLEDVRLOGRTSGGLLSEAPM EKLFFVDTGSKERGITKKRTKVQKKSLLLKKPLRVDLILENTSK VPAPKDVLAHQVDNAKKLRREGLHARGGSLIPGEVBRAQAG LLNPSATRARPGPODTVERPFYDLWASDNPLDRPLVGQDEFFLE CYKKKGVKRPARLHTKPSQAPAVBAGGSYNMPSFEDHQTLLS AAMEVELQRQKEAEKLERQLALPATEQAATQBSTPOELCEGLLE ESDGEGEPGQGEGPEAGDABUCFTPARLATTEKKTEQQRRREKA VHRIRVQQAALRAARLRHGGLFFLRGIKAQVALRLAELARRQRR RQARREAEADKPRRJGRLKYQAPDIDVQLSSIJTDSLETLLYPEC NILRDFRSFGPGRNMIFERFEAKKRYKKULVEKARFEETQL ARVDLQQOMTHI IDBIGKASAKADJAPITSASRMGSNRHVYV ILKDSSARPAGKGA I IGFIKVGYKKLFVLDDRRAHREVEPELCIL DFYTHESVGRHGHGRELFQYMLQKERVEPHOLAIDRFSQKLLKF LINKIYMLETTVPQVNIKVFVTFEGFFARLATTVASPTGARGNRHVYV AVDPTPAAPARKLPPKRAEGDIKFYSSSDREPKVAVEPPHDIN ARARRATPPAHPPBYSSSLGNSPERFLKVAVEPPHPIN ARARTPPAHPPBYSSSLGNSPERFLKVAVEPPHPIN ARARRATPPAHPPBYSSSLGNSPERFLKVAVEPPHPIN ARARRATPPAHPPBYSSSLGNSPERFLKVAVEPPHPIN LRCMQVOGNANATAFFRQGCTANDATTSYNSRAAQMYREKIRG LGSALARHGTOLMTUNGSSAVENHSPEKKODSFFTEHTQPPAM DAPATEPSGTQQPASTESSGLAQDPHGPOTTDLLGTSFKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAKVSSQSFSSIERQAQVAE KLREQQADAKKOAESSWASMISJOELQLIDR KKREQAADAKKOAESSWASMISJOELQLIDR 6474 3 462 LQRQGHPAAABVVVRCFFTCFTDLVIMPKRKSPENTEGKDGS KVTKQBPTTRSARLSAKGJAGKVSSQSFSSIERQAQVAE KLREQQADAAKKOAESSWASMISJOELQLIDR KKREQAADAKKOAESSWASMISJOELQLIDR KKREKGPAARAGTAPSENGETKAEETHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN ARAMAQYKGTWREAGRAPSHDEFKRAEETHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN ARAMAQYKGTWREAGRAPSHDEFKRAEETHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN ARAMAQYKGTWREAGRAPSHDEFKRREGHLYGGLVKRIAEETIL KSSJOKRFSAHTDAWAELKSSTVGLVTLNDMKARQBALVRERE RQLAKRQHLEEGGRLQGRREGRORGERKRKISCLSFALDDLDD QAAABARRAANLGKARDPAAELKSSTVGUVTLNDMKARQBALVRERE RQLAKRQHLEEGGRLQGRREGRORGERKRKISCLSFALDDLDD QAAABARRAANLGKARDPAAELKSSTVGLVTLNDMKARQBALVRERE RQLAKRQHEEGGRLGDRREGNERERKERKELELGERGE BAQREKVKDEEMEVTFSYWDGSGHRRTVRVRKGNTVQQFLKKAL GGLAKROHELBGRLGORGCORGERERKERKIELGLIGER	1	1	1	YFQQQLTFQESVLKLCQPELESSQIHISVLPMEVLMYIFRWVVS
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GPRNKKRGWRRLAGEPLGLEUDGLEUTGLETTSGGLLSEADN EKLFFVDTGSKEKGLTKKRTVOKKSLLLKUPLEVDLILENTSK VPAPROVLAHQVPNAKKLRRKEQLWEKLAKQGELPREVRRAQAR LLNPSATRAKPGPQDTVERFFYDLWASDNFLDEPLUVGODEFFLE GTKKKGVKRTARLHTKPSQAPAVEVAPAGASYMPSFEDHOTILS AAHEVELQRQKEABKLERQLAIPATEADATQESTFQELCEGLLE ESDGGEGGGGGEGGGEGAGADEVCPTPARLATTEKKTEQORREKA VHRLRVQQAALRARLENGELFRLRGATQESTFQELCEGLLE ESDGGEGGGGGGAGGABEVCPTPARLATTEKKTEQORREKA VHRLRVQQAALRARLENGELFRLRGIKAQVALRLABLARRQRR ROARREAEDAVRPRELGRLKYQAPDIDVQLSSELTDSLRTLKDEG NILRDRFKSFQRRNMIEPRERAKFKRYKVKLVEKRAFREIQL 6472 3 897 SCGSDRRQWAWEFFFDUDALFPERITVLDCHLRPPARRFGTTTF ARVDLQQQIMTI IDELGKASKAQNLSAPITSASRMGSNRHVVY ILKDSSARPAGKGAIIGFIKVGVKKLFVLDDRRAHNBVEPLCIL DFYTHESVORIBHGRELFGVMCKERVEPHOLAILORSCHLKF LNKHYNLETTVPQVNNFVIFGFFAHQHRPPAPSLRATRHSRAA AVDPTPAAPARKLPPKRAEGDIRYSSSCREFLKVAVEPPWPLLN RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP 6473 22 912 SSAVEFVWEGEKMAAEPNKTEIGTLFKLRAVFTNKACFDCGAK NPSWASITYGVFLCIDCSGYNGERGPLRPFVP 6473 22 912 SSAVEFVWEGEKMAAEPNKTEIGTLFKLRAVFTNKACFDCGAK NPSWASITYGVFLCIDCSGYNGERGUFLGVHLSFITSELDSNNWFQ LGCMQUGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRG LGSAALARHGTDLWIDMSSAVPNHSPEKKDSDFFTEHTQPPAW DAPATEPSGTQQFAPSTESSGLAOPHGPNTDLLGTSPKASLEL KSSIIGKKRAAANKGIGAKKGLGAKKVSQGSESTERQAQVAE KLREQQAADAKKQAESSMARALAYGELQIDR 6474 3 462 LQRQGHAAAPAVPVRCFFFCFTDIVIMPKRKSPENTEGKDGS KVYKQBFTRSARLSAKDAPBPEPPRFRTSAKKEPGAKISRGA KGKKEEKQEAGKGGTAPSRNGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKSTEN 6475 462 LQRQGHAAAPAVPVRCFFFCFTDIVIMPKRKSPENTEGKDGS KVYKQBFTRSARLSAKAPAPPPREPPRRTSAKKEPGAKISRGA KGKKEEKQEAGKGGTAPSRNGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKSTEN 6476 6476 106 1090 ARAMAQYKGTMERAGRAWHILKKRERQREQMEVLKQRIAEEETLL KSCUDKRFSAHYDAVERELKSSTVGLVTLNDMKARQEALVRERE RQLAKRQHLEEQRLQGERQEGGREGRERKKISCLSFALDDLDD QADAABARRRGINGSMPDUTSFLPDRDEEEEERNILEEILGRGW EAQREKVEDEEMBVTTSYWDGSGHRTTVRVRKGNTVQQFLKKML EAQREKVEDEEMBVTTSYWDGSGHRTTVRVRKGNTVQQFLKKKLIF EAQREKVEDEEMBVTTSYWDGSGHRTVRVRKGNTTVQQFLKKML EAQREKVEDEEMBVTTSYWDGSGHRTVRVRKGNTTVQFLKKKLIF EAQREKVEDEEMBVTTSYWDGSGHRTVRVRKGNTTVQFLKKMLIF	6471	1750	299	
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ARVDLQQQIMTI IDELGKASAKAQNLSAPITSASRMQSNRHVVY ILKDSSARPAGKGAI IGFI KVGYKKLFVLDDREAHNEVEPLCIL DFYIHESVQRHGHGRELFQYMLQKERVEPHQLAIDRFSQKLKF LNKHYNLETTVPQVNNFVI FEGFFAHGHRPPAPSLRATHSKRAA AVDPTPAAPARKLPPKRAEGDI KPYSSSDREPLKVAVEPPWPLN RAPRRATPPAHPPPRSSSLGNSPERGELRPFVP SSAVEFVWEGEKMAAEPNTTEI QTLFKRLRAVPTNKACFDCGAK NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWNNFQ LRCMQVGGNANATAFFRCHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTULDIMSSAVPNHSPEKKDSDFFTEHTQPPAW DAPATEPSGTQQPAPSTESGLAQPEHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGACKVSQSFSEIERQAQVAE KLREQQAADAKKQAESMVASMRLAYQELQIDR 6474 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6475 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKRTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEBIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAHHLLKRERGREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVVEALKSSTVGLVTLNDMKARQEALVRERE RQLAKRCHLEEQRLQQERQRRGEGRREKKRISCLSFALDDLDD QADAAEARRAGNLGKNPDVDTSFLPDRDREEEENRLREELRQEW EAQREKVKDEEMEVTFSYWDGSGHRRTVRVKKGNTVQQFLKKAL QQLKKDFLELRSAGVEQLMFIKEDLILPHYHTYPDFI LARARGK SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF	L			NILRDRFKSFORRNMIEPRERAKFKRKYKVKLVEKRAFREIOL
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912 SSAVEFVWEGEKMAAEPNKTEIQTLFKRLRAVPTNKACFDCGAK NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWNWFQ LRCMQVGGNANATAFFGHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDMMSSAVPNHSPEKKDSDFFTEHTQPPAW DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASIEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE KLREQQAADAKKQAEESMVASMRLAYQELQIDR 6474 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPKKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKABEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6475 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPKKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE RQLAKRQHLEEQRLQQERQREQEQRRERKRKISCLSFALDDLDD QADAAEARRAGNLGKNPDVDTSFLPPDRDREEENRLREELRQEW EAQREKVKDEEMBVTFSYWDGSGHRRTVRVRKGNTVQQFLKKAL QGLRKGFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF		ļ		
NPSWASITYGVFLCIDCSGVIRSLGVHLSFIRSTELDSNWNWFQ LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAW DAFATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASLEL KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE KLREQQAADAKKQAEESMVASMRLAYQELQIDR 6474 3 462 LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAPEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6475 3 462 LQRQRQHPAAAPAVPVRCPTFCFTDIVIMPKRKSPENTEGKDGS KVTKQEPTRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP PSTLSVKGQIETVRVKGTEN 6476 106 1090 ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE RQLAKRQHLEEQRLQQERQREQEQRERKRKISCLSFALDDLDD QADAAEARRAGNLGKNPDVDTSFLPDRDREEEENRLREELRQEW EAQREKVKDEEMEVTFSYWDGSGHRRTVRVRKGNTVQQFLKKAL QGLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF				RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP
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RQLAKRQHLEEQRLQQERQREQEQRRERKRKISCLSFALDDLDD QADAAEARRAGNLGKNPDVDTSFLPDRDREEEENRLREELRQBW EAQREKVKDEEMBVTFSYWDGSGHRRTVRVRKGNTVQQFLKKAL QGLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF	j .			
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SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF				
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	L I			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	Name of the state
ľ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
6477	227	915	\=possible nucleotide insertion)
04//	221	915	LQGHLMGIMAASRPLSRFWEWGKNIVCVGRNYADHVREMRSAVL
]		[SEPVLFLKPSTAYAPEGSPILMPAYTRNLHHELELGVVMGKRCR
1	į.	[AVPEAAAMDYVGGYALCLDMTARDVQDECKKKGLPWTLAKSFTA
ı	ļ		SCPVSAFVPKEKIPDPHKLKLWLKVNGELRQEGETSSMIFSIPY
1	•	j	IISYVSKIITLEEGDIILTGTPKGVGPVKENDEIEAGIHGLVSM
			TFKVEKPEY
6478	2	1495	FVSSRILPESLASSEASTLEAMGRKEEDDCSSWKKQTTNIRKTF
		!	IFMEVLGSGAFSEVFLVKQRLTGKLFALKCIKKSPAFRDSSLEN
		ł	EIAVLKKIKHENIVTLEDIYESTTHYYLVMQLVSGGELFDRILE
		l	RGVYTEKDASLVIQQVLSAVKYLHENGIVHRDLKPENLLYLTPE
1	1	ł	ENSKIMITDFGLSKMEQNGIMSTACGTPGYVAPEVLAQKPYSKA
1	ì		VDCWSIGVITYILLCGYPPFYEETESKLFEKIKEGYYEFESPFW
İ			DDISESAKDFICHLLEKDPNERYTCEKALSHPWIDGNTALHRDI
1	· ·		YPSVSLQIQKNFAKSKWRQAFNAAAVVHHMRKLHMNLHSPGVRP
			EVENRPPETQASETSRPSSPEITITEAPVLDHSVALPALTQLPC
1	:		QHGRRPTAPGGRSLNCLVNGSLHISSSLVPMHQGSLAAGPCGCC
{			SSCLNIGSKGKSSYCSEPTLLKKANKKONFKSEVMVPVKASGSS
Į.			HCRAGQTGVCLIM
6479	3	949	SCRGPGWHPAGGQAGAMELLSALSLGELALSFSRVPLFPVFDLS
1			YFIVSILYLKYEPGAVELSRRIIPIASWLCAMLHCFGSYILADLL
1	1		LGEPLIDYFSNNSSILLASAVWYLIFFCPLDLFYKCVCFLPVKL
1			IFVAMKEVVRVRKIAVGIHHAHHHYHHGWFVMIATGWVKGSGVA
1			LMSNFEQLLRGVWKPETNEILHMSFPTKASLYGAILFTLQQTRW
1			LPVSKASLIFIFTLFMVSCKVFLTATHSHSSPFDALEGYICPVL
	1		FGSACGGDHHHDNHGGSHSGGGPGAQHSAMPAKSKEELSEGSRK
]	ļ		KKAKKAD
6480	192	514	DFMSIYFPIHCPDYLRSAKMTEVMMNTOPMEEIGLSPRKDGLSY
1			QIFPDPSDFDRCCKLKDRLPSIVVEPTEGEVESGELRWPPEEFL
1			VQEDEQDNCEETAKENKEO
6481	. 110	1131	KSRMDLDVVNMFVIAGGTLAIPILAFVASFLLWPSALIRIYYWY
1			WRRTLGMQVRYVHHEDYQFCYSFRGRPGHKPSILMLHGFSAHKD
			MWLSVVKFLPKNLHLVCVDMPGHEGTTRSSLDDLSIDGQVKRIH
			QFVECLKLNKKPFHLVGTSMGGQVAGVYAAYYPSDVSSLWLVCP
			AGLQYSTDNQFVQRLKELQGSAAVEKIPLIPSTPEEMSEMLQLC
1 .			SYVRFKVPQQILQGLVDVRIPHNNFYRKLFLEIVSEKSRYSLHQ
}			NMDKIKVPTQIIWGKQDQVLDVSGADMLAKSIANCQVELLENCG
			HSVVMERPRKTAKLI I DFLASVHNTDNNKKLD
6482	2517	568	EPVSKVSQSRRKAGVPTANIEESQAVEAAMANVPWAEVCEKFOA
j i		= = =	ALALSRVELHKNPEKEPYKSKYSARALLEEVKALLGPAPEDEDE
. I	 		RPEAEDGPGAGDHALGLPAEVVEPEGPVAORAVRLAVIEFHLGV
, l	 		NHIDTEELSAGEEHLVKCLRLLRRYRLSHDCISLCIQAQNNLGI
1			LWSEREEIETAQAYLESSEALYNQYMKEVGSPPLDPTERFLPEE
j l			EKLTEQERSKRFEKVYTHNLYYLAQVYQHLEMFEKAAHYCHSTL
[ĺ	
]			KRQLEHNAYHPIEWAINAATLSQFYINKLCFMEARHCLSAANVI
1 1	İ		FGQTGKISATEDTPEAEGEVPELYHQRKGEIARCWIKYCLTLMQ
1 I			NAQLSMQDNIGELDLDKQSELRALRKKELDEESIRKKAVQFGT
			GELCDAISAVEEKVSYLRPLDFEEARELFLLGQHYVFEAKEFFQ
į į		į	IDGYVTDHIEVVQDHSALFKGLAFFETDMERRCKMHKRRIAMLE
[PLTVDLNPQYYLLVNRQIQFEIAHAYYDMMDLKVAIADRLRDPD
; {			SHIVKKINNLNKSALKYYQLFLDSLRDPNKVFPEHIGEDVLRPA
} [MLAKFRVARLYGKIITADPKKELENLATSLEHYKFIVDYCEKHP
⊢			RAAQEIEVELELSKEMVSLLPTKMERFRTKMALT
6483	3	623	NSHLLCGLRARAPLSANGREARAMEQRLABFRAARKRAGLAAQP
1 1			PAASQGAQTPGEKAEAAATLKAAPGWLKRFLVWKPRPASARAQP
]	ļ	GLVQEAAQPQGSTSETPWNTAIPLPSCWDQSFLTNITFLKVLLW
1 1	1	i	LVLLGLFVELEFGLAYFVLSLFYWMYVGTRGPBEKKEGEKSAYS

No.	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Indication Cortesponding	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
location corresponding to first amino acid arisoleucine, Kelysine, leleucine, methodine, Neaparagine, amino acid residue of sequence P=Proline, Q=Glutamine, R=Axginine, Section, Section, Section, Section, X=Ukhnown, *=Stop Codon, /=possible nucleotide deletion, legisle nucleotide Codon, /=possible nucleotide Codon, /=	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
corresponding to first amino acid residue of residue of amino acid residue of amino acid residue of amino acid residue of amino acid sequence seque		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid asequence Perfoline, G-Glutamine, R-Atginine, Serine, T-Threonine, Y-Valine, W-Tryptophan, Y=Tyrosine, X-Unknown, *=Stop codon, /=possible nucleotide deletion, Vepossible nucleotide insertion) PERFORMANCE TRADERS TO TRAD		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence codon, /=possible nucleotide deletion) 4-possible nucleotide insertion) 4-p		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
residue of amino acid sequence codon, /=possible nucleotide deletion) 4-possible nucleotide insertion) 4-p	i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
6484 201 965 GLAWATKINGERPOTO/DEE IELFVKANSGESIGNCEPCORLE MILMILKOVERWITTUMMTKPEELKULAPOTREPFLYWRIELT DPIKTEERLEGTLAPPRYPHISPKKSELKOZLERAKESAYIK NOKEANKINFEKSILKEPKRILDDYLATPILDEIDPDSAEPPYS RELPLDOOLITLAPORYPHISPKYKSEPDOTREPFLYWRIELT OPKIREPLEGTLAPORYPHISPKYKSEPTOTREDIT PARFSGYW RYLHINAYAREEFTHTCPEDKEIENTYANVAKOKS 6485 6 1091 PYDLVRAWEPJPCPDSOKIKEECOSSEESSISSMSKRITLEEDEE DEEPPRVILTYBERSFEVOMLUURHKHKYPFUPDAVVKSVORDK KASVIJISIAMINPKMEGTTYJKEISKLEPERCEGTLANDAEDE NODIGKOVSLITTOYRVRIGOGSPAGSFIRTYAADISTYPYRSIO ODVICTKLOOLOLUVKKILOOCPHISOROPHIOTRESSOVY CVETYLEDEGOLOLUVKKILOOCPHISOROPHIOTRESSOVY CVETYLEDEGOLOLUVKKILOOCPHISOROPHIOTRESSOVY TOTTYLEDEGOLOLUVKKILOOCPHISOROPHIOTRESSOVY TOTTYLEDEGOLOLUVKKILOOCPHISOROPHIOTRESSOVY TOTTYLEDEGOLOLUVKKILOOCPHISOROPHIOTRESSOVY TOTTYLEDEGOLOLUVKKILOOCPHISOROPHIOTRESSOVY TOTTYLOHOLOLUVKKILOOCPHISOROPHIOTRESSOVY TOTTYLOHOLOLUVKKILOOCPHISOROPHIOTRESSOVY TOTTYLOHOLOLUVKKILOOPHISOROPHIOTRESSOVY TOTTYLOHOLOLUVKKILOOPHISOROPH	1	amino acid	sequence	Codon, /=possible nucleotide deletion.
6484 201 965 GLAWATKINGERPOTO/DEE IELFVKANSGESIGNCEPCORLE MILMILKOVERWITTUMMTKPEELKULAPOTREPFLYWRIELT DPIKTEERLEGTLAPPRYPHISPKKSELKOZLERAKESAYIK NOKEANKINFEKSILKEPKRILDDYLATPILDEIDPDSAEPPYS RELPLDOOLITLAPORYPHISPKYKSEPDOTREPFLYWRIELT OPKIREPLEGTLAPORYPHISPKYKSEPTOTREDIT PARFSGYW RYLHINAYAREEFTHTCPEDKEIENTYANVAKOKS 6485 6 1091 PYDLVRAWEPJPCPDSOKIKEECOSSEESSISSMSKRITLEEDEE DEEPPRVILTYBERSFEVOMLUURHKHKYPFUPDAVVKSVORDK KASVIJISIAMINPKMEGTTYJKEISKLEPERCEGTLANDAEDE NODIGKOVSLITTOYRVRIGOGSPAGSFIRTYAADISTYPYRSIO ODVICTKLOOLOLUVKKILOOCPHISOROPHIOTRESSOVY CVETYLEDEGOLOLUVKKILOOCPHISOROPHIOTRESSOVY CVETYLEDEGOLOLUVKKILOOCPHISOROPHIOTRESSOVY TOTTYLEDEGOLOLUVKKILOOCPHISOROPHIOTRESSOVY TOTTYLEDEGOLOLUVKKILOOCPHISOROPHIOTRESSOVY TOTTYLEDEGOLOLUVKKILOOCPHISOROPHIOTRESSOVY TOTTYLEDEGOLOLUVKKILOOCPHISOROPHIOTRESSOVY TOTTYLOHOLOLUVKKILOOCPHISOROPHIOTRESSOVY TOTTYLOHOLOLUVKKILOOCPHISOROPHIOTRESSOVY TOTTYLOHOLOLUVKKILOOPHISOROPHIOTRESSOVY TOTTYLOHOLOLUVKKILOOPHISOROPH	1	sequence	: •	\=possible nucleotide insertion)
MILLIKOVEFRVITVOMTEKEDELKOLAGGINPPELVINKELET DPIKTERELEGOTLAPAPENJSPKYKESDYGCNLEPAFSAYIK N°CKEANKNPEKSLIKEPKRLDDYLNIPILDELDIPDSABEEPVS RRI-PLIDGOLITLADGSLIKENI KIVAMENDEI 1PAEFSGWW RYLHINAYARESPTHICPEDKKII KIVAMENDEI 1PAEFSGWW RYLHINAYARESPTHICPEDKKII KIVAMENDEI 1PAEFSGWW RYLHINAYARESPTHICPEDKKII KIVAMENDEI 1PAEFSGWW RYLHINAYARESPTHICPEDKKII KIVAMENDEI 1PAEFSGWW RYLHINAYARESPTHICPEDKKII KIVAMENDEI 1PAEFSGWW RYLHINAYARESPTHICPEDKII KOKIKKI COSSESSIASINAMESTILEEDEE DEEPPRULLYHEPRSPEVOMLUWIKHKKYPPWADVYKSURGROK KASULYIE KOHINDPRIMGETYSLIKSIKKIPKENTITLEEDEE DEEPPRULLYHYPELSPEVOLKIKOSPESSIASINASI LIKEEDEE NODIGKCVSLITTDYRVSLICCUS PRAGSELSYTAADIS YPURSI 10 ODVLGYKLOOLIKOSPEDEVOUGLIGOROCHINDRIRARARI RANKKUPTY-GKAKGAESILRAI LIKSEKSSENRIQTELSSOYVT CVETYLEDESGOLDI.VVELVIGOYOOVOKADENDRIRETILD VLLPEALITCA SAADEVOYKTAEEKYIKGPSLSYREKSI FONQL LEERBIRRRS RANKKUPTY-GKAKGAESILRAI LIKSEKSESSRUQTELSSOYVT CVETYLEDESGOLDI.VVELVIGOYOOVOKADENDRIRETILD VLLPEALITCA SAADEVOYKTAEEKYIKGPSLSYREKSI FONQL LEERBIRRRS GOTGRESGOLIRADMENTROGRMGI HOUGHTENDEITETILD LEERBIRRRS 1SEPERJAKRIKSSYTLHTOVODIKIS EVYTEETPYTCOPPILLICASA YYNOCI FIRMI KIGHWO/TODPICTORGCAS INGKEEDENS SETL HUNGVOLVAMANINOPATINASOPPITYOKOHUMKYTVIPGKVID GLETILDELEKLPVUNKTYYDIJAMI KIDITIHAMPENA HUNGVOLVAMANINOPATINASOPPITYOKOHUMKYTVIPGKVID GLETILDELEKLPVUNKTYYDIJAMI KIDITIHAMPENA HENDEVIKSTOPPICARIA PASTORDEPHTENDENSPERSPEN PROPINLYPHILATOROKANINOPATINASOPPITYOKOHUMKYTYTOKOKUD KASHONINASORI SSECPROGRAMIA PASTORDEPHTENDENSPERSPEN PROPINLYPHILATOROKANINASORI SEPENJATIOLIS SILEMIA SIL				VFNPGCEAIQGTLTAEQLERELQLRPLAGR
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DFIKTREFLEOTLAPRYPHLSPKYRESDVGCNLFAKFSAYIK NCKEANKIPEKSLLKEPKIDDULAPSAEPPVS RIFLIDDQLITLADCSLIPKUNI KVAAKKYRDF01PAEFSGWW RYLHINYARERSFITHTCPERKEI ENTYANKOKS 6485 6 1091 PYDLWRAVEFLECDSCKLEKECGSSESSMSSISMSTLEEDEE DEEPPPWLIVHEPRSFEVGKLEWELGKEFDCKEKTLINDAEEDE NQDIGMCVSLITDVRVELGCSFAGSELFAAD1SYPYRES10 QDVLSTKLDOLGKSPEEPVVSCHLGGROPCROMLDERRAARD RANGKLVEFY-GKAKGASSLIKABLUKSERSPSKULGTLLANDAEDE RANGKLVEFY-GKAKGASSLIKABLUKSERSPSKULGTILSSSOTYT CVETYLEDEGOLDLVVKYLQGVYQEVGRKVLQKTNODRI RETILD VLDFERLI CALSAGDEVDYKTAEEKTI KOPSLSYRKEI PINGL LEERNRRR 6486 10 581 LVLQAGGAHLSPSRVVTQTIYWLAFSEMPKPPDYSELSDSLTLA GGTGRFSGFJLRRARRMMFRORMG IGVGLYLLAGAAFYYVE ISETYMRLALBHIQQHPEEPLEGTTYTHSLKAGLISLPFWWTY IFLVPFLAMFHFLYSCTTAAPKTVGCTIYWLAGAAFYYVE ISSTYMRLALBHIQQHPEEPLEGTTYTHSLKAGLISLPFWWTY KASNOLSKLOLIDT KHNYRGVVSHAMNEPSTNASOFPITYGGKORSI WKKKEEPLEYSETL KHNYRGVVSHAMNEPSTNASOFPITYGGKORSI WKKKEEPLEYSETL KHNYRGVVSHAMNEPSTNASOFPITYGGKOPHLOMKYTYFGGVID GLETLDELEKLPVUSKTYTPLNDVHIKDTTHANFER FERSTNATALSHIQQHPEEPLEGTTYTHSLKAGLISLPFWWTY TALQEFGTSGFPISLIRFAHPSGTGFRFFLFGARGFSWPFSFVVP MEPPHLYPVKLYVYDLSKGLARKLSPIMLGQLEGIWHTSIVVH KDEFFFGSGGTSJFSLGFFAHPSGTGFRFFLFGARGFSWPFSFVVP MEPPHLYPVKLYVYDLSKGLARKLSPIMLGQLEGIWHTSIVVH KDEFFFGSGGTISSCPPGGTLLAPDSVUNGTSTVETEI FLEYI SSLGESLFRGBAYNLFHHCNTTFSNEVAGFITGKTFSYTTDLD SCHLSFFFGGGGTSSCPDGTLLAPDSVUNGTSTVETEI FLEYI SSLGESLFRGBAYNLFHHCNTTFSNEVAGFITGKTFSYTTDLD SCHLSFFTGGGTSSCPTGGTTHYDLAFAAKRICKL GLEWEWEVVERRTFABITREFFRLQRERSEERLQGFTFFHTVLAR NLIKHTVGYLLDHRYBESTVENVERSSEELKAARRICKL GLEWEWEVVERRTFABITREFFRLQRERSEERLQGFTFFHTVLAR NLIKHTVGYLLDHRYBESTVENVERSSEELKAARRICKL GLEWERWEVVERRTFABITREFFRLQRESSEELKAARRICKL GREFHLAIATRIVATFTHYDPYHDIAFAPNL GGREFHLAIATRIVATFTHYDPYHDIAFAPNL GGREFHLAIATRIVATFTHYDPYHDIAFAPNL GGREFHLAIATRIVATFTHYDPYHDIAFAPNL GGREFHLAIATRIVATFTHYDPYHDIAFAPNL GGREFHLAIATRIVATFTHYDPYHDIAFAPNL GGREFHLAIATRIVATFTHYDRYRAKSEGGFTKEFTHIVARS HERGGEWEVVERNATTSTVTDKARKINGHLANGTSAGHTIE ARDOWNLSGGGGGGGGGGTTHESLOSHITFELONSINSSAGRKHIS HERGGEWEVLAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		1	1	
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KEONTGHNINGVOOPSGTSKTLYSTIMALGSSPGISAQQLVRT VGHTTTM-LI PALCTSSPOTLPMINSCLTNAVHLINIVSVUSPVN VHINTRTSAPSPTALKLATVAASMDRVPKVTPSSAISSIARENH EPERLIGINGIAETTVAMEVT AVAGGARPCSTPSSPHRRCREHRPRI-PRPPAAIMSASAVYLD LKGKVLI CRNYRGDVDMSEVEHFMPILMEKEEEGMLSPILAHGG VRFMWIKHINILYLVATSKKNACUSLVFSFLYKVUQVFSEYFKEL EESIRDMFVIIYELLDELMDFGYPOTTDSKILQEYITQEGHKL ETGAPRP PATVTINAVSMESGIKYRKNEVPLDVIBSVALLUSAN GNULRSEIVGSIKMRVFLSGMPELRIGLINDKVLFDNTGRGKSKS VELEDVERHSUSRIEVMIKAKSGFKRRSTANNVETHIPVPN DADSPRERTTUGSVENVENENSEIVMSIKSFPGGKEYLMRAHFGL PSVEAEDKEGKPPISVKEPIPYFTTSGIQVRYLKIIEKSGYQAL PWVRYITQNGDYQLRTQ AVAGGARPCSTPSSPHRRCRHRMPRPI-PRPAAIMSASAVVUD LKGKVLI CRNYRGDVDMSEVEHFMPILMEKEEEGMLSPILAHGG VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL EESIRDNFYIIYBILDELMDFGYPGTTDSKILQEYITQEGHKL ETGAPRP PATVTNAVSMESGIKYRKNEVFLDVIESVNILLVSAN GNVLRSEIVGSIKMRVFLSGMPELRIGIADKVUFDNTGRGKSKS VELEDVKFHQCVRLSRFENDRTISIPPDGEFEIMSYRLNTHVK ETGAPRP PATVTNAVSMESGIKYRKNEVFLDVIESVNILLVSAN GNVLRSEIVGSIKMRVFLSGMPELRIGIADKVUFDNTGRGKSKS VELEDVKFHQCVRLSRFENDRTISIPPDGEFEIMSYRLNTHVK PILMIESVIEKHSHSRIEYMIKAKSQFKRRSTANNVEIHIPVPN DADSPKFKTTVGSVKWPENSEIVWSIKSFPGGKEYLMRAHFGL PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL PWWRYITQNGDYQLRTQ GASSILATDOORDYQLRTQ GASSILATDOORDYGLRTQ LKAVSLLPLQGDVQLRTQ BAVGICHPPSSELATDPPVVMNADTLSYCQKEAWCKLAFYLL SFFYYLYCMIYTLVSS GATNILLSRFTRNEFSHDSRTTIGVSFSTRTVMLGTAAVKAQIWD TAGLERYRAITSAYYRGAVGALLVFDLTKKQTYAVVERUKELY DIABATIVVMLVGMKSDLSQAREVPTEEARMFAENNOLLFJEETS	6493	557	1147	<u> </u>
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amino acid sequence Codon, /-possible nucleotide deletion,]			S=Serine, T=Threonine, V=Valine,
Sequence Seposeriac(SISI) SERICEPS(SISI)	1			w=Trypcophan, Y=Tyrosine, X=Unknown, *=Stop
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6501 1 570 LVGMSGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGE IHSRLLDHRPVIQGETRYFVKEFEEKRGLREMRVLENLKNMIHE TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKKI HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKFSTF 6502 213 1650 AGNKPDPWAGRNRTAVLPDVSVFHREDVGWNRSWLQQSYQAVKE KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCMEPDGPPELFDAWLSQFCLEEK KGEISELLVGSPSIRALYTKMVPAAVSHEFWHRYFYKVHQLEQ. EQARRDALKQRAEQSISEEPGWEEEEBELMGISPISPKEAKVPV AKISTFPEGEPGPOSPCEENLVTSVEPPAEVTPSESSESISLVT	1			KOLAVULKIAGVEAENAEDADGKDVENTKSVGDSI KEAMTIHEN
IHSRLLDHRPVIQGETRYFVKEFEEKRGLREMRVLENLKNMIHE TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKKI HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKFSTF 6502 213 1650 AGNKPDPWAGRNRTAVLPDVSVFHREDVGWNRSWLQQSYQAVKE KSSEALBFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ. EQARRDALKQRAEQSISEEPGWEEEEEELMGISPISPKEAKVPV AKISTFPEGEPGPOSPCEENLVTSVEPPAEVTPSESSESISLVT				QVVEGCCSDMAVTFNG5TFNQMHVMM1GV1KDRAFGF1FQ
TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKKI HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKFSTF 6502 213 1650 AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ. EQARRDALKQRAEQSISEEPGWEEEEEELMGISPISPKEAKVPV AKISTFPEGEPGPOSPCEENLVTSVEPPAEVTPSESSESISLVT	6501	1	570	LVGMSGGGTETPVGCEAAPGGGSKKKDSLGTAGSAMLIIKDLGE
HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ YAEMEKDLAKFSTF 6502 213 1650 AGNKPDPWAGRNRTAVLPDVSVFHREDVGWMRSWLQQSYQAVKE KSSEALBFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ. EQARRDALKQRAEQSISEEPGWEEEEEBLMGISPISPKEAKVPV AKISTFPEGEPGPOSPCEENLVTSVEPPAEVTPSESSESISLVT	{			
YAEMEKDLAKFSTF 6502 213 1650 AGNKPDPWAGRNRTAVLPDVSVFHREDVGWNRSWLQQSYQAVKE KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS SGATEKMKKGLSDFLGVISDFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ. EQARRDALKQRAEQSISEEPGWEEEEEBLMGISPISPKEAKVPV AKISTFPEGEPGPOSPCEENLVTSVEPPAEVTPSESSESISLVT	1		1	TNEHTLEKCROTMROSLSQV LQRLQAANUSVCRLQQREQERRRI
6502 213 1650 AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCMEPDGPPELFDAWLSQFCLEEK KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ. EQARRDALKQRAEQSISEEPGWEEEEBELMGISPISPKEAKVPV AKISTFPEGEPGPOSPCEENLVTSVEPPAEVTPSESSESISLVT	1			
KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ. EQARRDALKQRAEQSISEEPGWEEEEBELMGISPISPKEAKVPV AKISTFPEGEPGPOSPCEENLVTSVEPPAEVTPSESSESISLVT	L			
SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT AEPYDGTKARLYSLQSDPATYCMEPDGPPELFDAWLSQFCLEEK KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ. EQARRDALKQRAEQSISEEPGWEEEEBELMGISPISPKEAKVPV AKISTFPEGEPGPOSPCEENLVTSVEPPAEVTPSESSESISLVT	6502	213	1650	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE
AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ. EQARRDALKQRAEQSISEEPGWEEEEEELMGISPISPKEAKVPV AKISTFPEGEPGPOSPCEENLVTSVEPPAEVTPSESSESISLVT	1			KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS
KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ. EQARRDALKQRAEQSISEEPGWEEEEEELMGISPISPKEAKVPV AKISTFPEGEPGPOSPCEENLVTSVEPPAEVTPSESSESISLVT	1	1	1	SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
EQARRDALKQRAEQSISEEPGWEEEEEELMGISPISPKEAKVPV AKISTFPEGEPGPOSPCEENLVTSVEPPAEVTPSESSESISLVT	1	1	}	AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK
AKISTFPEGEPGPOSPCEENLVTSVEPPAEVTPSESSESISLVT	1			KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ.
AKISTFPEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT				EQARRDALKQRAEQSISEEPGWEEEEEELMGISPISPKEAKVPV
I I I I I I I I I I I I I I I I I I I	1		1 .	AKISTFPEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT
QIANPATAPEARVLPKDLSQKILLBASILEEQGLAVDVGBIG:011				QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
	T		IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFELNSDSG
	ł		KSTPSNNGKKGSSTDISEDWEKDFDLDMTEEEVQMALSKVDASG
1	1		EVSGPGGSEGSEPNGPGCESSPOPAOLSPOEGPCSCLR
6503	213	1650	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE
	1		KSSEALEFMKRDLTEPTQVVQHDTACTIAATASVVKEKLATEGS
1			SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
1			AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK
j			KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ
			EQARRDALKQRAEQSISEEPGWEEEEEELMGISPISPKEAKVPV
1			AKISTFFEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT
			QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP
			IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFELNSDSG
			KSTPSNNGKKGSSTDISEDWEKDFDLDMTBEEVQMALSKVDASG
L			EVSGPGGSEGSEPNGPGCESSPQPAQLSPQEGPCSCLR
6504	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG
i		•	SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKEGDEPITQ
1	1		WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
ļ			DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA
i	1 1		PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
	i		REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF
			DDDFHIYVYDLVKKS
6505	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG
1	1		SANMTKKKVSQKKQRGRPSSOPCRNIVGCRISHGWKEGDEPITQ
			WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
į	1		DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA
1			PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
1	i i		REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF
6506	<u> </u>	1350	DDDFHIYVYDLVKKS
1 0300)	1320	EVSPPTSCCLTVAVADPGVSEGFRGFGAGCEMPGRGRCPDCGST
Į.	1 1		ELVEDSHYSQSQLVCSDCGCVVTEGVLTTTFSDEGNLREVTYSR
}	1		STGENEOVSRSQQRGLRRVRDLCRVLQLPPTFEDTAVAYYQQAY
			RHSGIRAARLQKKEVLVGCCVLITCRQHNWPLTMGAICTLLYAD
1	1 1		LDVFSSTYMQIVKLLGLDVPSLCLAELVKTYCSSFKLFQASPSV
1	ļ		PAKYVEDKEKMLSRTMOLVELANETWLVTGRHPLPVITAATFLA
			WQSLQPADRLSCSLARFCKLANVDLPYPASSRLQELLAVLLRMA EQLAWLRVLRLDKRSVVKHIGDLLQHRQSLVRSAFRDGTAKVET
1			REKEPPGWGQGGEGEVGNNSLGLPGGKRPASPALLLPPCMLKS
i			PKRICPVPPVSTVTGDENISDSEIEQYLRTPQEVRDFQRAQAAR
1		j	QAATSVPNPP
6507	1878	929	RSHASRLPELPSGCLVLQVQELVQMSGMEATVTIPIWQNKPHGA
		·-	ARSVVRRIGTNLPLKPCARASFETLPNISDLCLRDVPPVPTLAD
1			IAWIAADEEETYARVRSDTRPLRHTWKPSPLIVMQRNASVPNLR
1			GSEERLLALKKPALPALSRTTELQDELSHLRSQIAKIVAADAAS
			ASLTPDFLSPGSSNVSSPLPCFGSSFHSTTSFVISDITEETEVE
1	1		VPELPSVPLLCSASPECCKPEHKAACSSSEEDDCVSLSKASSFA
			DMMGILKDFHRMKQSQDLNRSLLKEEDPAVLISEVLRRKFALKE
			EDISRKGN
6508	862	342	WEARKRPQRWPSERREVRVPPPHLQRGRSGLEPGTFRKMAAARP
į į	İ	i	SLGRVLPGSSVLFLCDMQEKFRHNIAYFPQIVSVAARMLKNTTL
			DLLDRGLQVHVVVDACSSRSQVDRLVALARMRQSGAFLSTSEGL
	<u> </u>		ILQLVGDAVHPQFKEIQKLIKEPAPDSGLLGLFQGQNSLLH
6509	2	1053	FVWNPRGGRKRRRQAAVTQAATRASGTPSPRDGTMTQGKLSVAN
ĺĺĺ		ĺ	KAPGTEGQQQVHGEKKRAPAVPSAPPSYEEATSGEGMKAGAFPP
]]	l		APTAVPLHPSWAYVDPSSSSSYDNGFPTGDHELFTTPSWDDOKV
[]	j		RRVFVRKVYTILLIQLLVTLAVVALFTFCDPVKDYVQANPGWYW
<u></u>			ASYAVFFATYLTLACCSGPRRHPPWNLILLTVFTLSMAYLTGML

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	C-Comine M. Mharaniane, R=Arginine,
J	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
.	Ì	}	SSYYNTTSVLLCLGITALVCLSVTVFSFQTKFDFTSCQGVLFVL
1		!	LMTLFFSGLILAILLPFQYVPWLHAVYAALGAGVFTLFLALDTQ
			LLMGNRRHSLSPEEYIFGALNIYLDIIYIFTFFLQLFGTNRE
6510	37	1156	PCALDGCPQRGAVHPLLSSAMGLLAFLKTQFVLHLLVGFVFVVS
l		j	GLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLVMLLEWW
1	i		SCTECTLFTDQATVERFGKBHAVIILNHNFEIDFLCGWTMCERF
ł			GVLGSSKVLAKKELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVV
	1		EGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSMEVAAAKGLPVL
1			KYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGIL
	!		YGKKYEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIY
ì	İ	i	NQKGMFPGEQFKPARRPWTLLNFLSWATILLSPLFSFVLGVFAS
			GSPLLILTFLGFVGAGNGHCR
6511	2541	1425	GEEQPLAAAPTECLEQVIGGAGDPGTWASFPSPLPGPAPLKGGK
1	ļ		TMATNFSDIVKQGYVKMKSRKLGIYRRCWLVFRKSSSKGPQRLE
1	ł		KYPDEKSVCLRGCPKVTEISNVKCVTRLPKETKRQAVAIIFTDD
1	ľ		SARTFTCDSELEAEEWYKTLSVECLGSRLNDISLGEPDLLAPGV
J	l .		QCEQTDRFNVFLLPCPNLDVYGECKLQITHENIYLWDIHNPRVK
1			LVSWPLCSLRRYGRDATRFTFEAGRMCDAGEGLYTFQTQEGEQI
ł			YQRVHSATLAIAEQHKRVLLEMEKNVRLLNKGTEHYSYPCTPTT
			MLPRSAYWHHITGSQNIAEASSYAGEGYGAAQASSETDLLNRFI
1			LLKPKPSQGDSSEAKTPSO
6512	159	807	FGKKSTWFPLSRSLRVASGRSCKLGHGGYTGSGPGFGEPRDSGA
ŀ			EVPSGSGRATGCERGGVRGARQGRAPGSSIWRKEPRMVCTRKTK
1			TLVSTCVILSGMTNIICLLYVGWVTNYIASVYVRGQEPAPDKKL
1			EEDKGDTLKIIERLDHLENVIKQHIQEAPAKPEEAEAEPFTDSS
			LFAHWGQELSPEGRRVALKQFQYYGYNAYLSDRLPLDRP
6513	2	756	FVSPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTA
ĺ	[LFPDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQV
			AAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQ
i i			GVPLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPV
			LQQDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSF
1 1			SPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALF
1			PDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAA
1			PYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGV
1			PLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQ
1			QDAHSSVTITPQRSPTGAVEVQVPEDPVVALVGTDATLRCSFSP
1 1			EPGFSLAQLNLIWQLTDTRQLVHSFTEGR
6514	985	302	VGIPGPTISSAAEMEDLLDLDEELRYSLATSRAKMGRRAQQESA
			QAENHLNGKNSSLTLTGETSSAKLPRCRQGGWAGDSVKASKPRR
1 1			
1 1	Ī	i	KASERIEDFRLRPQSLNGSDYGGDIPIIPDLEEVQEEDFVLQVA APPSIQIKRVMTYRDLDNDLMKYSAIQTLDGEIDLKLLTKVLAP
1 1	1		EREALE ENDINGROUP TO THE TRANSPORT OF TH
1	ſ	1	EHEVRERNPSWQDDVGWDWDHLFTEVSSEVLTEWDPLQTEKEDP AGOARHT
6515	1345	305	
		303	GRVGSRRRGAAVPGGCGAGSTQLEVSASASCGALGSADMPIVV
1 1	ł	•	VHGGGAGPISKDRKERVHQGMVRAATVGYGILREGGSAVDAVEG
	İ		AVVALEDDPEFNAGCGSVLNTNGEVEMDASIMDGKDLSAGAVSA
1 1	ļ	ļ	VQCIANPIKLARLVMEKTPHCFLTDQGAAQFAAAMGVPEIPGEK
į /	ļ		LVTERNKKRLEKEKHEKGAQKTDCQKNLGTVGAVALDCKGNVAY
1			ATSTGGIVNKMVGRVGDSPCLGAGGYADNDIGAVSTTGHGESIL
1			KVNLARLTLFHIEQGKTVEEAADLSLGYMKSRVKGLGGLIVVSK
1 6636			TGDWVAKWTSTSMPWAAAKDGKLHFGIDPDDTTITDLP
6516	1	1402	FRRLRYLGQDATAAARDLRTRGLQGYCPSATARQQVLVSALQQL
		ļ	KGRRSEHRNENQEMPYSTNKELILGIMVGTAGISLLLLWYHKVR
	-		KPGIAMKLPEFLSLGNTFNSITLQDEIHDDQGTTVIFQERQLQI
Į i		Í	LEKLNELLTNMEELKEEIRFLKEAIPKLEEYIQDELGGKITVHK
LL			ISPQHRARKRRLPTIQSSATSNSSEEAESEGGYITANTDTEEQS

SEQ	Predicted	Predicted end	Amino acid coment containing disease
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
İ	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	(W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į.	1	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1	1	ļ	FPVPKAFNTRVEELNLDVLLQKVDHLRMSESGKSESFELLRDHK
1	1	1	EXFRDEIEFMWRFARAYGDMYELSTNTQEKKHYANIGKTLSERA
-		1	INRAPMNGHCHLWYAVLCGYVSEFEGLQNKINYGHLFKEHLDIA
]	-	ł	IKLLPEEPFLYYLKGRYCYTVSKLSWIEKKMAATLFGKIPSSTV
]	!		QEALHNFLKAEELCPGYSNPNYMYLAKCYTDLEENQNALKFCNL
			ALLLPTVTKEDKEAQKEMQKIMTSLKR
6517	3	1414	GRVWGGSSSLNAMVYVRGHAEDYERWQRQGARGWDYAHCLPYFR
1			KAQGHELGASRYRGADGPLRVSRGKTNHPLHCAFLEATQQAGYP
			LTEDMNGFQQEGFGWMDMTIHEGKRWSAACAYLHPALSRTNLKA
		!	EAETLVSRVLFEGTRAVGVEYVKNGQSHRAYASKEVILSGGAIN
1	1	i	SPQLLMLSGIGNADDLKKLGIPVVCHLPGVGQNLQDHLEIYIQQ
1	1		ACTRPITLHSAQKPLRKVCIGLEWLWKFTGEGATAHLETGGFIR
1			SQPGVPHPDIQFHFLPSQVIDHGRVPTQQEAYQVHVGPMRGTSV
1	1		GWLKLRSANPQDHPVIQPNYLSTETDIEDFRLCVKLTREIFAQE
1			ALAPFRGKELQPGSHIQSDKEIDAFVRAKADSAYHPSCTCKMGQ
ļ	1		PSDPTAVVDPQTRVLGVENLRVVDASIMPSMVSGNLNAPTIMIA
			EKAADIIKGQPALWDKDVPVYKPRTLATQR
6518	242	1098	PAWNPGSEPRTRVRPRARSFPLPPPRAPRRRHRLLRAVPGPSR
1			RHRCRRRAPPPPSTMGDAGSERSKAPSLPPRCPCGFWGSSKTMN
i			LCSKCFADFQKKQPDDDSAPSTSNSQSDLFSEETTSDNNNTSIT
			TPTLSPSQQPLPTELNVTSPSKEECGPCTDTAHVSLITPTKRSC
1			GTDSQSENEASPVKRPRLLENTERSEETSRSKQKSRRRCFQCQT
			KLELVQQELGSCRCGYVFCMLHRLPEQHDCTFDHMGRGREEAIM
			KMVKLDRKVGRSCQRIGEGCS
6519	3	1113	ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS
			AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPQSYGSPAS
	l		WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSQPGPRKLL
			VPPTLLHAQPHHLLL:PAAAAAASANAKSRRPKEKREKERRRHGL
			GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK
	i		VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKKK
			ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG
1			KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI
	·		HIEHQPNGGASVIHCLQ
6520	3	1113	ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS
1 1			AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPQSYGSPAS
]			WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSQPGPRKLL
			VPPTLLHAQPHHLLLPAAAAAASANAKSRRPKEKREKERRRHGL
1 1			GGARBAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK
			VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKKKK
1 1			ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG
]			KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI
<u> </u>			HIEHQPNGGASVIHCLQ
6521	. 184	1798	KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP
]	·		IRRTVNSTRETPPKSKLAEGEEEKPBPDISSEESVSTVEEOENE
1			TPPATSSEAEQPKGEPENBEKEENKSSEETKKDEKDQSKEKEKK
]	[VKKTIPSWATLSASQLARAQKQTPMASSPRPKMDAILTEAIKAC
1 1	[ĺ	FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKRELNRGVI
]	į		KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE
!!	ļ	ļ	DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLKVDIRPQLLKNA
[]	ļ		LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS
		}	AIAAMNBPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLOKCB
1 1	ļ		KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE
j]		DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKORGSKPA
j 1			PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS
]	1		KKPATSARKE
6522	1042	391	
للتتا		33-	NKWLRPSPRSHRTPESGRVLSLFRLPPPGMALSGSTPAPCWEED

		1 10 - 32 ab - 3 3	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
!	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
[corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
]	to first	amino acid	S=Serine, T=Threonine, V=Valine,
[[amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
j .	residue of	amino acid	W=Tryptopnam, Y=Tyrosine, X=Unknown, *=Scop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ECLDYYGMLSLHRMFEVVGGQLTECELELLAFLLDEAPGAAGGL
(ł	ì	SRARSGLKLLLELERRGQCDESNLRLLGQLLRVLARHDLLPHLA
	<u> </u>	}	RKRRRPVSPERYSYGTSSSSKRTEGSCRRRRQSSSSANSQQGSP
	[PTKRQRRSRGRPSGGARRRRRGPQPHPSSSQSPPDLPLKAK
6523	2	1097	ASCQTRRRTAALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI
Į .	1	ŀ	RSRKLGIFRRCWLVFKKASSKGPRRLBKFPDEKAAYFRNFHKVT
	İ		ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC
1			KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN
1		[LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
ì	1	1	WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER
1		1	LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGE
1	i	1	IYSLQGNHENRHSDLTGKSCKTSENRFLEENAPLVMYGITHHLF
1	1		MDTSTCKVVHDLE
6524	2	1097	ASCQTRRRTAALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI
			RSRKLGIFRRCWLVFKKASSKGPRRLEKFPDEKAAYFRNFHKVT
1			ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC
1			KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN
			LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
1			WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER
1			LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGE
	1		IYSLQGNHENRHSDLTGKSCKTSENRFLBENAPLVMYGITHHLF
1	1]	MDTSTCKVVHDLE
6525	1	1859	GESPFSEEESIEFNPSSSGRSARTVSSNSFCSDDTGWPSSQSVS
1	1 -		PVKTPSDAGNSPIGFCPGSDEGFTRKKCTIGMVGEGSIQSSRYK
i			KESKSGLVKPGSEADFSSSSSTGSISAPEVHMSTAGSKRSSSSR
1		1	NRGPHGRSNGASSHKPGSSPSSPREKDLLSMLCRNQLSPVNIHP
}	ļ	ł	SYAPSSPSSSNSGSYKGSDCSPIMRRSGRYMSCGENHGVRPPNP
i	1		EQYLTPLQQKEVTVRHLKTKLKESERRLHERESEIVELKSQLAR
l	i		MREDWIEEECHRVEAQLALKEARKEIKQLKQVIETMRSSLADKD
			KGIQKYFVDINIQNKKLESLLQSMEMAHSGSLRDELCLDFPCDS
1)		PEKSLTLNPPLDTMADGLSLEEQVTGEGADRELLVGDSIANSTD
i	1 .	1	LFDEIVTATTTESGDLELVHSTPGANVLELLPIVMGQEEGSVVV
1	1		ERAVQTDVVPYSPAISELIQSVLQKLQDPCPSSLASPDESEPDS
1			MESFPESLSALVVDLTPRNPNSAILLSPVETPYANVDAEVHANR
1	1	1	LMRELDFAACVEERLDGVIPLARGGVVRQYWSSSFLVDLLAVAA
1	1		PVVPTVLWAFSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR
1		1	IKT
6526	2	2034	SGRAGEPEEWRGRQIIDSKETWIPFNSEDSQQLEEAYSSGKGCN
-555	1 -		GRVVPTDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD
ì		1	NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREIIILHNP
1		1	KLMVHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDIHCGEP
1	1	1	LQIDHLVFVVHGIGPACDLRFRSIVQCVNDFRSVSLNLLQTHFK
	1		KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLQRITLPSINRLRH
	1		FINDTILDVFFYNSPTYCQTIVDTVASEMNRIYTLFLQRNPDFK
1 .	1		GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD
1			TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP
l .	1		LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSN
Į	1	1	TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL
1			KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI
f	1		PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY
1	1	l .	PHHKGRKRMHLELREGLTKMSMDLKNNLLGSLKMAWASFTKAFT PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV
	Į.		
ł		ļ	PALUASET PER TRANSPES TO EXPOSE VALUE COME COME COME COME COME COME COME COM
			GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV
			GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYOTOGIFLDOPLQ
6527	1	922	GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCQRGDLS
6527	1	922	GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYOTOGIFLDOPLQ

SEQ	Predicted	Predicted end	Amino acid sagment and
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
Ĺ	sequence		\=possible nucleotide insertion)
			LVLESRKRREHLSEEDILRNKAIMESLSKGGNIMEQNFEPIRRQ
]			SLTPPPQNTITWEEYISAENGKAPHLGRELVCKESKKTFKATIA
l l			MSQEFPLGIELLLNVLEVVAPFKHFNKLREFVQMKLPPGFPVKL
			DIPVFPTITATVTFQEFRYDEFDGSIFTIPDDYKEDPSRFPDL
6528	1	1073	LTGPAAAEPRCAADAGMKRALGRRKGVWLRLRKILFCVLGLYIA
ŀ	}		IPFLIKLCPGIQAKLIFLNFVRVPYFIDLKKPQDQGLNHTCNYY
{	1		LQPEEDVTIGVWHTVPAVWWXNAQGKDQMWYEDALASSHPIILY
ĺ			LHGNAGTRGGDHRVELYKVLSSLGYHVVTFDYRGWGDSVGTPSE
].		RGMTYDALHVFDWIKARSGDNPVYIWGHSLGTGVATNLVRRLCE
· ·			RETPPDALILESPFTNIREEAKSHPFSVIYRYFPGFDWFFLDPI
}	1		TSSGIKFANDENVKHISCPLLILHAEDDPVVPFQLGRKLYSIAA
1			PARSFRDFKVQFVPFHSDLGYRHKYIYKSPELPRILREFLGKSE
			РЕНОН
6529	363	2215	THIRYNKIGVVKTMSCGNEFVETLKKIGYPKADNLNGEDFDWLF
i			EGVEDESFLKWFCGNVNEQNVLSERELEAFSILQKSGKPILEGA
1	i -		ALDBALKTCKTSDLKTPRLDDKELEKLEDEVQTLLKLKNLKIOR
1			RNKCQLMASVTSHKSLRLNAKEEEATKKLKOSOGILNAMITKIS
1			NELQALTDEVTQLMMFFRHSNLGQGTNPLVFLSOFSLEKYLSOF
[ĺ		EQSTAALTLYTKKQFFQGIHEVVESSNESOFFNFI,KTOTPSTCD
			NQEILEERRLEMARLQLAYICAOHOLIHLKASNSSMKSSTKWAR
1			ESLHSLTSKAVDKENLDAKISSLTSEIMKLEKEVTQIKDRSLPA
			VVRENAQLINMPVVKGDFDLQINKQDYYTARQELVLNQLIKQKA
			SFELLQLSYEIELRKHRDIYRQLENLVQELSQSNMMLYKQLEML
			TDPSVSQQINPRNTIDTKDYSTHRLYQVLEGENKKKELFLTHGN
			LEEVAEKLKQNISLVQDQLAVSAQEHSFFLSKRNKDVDMLCDTL
	l l		YQGGNQLLLSDQELTEQFHKVESQLNKLNHLLTDILADVKTKRK
1 1			TLANNKLHOMEREFYVYFLKDEDYLKDIVENLETOSKIKAVSLE
6530	128	2986	GAAHHGAIVQVHPLLPGSSTIMIHDLCLVFPAPAKAVVYVSDIQ
1 1			ELYIRVVDKVEIGKTVKAYVRVLDLHKKPFLAKYFPFMDLKLRA
1 1			ASPIITLVALDEALDNYTITFLIRGVAIGQTSLTASVTNKAGQR
1			INSAPQQIEVFPPFRLMPRKVTLLIGATMQVTSEGGPQPQSNIL
1 1	i		FSISNESVALVSAAGLVQGLAIGNGTVSGLVQAVDAETGKVVII
1 1			SQDLVQVEVLLLRAVRIRAP_MRMRTGTQMPIYVTGITNHQNPF
1 1	İ		SFGNAVPGLTFHWSVTKRDVLDLRGRHHEASIRLPSQYNFAMNV
1 1			LGRVKGRTGLRAVVKAVDPTSGQLYGLARELSDEIQVQVFEKLQ
1	i		LLNPBIEAEQILMSPNSYIKLQTNRDGAASLSYRVLDGPEKVDV
1 1			VHVDEKGFLASGSMIGTSTIEVIAQEPFGANOTIIVAVKVSPVS
1 1			YLRVSMSPVLHTQNKEALVAVPLGMTVTFTVHFHDNSGDVPHAH
1 1			SSVLNFATNRDDFVQIGKGPTNNTCVVRTVSVGLTLLRVWDAKH
	1		PGLSDFMPLPVLQAISPELSGAMVVGDVLCLATVLTSLEGI.SGT
1 1			WSSSANSILHIDPKTGVAVARAVGSVTVYYEVAGHLRTVKEVVV
1 1			SVPQRIMARHLHPIQTSFQRATASKVIVAVGDRSSNLRGECTDT
1 1	1		QREVIQALHPETLISCQSQFKPAVFDFPSQDVFTVEPOFDTALG
1 1			QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEOVGA
1	1	i i	EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS
, i	1	ľ	PAVLAFAKEKSFGWPSFITYTVGVLDPAAGSOGPLSTTLTFSSD
	ļ	j	VTNQAIAI PVTVAFVVDRRGPGPYGASLFQHFLDSYOVMFFTLF
]]	ł	ALLAGTAVMIIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS
6531	0/15		SPTSPNALPPARKASPPSGLWSPAYASH
""	845	1425	PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS
1	ļ	i	SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFAEYWYQA
	ì		QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL
	İ		NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS
6532	2		SGLLVLPQAGLLTPHPS
		954	AAGPPSEVVNQDSLFPEPEPGPAPQVLLGPQGPGL1KGVAPPTL

SEQ	Predicted	I Dundietad and	
ID	beginning	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
10.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			ITDSTGTHLVLTVTNKNAHSPGLSRGSPQQPSSQPGSPAPAPSA
1		ĺ	QMDLEHPLQPLFGTPTSLLKKEPPGYEEAMSQQPKQQENGSSSQ
1	j		QMDDLFDILIQSGEISADFKEPPSLPGKEKPSPKTVCWSPLAAQ
	[[PSPSAELPQAAPPPPGSPSLPGRLEDFLESSTGLPLLTSGHDGP
			EPLSLIDDLHSQMLSSTAILDHPPSPMDTSELHFVPEPSSTMGL
			DLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLFSTDFLDGHD
			LQLHWDSCL
6533	1798	373	STISWLARVEPPRRSSGVGAARLRFPGGSRPLRARACVLALAVL
ſ		ĺ	ALLERNNADSMSAHSMLCERIAIAKELIKRAESLSRSRKGGIEG
1	1		GAKLCSKLKAELKFLQKVEAGKVAIKESHLQSTNLTHLRAIVES
1			AENLEEVVSVLHVFGYTDTLGEKQTLVVDVVANGGHTWVKAIGR
i		ļ	KAEALHNIWLGRGQYGDKSIIEQAEDFLQASHQQPVQYSNPHII
1			FAFYNSVSSPMAEKLKEMGISVRGDIVAVNALLDHPEELQPSES
1		Ì	ESDDEGPELLQVTRVDRENILASVAFPTEIKVDVCKRVNLDITT LITYVSALSYGGCHFIFKEKVLTEQAEQERKEQVLPOLEAFMKD
ļ		•	KELFACESAVKDFQSILDTLGGPGERERATVLIKRINVVPDOPS
i			ERALRLVASSKINSRSLTIFGTGDTLKAITMTANSGFVRAANNQ
ľ	1		GVKFSVFIHQPRALTESKEALATPLPKDYTTDSEH
6534	47	596	KATRFISAAFVVLNKQGVSPAKLPHTSWSWSLQTLSFLFSGDLA
i			EKSLQCFPCSAMLLELIPLLGIHFVLRTARAQSVTQPDIHITVS
ŀ			EGASLELRCNYSYGATPYLFWMERTVEEAFILLVCLKPWRVASS
İ			LEKKEKEDESFOLLLGSRYNVLKAHCLLPLIRWLTSGDSLLSAO
			PHCPQGL
6535	250	964	LIKTFFRDVAIQRDLLPKEKNLETLLTLAFLEIDKAFSSHARLS
1			ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL
			TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD
}	i i		LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW
			DFVNQCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN
6536	242	1174	SEINFSFSRSFASSGRWA
6536	242	11/4	SLVKEMTNQYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS
			LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSOYLATGTHV
			GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI
1			INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK
1			IYDVQHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW
1	[DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC
1	[PI
6537	1638	921	NRFNPPPTQGPDPSLVYRPDVDPEVAKDKASFRNYTSGPLLDRV
1			FTTYKLMHTHQTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV
1			DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV
1			LALFGEPQWAVVGDTFPVGCRPQASVVFCDSTFQDNPDLQDPRY
			STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG
			AEAVPAGDTLSPQSTCTR
6538	3345	2412	PYLYDFLDALITCQTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE
]			ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV
1			EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPIVK
(KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL
]			SYDDPNRKMYHLCIVNLVIGTLYCAKGNYBFGISRVIKSLEPYN
			KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC
	ľ		ELYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW
6539	210		NK
6540	218	339	FLGAASPHPHFSSLAPHPDQPEFTPVQDELEAMELWGPGV
0.540	3	391	LERLWILLLRRPEDAMAECPTLGEAVTDHPDRLWAWEKFVYLDE
1 1	}		KQHAWLPLTIEIKDRLQLRVLLRREDVVLGRPMTPTQIGPSLLP
			IMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPDD

SEO Predicted end Inino acid segment containing signal pe (a=hlanine, C=Cytesine, D=Appartic Acid No: nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence seq	
NO: nucleotide location corresponding to first amino acid amino acid residue of amino acid residue of amino acid sequence sequence sequence (Codon, -possible nucleotide deletion, -possible nucleotide deletion, -possible nucleotide deletion, -possible nucleotide deletion, -possible nucleotide sequence (Codon, -possible nucleotide sequence (Codon, -possible nucleotide sequence) (Codon, -possible nucleotide	
location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid residue of amino acid sequence codon, /=possible nucleotide deletion, >=possibl	
Corresponding to first amino acid amino acid residue of several residue of amino acid residue of amino acid sequence sequence S=Serime, T=Threonime, V=Valime,	me,
to first amino acid residue of amino acid residue of amino acid sequence 6541 1165 536 RTLVQRRILMERRARGRDLRGGGGTFRGGRKGILDT RPEGGKPDSMORNEEPGGHERPIDTPRDHEPBIGHE RSSLOGMUMASLPPRKRPMHDGPGTSEHREMEAPGGPS KGRGGFGPARVPKSGRSSSLLOEHHIDTHRDEPFGGFE RSSLOGMUMASLPPRKRPMHDGPGTSEHREMEAPGGPS KGRGGFGPARVPKSGRSSSLLOEHHIDTHRDEPFGGFE RSSLOGMUMASLPPRKRPMHDGPGTSEHREMEAPGGPS KGRGGFGPARVPKSGRSSSLLOEHHIDTHRDEPFGGFE RSSLOGMUMASLPPRKRPMHDGPGTSEHREMEAPGGPS KGRGGFGPARVPKSGRSSSLLOEHHIDTHRDEPFGGFE RSSLOGMUMASLPPRKRPMHDGPGTSEHREMEAPGGPS KGRGGFGPARVPKSGRSSSLLOEHHIDTHRDEPFGGFE RSSLOGMUMASLPPRKRPMHDGPGTSEHREMEAPGGPS KGRGGFGPARVPKSGRSSSLLOEHHIDTHRDEPFGGFE RSSLOGMUMASLPPRKPMHABALYONVLFYFEGGSCRP RGGSCSCRTPAPPRAGAGGGVBDALDKOYYFTVLGGHES LRCEEEQDKEMMEAIHOASYADILIERBVLMQKYTHLU EKIAANQLRHQLEDQDTFIERKSEIIALNKTKERMRPY DEDPDIKKIKKVQSFMRGWLCRRKWKTIVQDYICSPHABE NQIVETMVEABESEVYHQLYILVGFLRPERMASSKKPE VSSIFINSETIHFLHEIFHGGLKARIANMPTLILADLEFT LAHIYQGFVRHNYSLOVLANKONDFDKLLKQVFENNPP LETFLTYPMFQIPRYSLOVLANKONDFDKLLKQVFENNPP LETFLTYPMFQIPRYSLOVLANKONDFDKLLKQVFENNPP LETFLTYPMFQIPRYSLOVLANTHERVEKSLEFF ELSRVMHDEVSDTENIKKEBERQCFLFTKHHI SGGKLHLLKTGGVISLIDCTLIBEPDASDDDSKGSGQVF KIVVEPPDRAFTVVLLAPFRGRAMMSDISGCVDNIT TIVFEENSKVTVPHNIKSDARLHKDDTDLCFSKTLNSCG VASVERLLERLIDLEFFISIDLERFLISTIFLHTHITFLTTRIFTTHTTHTTTHTTTHTTTTTTTTTAVV IYKRPFTSIPVESLEIFFATGQNNGGHLUDGKSPRLCC VASVERLLERLIDLERFSIDLERFRATGQNNGGHLUDGKSPRLCC PPLAVSRTSSPWARKISLITSNKTGADLJTTSSSPJ PAASPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNRW LKRSICKAVLESSPADRARKSGDQDDDDIHKKEMDI MKAECFESLSAMELAEQITLLDHVIFFSIPVEFFIGGGM NERTFYIMKTSAGDDDDDIKKSRANATH ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKOT KLQKTVSSEGRFKNLRETLKNCNPPPAVPILIGMYLTDLLAB PRFTEEGLUNFSKNMMISHITERGPQOTSVSHICHDEP LKVHLQTOQEVKLRMTGMALRVVRTOGILALYSGLABAI VSLTRPAITETVRDEVAKGSGGAINMYADVSSRANATH ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKOT KLQKTVSSEGRFKNLRETLKNCNPPAVPILIGMYLTDLLAB PRFTEEGGLUNFSKNMMISHITERGPQOTSVSHICHDEP LKVHLQTOQEVKLRMTGMALRVVRTOGILALYSGLABAI VSLTRPAITETVRDEVAKGSGOALMYSGWYGGGLASCGAACCT LKVHLQOTOQEVKLRMTGMALRVVRTOGILALYSGLABAI VSLTRPAITETVRDEVAKGSGOALMYSGWYGGGLASCGGAACCT	
amino acid residue of amino acid sequence 6541 1165 536 RTLVQRTIMLLIKRPARGRIEGRGTFTRGGKGLEFI RFEGGKEDSWDGNREEGPGHEHRUTPRPDHEPHGHE RSSLQGMDMASLPPRRPWHDGPCTSEHREMEAPGGP SKGRGFGPRARVPKSGRSSSLDGEHHDGYHRDEPFGGFE SKGRGSGPRARVPKSGRSSSLDGEHHDGYHRDEPFGGFE SKGRGSGPRARVPKSGRSSSLDGEHHDGYHRDEPFGGFE SKGRGSGPRARVPKSGRSSSLDGEHHDGYHRDEPFGGFE SKGRGSGPRARVPKSGRSSSLDGEHHDGYHRDEPFGGFE SKGRGSGPRARVPKSGRSSSLDGEHHDGYHRDEPFGGFE SKGRGSGPRARVPKSGRSSSLDGEHHDGYHRDEPFGGFE SKGRGSGPRARVPKSGRSSSLDGEHHDGYHRDEPFGGFE SKGRGSGPRARVPKSGRSSSLDGEHHDGYHRDEPFGGFE SKGRGSGPRARVPKSGRSSSLDGEHHDGYHRDEPFGGFE SKGRGSGPRARVPKSGRSSSLDGEHHDGYHRDEPFGGFE SKGRGSGPRARVPKSGRSSSLDGEHHDGYHRDEPFGGFE SKGRGSGSMWGRGSMMNSGPPRGASGRGGRGR KRGFLSKKTARASRHHEKWPALVONLFYFEGEGSCRP EGCSCERTPAPPRAGAGGGVRDALDKOYYFTVLFGHEG LRCEEEQDGKEMMEAINGASVANTHUKAFLE EKIAANQLHQLEDQDTEIERLKSEIIALMKYKEMRPYP DEDPDIKKIKKVGSMRGWLGAKTANMFULILADLEP LRIYQEFVRNHQVSLQVLANCKQNRDFDKLLKQYEANPA LETFLITYPMFQIPENILITLLELLAHTPHEHVERKSLEFF ELSRYMHDEVSITENIKNIALITLLADLET LANIYQEFVRNHQVSLQVLANCKQNRDFDKLLKQYEANPA LETFLITYPMFQIPENILITLLELLAHTPHEHVERKSLEFF SGKHLLKTGGVSLJCDTLLADLERTUSGCDLLDTSGT SLIQVPSVERGKLSKVRIGSLSLKKEGERGCFLFTKHFI SGKKLHLLKTGGVSLJCDTLLADLEFT SKGSGQVW KIVVEPPDRAAFTVVLLAPSRQEKANAMSDISQCVDNIT TIVFEENSKVTVPHMIKSDARLHKUDTDLCFSKTLNSCK YASVERLEERLIDLRFISIDFLNYFLHTKRIFTTAAVVI IXKRPFTSIPVSSLELFFATSQNNRGEHLVDGKSFRLCG PPLAVSRTSSPVPARKISLISTNSKIGALDLTTSSSFT PAASPPPHTGOIPLDLERGLSSPEQSFGTVEENVINNFRU LKRS JOKAVLESAPADRRGUSSPRADATTELSEPCSPST YRQPGGGTADNAHCSVSPASAFAIATAAAGHGSPPGFNN DKEFIIRTATRRVINVILRHWVSKHAQDDQDDIHKKEDII MRAECFESLSAMELABGITLLDHVIFRSIPYEFFIGGGM NERTFYIMKTSGHPNDMSHLVASGINMYADVSSRANAIE ADICRCLHNYNGVLSITSALNRSAIYRLKKTWAKVSKOT KLOKKYSSEGRAFWLRETLKNINSGSTANTHADASGRACT LKVHLQTYQGEVKLRMTGMALRVVRTOGILALYSGLASGL YSLTRPATYETVYRDNAKGSGPRPTERKVLLSSVGLA SGATMASSRGALVTVERDRAKASGRYGFGGLASCGAACCT LKVHLQTYQGEVKLRMTGMALRVVRTOGILALYSGLASGI TPADLVNVRMQNDVKLPGGLSCYDGAKGLVKSTGYLSDNIT SFIAGGCATFICTURNSKGEYGGVPHCAVET	
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SWPRGRETGHPGALRTRTMQKSVRYNEGHALYLAFLE KRGFLSKKTAEASRMHEKWFALYQNULFYTEGEGSCREP EGGSCERPAPPRAGGGGGVBTALDKOKYYFTULFGHEG LRCEEEQDGKEWMEAIHQASYADILIEREVLMQKYIHLU EKLAANQLRHQLEDQDTEIERKSEILALKKTKERMRYY DEDDDILKKIKKYOSMRGMLCRKWKKTIVQDYICSPHAE NQIVFTMVEAESEYVHQLYILVNGFLRPLRMAASSKKPF VSSIFLNSETIMFLHEIFHGGLKARIANWFPLILADLFF LNIYQEFVRHQYSLQVLANCKONDFDKLLKQVYEANPP LEFFLTYPMFGIPRYIITLHELLAHTPHEHVERKSLEFF ELSRVMHDEVSDTENIRKNLAIERMIVEGCDILLDTSQT SLIQVPSVERGKLSKNLGSLSLKKEGERQCFLFFKHFI SGGKLHLLKTGGVLSI.IDCTLIEEPDASDDDSKGSGQVW KIVVEPPDRAAFTVVLLAPSRQEKAAWMSDISQCVDNIK TIVFEENSKVIVPHNIKSDARLHKDDTDICFSKTLNSCK YASVERLLERI.DLRFLSIDFNTFLHTYRIFTTAAVVI IYKRPFTSIPVRSLELFFAATSQNNRGEHLVDGKSPRLCE PPLAVSRTSSPVRARKLSLTSPLNSKLGALDLTTSSSFI PAASPPPHTGGIPLDLSRGLSSPEQSFSTVEENVDNREV LKRSIQKAVLESSPAADRAGVESSPAADTTELSFCRSPST YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNN DKEFIIRRTATMRVLNVLRHWYSKHAQDFELNNELKMYV EVLRDPDLLPQERKAAANILMALSGDQDDDIHLKLEDII MKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLGGGG NERTPYIMKTSQHFNDMSNILVASQIMNYADVSSRANAIE ADICRCLHNYNGVLESTSALNRSAIYRLKKTWARVSKOT KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAF PNFTEGLVNPSKMRMISHIIRERQFQQTSYRIDHQPK LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASI VSLTRFAIYETVDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVVRMQNDVKLPQCGRRNYAHALDGLYRVARESG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFFLCQPLDVLKTRLMNSKGEYGCVFHCAVET	PGSGTP
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EGCSCERTPAPPRAGAGGGGRDALDKOYYFTVLFGHEG LRCEEQOBKEMMEAHAGAYADILIERRVLMGKYJHIV EKIAANQIRHQLEBQPTEIBELKSEIJALMKKERMRYY DEDPDIKKIKKVQSFMRGWLCRKWKTIVQDYICSPHAE NQIVFTMYEAESEYVÜGLYILVNGFLRPLEMAASSKKPE VSSIFINSETIMFHEIFHGGLKARIANWFTLILADLEF LNIYQEFVRNHQYSLQVLANCKQNRDFDKLLKQYEANPP LETFLTYPMFQIPRYIITHELLAANTPHENVERSLEFP ELSRVMHDEVSDTENIKKNLAIERNIVEGGIDILDTSGT SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLFFKHFI SGGKLHLLKTGGVUSLIDCTTLIEEPDASDDDSKGSGQVF KIVVEPPDRAAFTVVLLAPSRQEKAAWMSDISQCVDNIT TIVPEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCR YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVI IYKRPFTSIPVRSLEJFFATSQNNRGEHLVDGKSFRLCR PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPP PAASPPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNPRV LKRSIQKAVLESAFANRAGVESSPAADTTELSPCRSPST YRQPGGGTADNAHCSVSPASAFAIATAAAGHGSPPGFNN DKEFIIRRTATNRVLNVLRHWVSKHAQDFELNNELKMNV EVURDPDLLPQERKAANIIMALSQDDQDDIHLKLEDII MKABCFESLSAMELABGITLLDHVIFRSIPYEEFLGGGW NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIE ADICRCLHNYNGVLEITSALNKSATYRLKKTWAKVSKOT KLQKTVSSEGRFKNLBRILKNCNPPAVPYLGMYLTDLAF PNFTEEGLVNFSKMRMISHIREIRQFQQTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA 6543 1857 950 FVSGGRAGIGLSWAMAREARVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASI TPADLVNVRMQNDVKLPQGGRRNYAHALDGLYRVAREEG SGATMASSRGALVTVEQGLSCYDQAKQLVLSTGYJLSDNIF SFIAGGCATFLCQPLDVLKYRLMNSKGEYQGVFRCAVET	
LRCEEEQDKEWMEAIHQASYADILIEREVLMQKYIHLU EKLAANQLRHQLEDQDTEIBRLKSSIIALMKTKERMRPY DEDDDIKIIKVGSFMRGWLCRRKWTIVQDYICSPHAB NQIVFTMVEAESEYVHQLYILVNGFLRPLRMAASSKKPF VSSIFLNSETIMFLHEIFHGLKARIANMPTLILADLFT LNIYQEFVRNHQVSLQVLANCKQNRDFDKLLKQYEANDF LETFLTYPMFQIPRYIITLHELLAHTPHEHVERKSLEFP ELSRVMHDEVSDTENIKKNLAIERMIVEGCDILLDTSGT SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLFTKHFI SGGKLHLLKTGGVLSLIDCTLIEEPDASDDDSKGSGQVF KIVVEPPDRAAFTVVLLAPSRQEKAAWMSDISQCUDNIR TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCK YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVI IYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSFRLCR PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPI PPAASPPPHTGQIIPLDLSRGLSSPEQSPGTVEENVDNRPX LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPST YRQPGGQTADNAHCSVSPASAFAIATAAACHGSPPGFNN DKEFIIRTATNRVLNVLRHWYSKHAQDFELNNELKMW EVLRDPDLLPQERRAANILMALSQDDQDDIHLKLEDII MKAECFESLSMELBEQITLLDHVIFRSIPYEEFLGGGW NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIE ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKOT KLQKTVSSEGRFKNLBETLKNCNPPAVPILGMYIDLAF PNFTEEGLVNFSKMRNISHIIREIRGFQCTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA 6543 1857 950 PVSGCGRAGIGLSWAMAERRVSRWYFGGLASCGAACCT LKVHLQTQQEVKLURMTGMALRVVRTDGILALYSGLSASI YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA SGATMASSRGALVTVGQLSCYDQAKQLVLSTGTSJNSDNIS SGATMASSRGALVTVGOLSCYDQAKQLVLSTGTSJNSDNIS SGATMASSRGALVTVGOLSCYDQAKQLVLSTGTSJNSDNIS	
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VSSIFINSETIMFLHEIPHQGLKARIANWPTLILADLFI LNIYQGEVRNHQYSLQVLANCKQNRDFDKKLLKQYEANPA LETFLTYPMFQIPRYIITLHELLAHTPHEHVERKSLEFA ELSRVMHDGVSDTENIRKNLAIERMIVEGCDILLDTSQT SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLFTKHFI SGGKLHLLKTGGVLSLIDCTLIEEPDASDDDSKGSGQVF KIVVEPPDRAAFTVVLLAPSRQEKAAMMSDISQCVDNIR TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCK YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVI IYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCR PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPI PAASPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNRPX LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPST YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPFGTNN DKEFIIRTATNRVLNVLRHWVSKHAQDFELNHELKMNV EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDII MKAECFESLSAMELABQITLLDHVIFRSIPYEEFLGQGW NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIE ADICRCLHNYNGVLEITSALNRSATYRLKKTWAKVSKGT KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAF PNFTEEGLVNFSKMRMISHIIREIRQFQCTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA FVSGCGRAGGIGSWAMAABARVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASI YSLTRFAIYETVRDRVKAGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVLPQGGRRNYAHALDGLYRVAREEG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
LNIYQEFVRNHQYSLQVLANCKQNRDFDKLLKQYEANPA LETFLIYYPMFQIIPYIITLHELLAHTPHEHVERKSLEFA ELSRVMHDEVSDTENIRKNLAIERMIVEGCDILLDTSQT SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLFTKHFI SGGKLHLLKTGGVLSLIDCTLIEEPDASDDDSKGSQQVE KIVVEPPDRAAFTVVLLAPSRQEKAAWMSDISQCVDNIR TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCK YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVI IYKRPFTSIPVRSLEFFATSQNNRGEHLVDGKSPRLCR PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPT PAASSPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNRPX LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPST YROPGGGTADNAHCSVSPASAFAIATAAAGHGSPPGFINN DKEFIIRRTATNRVLNVLRHWVSKHAQDFELNNELKMNV EVLRDPDLLPQERKAAANILMALSQDDQDDTHLKLEDII MKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLGQGW NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIE ADICRCLHNYGVLEITSALNRSAIYRLKKTWAKVSKOT KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAF PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHOPK LDKDLIIDEDTLYELSLKIEPRLPA FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASI YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGGRRNYAHALDGLYRVAREG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
LETFLTYPMFQIPRYIITLHELLAHTPHEHVERKSLEFA ELSRVMHDEVSDTENIRKNLAIERMIVEGCDIILDTSQT SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLFTKHFI SGGKLHLLKTGGVLSLIDCTLIEEPDASDDDSKGSGQVF KIVVEPPDRAAFTVVLLAPSRQEKAAMMSDISQCVDNIR TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCK YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVI IYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCR PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPT PAASPPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNPRV LKRSIQKAVLESAPADRAGVESSPAADTTELSPCSPST YRQPGGGYADNAHCSVSPASAFAIATAAAGHGSPPGFMN DKEFIIRRTATNRVLNVLRHWVSKHAQDFELNNELKNNV EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDII MKAECFESLSAMELABQITLLDHVIFRSIPYEEFIGGGW NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIE ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKQT KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAF PNFTEEGLVNPSKMRNISHIIREIRQFQQTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA 6543 1857 950 FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASI YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEG SGATMASSRGALVTVGQLSCTDQAKQLVLSTGYLSNNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
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SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLFTKHFI SGGKLHLLKTGGVLSLIDCTLIEEPDASDDDSKGSGQVI KIVVEPPDRAAFTVVLLAPSRQEKAAWMSDISQCVDIK TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCK YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVI IYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCR PPLAVSRTSSFVRARKLSLTSPLNSKIGALDLTTSSSPT PAASPPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNPRV LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPST YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNN DKEFIIRRTATNRVLNVLRHWVSKHAQDFELNNELKNNV EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDII MKABECFESLSAMELAEQITLLDHVIFRSIPYEEFLGQGIW NERTPYIMKTSQHFNDMSNLVASQIMMYADVSSRANAIE ADICRCHNYNGVLEITSALNRSAIYRLKKTWAKVSKQT KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAF PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPK LDKDLIIDEDTLYELSLXIEPRLPA FVSGCGRAGIGLSWAMAAEARVSWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASI YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLAS TPADLVNVRMQNDVKLPQGGRRNYAHALDGLYRVAREGS GGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
SGGKLHLLKTGGVLSLIDCTLIEEPDASDDDSKGSGQVF KIVVEPPDRAAFTVVLLAPSRQEKAAMMSDISQCVDNIR TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCK YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVI IYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCG PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSPT PAASPPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNPRV LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPST YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNN DKEFIIRRTATNRVLNVLNHWVSKHAQDFELNNELKNNV EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDII MKAECFESLSAMELABQITLLDHVIFRSIPYEEFLGQGW NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIE ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKOT KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAF PNFTEEGLVNFSKNRMISHIIRETRQFQQTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA 6543 1857 950 FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASL YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLAF TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
KIVVEPPDRAAFTVVLLAPSRQEKAAWMSDISQCVDNIK TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCK YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVI IYKRPFTSIPVRSLELPFATSQNNRGEHLVDGKSPRLCK PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPT PAASPPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNPRV LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPST YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNN DKEFIIRTATNRVLNVLRHWVSKHAQDFELNNELKMNV EVLRPDDLLPQERKAAANILMALSQDDQDDIHLKLEDII MKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLGGGW NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIE ADICRCHHNYNGVLEITSALNRSAIYRLKKTWAKVSKQT KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAF PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA 6543 1857 950 FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASL YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREGG GGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCK YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVI IYKR PFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCR PPLAVSTSSPVRARKLSLTSPLNSKIGALDLTTSSSPI PAAS PPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNPRV LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPST YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNN DKEFIIRRTATNRVLNVLRHWVSKHAQDFELNNELKMNV EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDII MKAECPESLSAMELAEQITLLDHVIFRSIPYEEFLGGGW NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIE ADICRCHHYNNGVLEITSALNRSAIYRLKKTWAKVSKQT KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAF PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA 6543 1857 950 FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCT LKVHLQTQQEVKLMTGMALRVVRTDGILALYSGLSASL YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVI IYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCR PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPT PAASPPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNPRV LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPST YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNN DKEFIIRRTATNRVLNVLRHWVSKHAQDFELNNELKMNV EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDII MKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLGGGW NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIE ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKOT KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGNYLTDLAF PNFTEEGLVNPSKMRMISHIIREIRQFQQTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA 6543 1857 950 FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASI YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
IYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCR PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPT PAAS PPPHTGIPLDLSRGLSSPEQSPGTVEENVDNPRV LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPST YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNN DKEFIIRRTATNRVLNVLRHWVSKHAQDFELNNELKMNV EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDII MKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLGQGW NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIE ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKOT KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAE PNFTEEGLVNPSKMRMISHIIREIRQFQQTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA 6543 1857 950 FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASL YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	-
PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPT PAASPPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNPRV LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPST YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNN DKEFIIRTATNRVLNVLRHWVSKHAQDFELNNELKMND EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDII MKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLGGGW NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIE ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKQTI KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAE PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASI YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREGG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
PAAS PPPHTGQIPLDLSRGLSSPEQSPGTVEENVDNPRV LKRS I QKAVLESAPADRAGVESSPAADTTELSPCRSPST YRQPGGQTADNAHCSVSPASAFA I ATAAAGHGSPPGFMN DKEFI I RR TATTNRVLNVLRHWVSKHAQDFELNNELKMNV EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDI I MKABCFESLSAMELAEQ I TLLDHVI FRS I PYEEFLGQGW NERT PY I MKTSQHFNDMSNLVASQ I MMYADVSSRANA I E ADI CRCLHNYMGVLEITSALNRSAI YRLKKTWAKVSKQT KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAE PNFTEEGLVNFSKMRMISHI I REIRQFQQTSYRIDHQPK LDKDLI I DEDTLYELSLKI EPRLPA FVSGCGRAGIGLSWAMAAEAVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGI LALYSGLSASI YSLTRFAI YETVRDRVAKGSQGPLP FHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREGG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPST YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNN DKEFIIRTATNRVINVLRHWVSKHAQDFELNNELKMNV EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDII MKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLGQUE NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIE ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKQT KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAF PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA FVSGCGRAGIGLSWAMAAEAVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASI YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREGG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	_
YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNN DKEFIIRRTATNRVLNVLRHWVSKHAQDFELNNELKMNV EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDII MKAECPESLSAMELAEQITLLDHVIFRSIPYEEFLGGGW NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIE ADICRCHNYNGVLEITSALNRSAIYRLKKTWAKVSKQT KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAF PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA 6543 1857 950 FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCT LKVHLQTQQEVKLMTGMALRVVRTDGILALYSGLSASL YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
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MKAECFESLSAMELAEQITLLDHVIFRSIPYEEFLGQGW NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIE ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKQT KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAE PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA 6543 1857 950 FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASI YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIE ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKOT KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAF PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA 6543 1857 950 FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASI YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREGG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
ADICRCLHNYNGVLEITSALNRSATYRLKKTWAKVSKQT KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAF PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA FVSGCGRAGIGLSWAMAAARAVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASI YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREGG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAF PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA 6543 1857 950 PVSGCGRAGIGLSWAMAAEAVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASI YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREGG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
PNFTEEGLVNPSKMRMISHIIREIRQFQQTSYRIDHQPK LDKDLIIDEDTLYELSLKIEPRLPA 6543 1857 950 FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCT LKVHLQTQEVKLRMTGMALRVVRTDGILALYSGLSASL YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
LDKDLIIDEDTLYELSLKIEPRLPA 6543 1857 950 FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASL YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
6543 1857 950 FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCT LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASL YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	KVAQYL
LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASL YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLA TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEG SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	_
SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIF SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
* SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVET	
1 1 7	
I I I I I I I I I I I I I I I I I I I	
6544 630 79 PSPCFIRSRLDGQPWMAGLEAWLSQNFSLHQPQSRVRVR	
EPSDTDPEPRTLNPSPAGWFVQQHPBLELMSSFRERFGR	
RSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRPSPP	
GPQESPQKMSEBVRAEPQEEEEEKEGKEEKEEGEMAPLP	PEAHLG
EGKQKECP	
6545 176 560 PPHSHAALLPAAMTPLLTLILVVLMGLPLAQALDCHVCA	
CFNPMRCPAMVAYCMTTRTYYTPTRMKVSKSCVPRCFET	
SKHASTTSCCQYDLCNGTGLATPATLALAPILLATLWGL	`L_
6546 1657 364 HLINGLDEVAAFFVADLGAIVRKHFCFLKCLPRVRPFYA	AVKCNS
SPGVLKVLAQLGLGFSCANKAEMELVQHIGIPASKIICA	MPCKQ
IAQIKYAAKHGIQLLSFDNEMELAKVVKSHPSAKMVLCI	CATDDS
HSLSCLSLKFGVSLKSCRHLLENAKKHHVEVVGVSFHIG	
PQAYAQS I ADARLV FEMGTELGHKMHVLDLGGGFFGTEG	JAKV RF
EEIASVINSALDLYFPEGCGVDIFAELGRYYVTSAPTVA	
KKEVLLDQPGREEENGSTSKTIVYHLDEGVYGIFNSVLF	

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Judan	\=possible nucleotide insertion)
	-		TPILQKKPSTEQPLYSSSLWGPAVDGCDCVAEGLWLPQLHVGDW
1			LVFDNMGAYTVGMGSPFWGTQACHITYAMSRVAWEALRROLMAA
			EQEDDVEGVCKPLSCGWEITDTLCVGPVFTPASIM
6547	1	541	LHSKYLAPALCSQPGMMRCCRRRCCCRQPPHALRPLLLLPLVLL
			PPLAAAAAGPNRCDTIYQGFAECLIRLGDSMGRGGELETICRSW
1			NDFHACASQVLSGCPEEAAAVWESLQQEARQAPRPNNLHTLCGA
ŀ	i		PVHVRERGTGSETNQETLRATAPALPMAPAPPLLAAALALAYLL
			RPLA
6548	2	219	FVSRLSVRDVRFPTFLGGHGADAMHTDPDYSAAYVPIETDAEDG
	J -		IKGCGITFTLGKGTEVGELKILSRFQNA
6549	73	1490	ETGRVCEDARPACGSRSRRRRKEAAPGIPTPSPSSSSPTSSRPA
1	· -		ARAFSKAPARLSRPRAREEPPDPGRRYIQEEIIQARKHKLIKMC
1			SSVAAKLWFLTDRRIREDYPQKEILRALKAKCCEEELDFRAVVM
I			DEVVLTIEQGNLGLRINGELITAYPQVVVVRVPTPWVOSDSDIT
1	i ·		VLRHLEKMGCRLMNRPQAILNCVNKFWTFQELAGHGVPLPDTFS
}			YGGHENFAKMIDEAEVLEFPMVVKNTRGHRGKAVFLARDKHHLA
1			DLSHLIRHEAPYLFQKYVKESHGRDVRVIVVGGRVVGTMLRCST
j			DGRMQSNCSLGGVGMMCSLSEQGKQLAIQVSNILGMDVCGIDLL
			MKDDGSFCVCEANANVGFIAFDKACNLDVAGIIADYAASLLPSG
	ĺ		RLTRRMSLLSVVSTASETSEPELGPPASTAVDNMSASSSSVDSD
1			PESTERELLTKLPGGLFNMNQLLANEIKLLVD
6550	2293	922	FRVSRDGAPDCGIEQMGLAMEHGGSYARAGGSSRGCWYYLRYFF
			LFVSLIQFLIILGLVLFMVYGNVHVSTESNLQATERRAEGLYSQ
i]		LLGLTASQSNLTKELNFTTRAKDAIMQMWLNARRDLDRINASFR
l			QCQGDRVIYTNNQRYMAAIILSEKQCRDQFKDMNKSCDALLFML
1	!		NQKVKTLEVEIAKEKTICTKDKESVLLNKRVAEEQLVECVKTRE
l			LQHQERQLAKEQLQKVQALCLPLDKDKFEMDLRNLWRDSIIPRS
	i		LDNLGYNLYHPLGSELASIRRACDHMPSLMSSKVEELARSLRAD
			IERVARENSDLQRQKLEAQQGLRASQEAKQKVEKEAQAREAKLQ
<u> </u>			AECSRQTQLALEEKAVLRKERDNLAKELEEKKREAEQLRMELAI
}			RNSALDTCIKTKSQPMMPVSRPMGPVPNPQPIDPASLEEFKRKI
			LESQRPPAGIPVAPSSG
6551	157	748	IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE
Į į			ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN
ł			ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER
			EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ
			EKDKHAEEVRKNKELKEEASR
6552	157	748	IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE
1			ADTVDLNWCVISDMEVIBLNKCTSGQSFEVILKPPSFDGVPEFN
1			ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER
			EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ
			EKDKHAEEVRKNKELKEEASR
6553	2	1807	PVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD
]	1		EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV
	.		RPRLELMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD
			LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS
			LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG
j l	[SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIQNS
.			YVKLPPEKFAPKKQGDGGKDLPTEAKKLQLNSAEKLYAEIRDKN
			FNAVGSVLSKKAKI I SAAFEERHNAKTVGEI KQFVSQLPHMQAA
	j		RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN
[YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT
			YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE
			QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF
			EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSQL
t <u>. </u>			EDGGTEYVIATTKLMNGTSWIEALMEKPF

	·		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
]	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6554	119	1244	FEMGSQVSVESGALHVVIVGGGFGGIAAASQLQALNVPFMLVDM
			KDSFHHNVAALRASVETGFAKKTFISYSVTFKDNFRQGLVVGID
		1	LKNQMVLLQGGEALPFSHLILATGSTGPFPGKFNEVSSOOAAIO
1	İ		AYEDMVRQVQRSRFIVVVGGGSAGVEMAAEIKTEYPEKEVTLIH
1			SQVALADKELLPSVRQEVKEILLRKGVQLLLSERVSNLEELPLN
1			EYREYIKVQTDKGTEVATNLVILCTGIKINSSAYRKAFESRLAS
1		}	SGALRVNEHLQVEGHSNVYAIGDCADVRTPKMAYLAGLHANIAV
i		1	ANIVNSVKQRPLQAYKPGALTFLLSMGRNDGVGQISGFYVGRLM
<u></u>			VRLTKSRDLFVSTSWKTMRQSPP
6555	1552	498	IHMALLRKINQVLLFLLIVTLCVILYKKVHKGTVPKNDADDESE
1	1	1	TPEELEEEIPVVICAAAGRMGATMAAINSIYSNTDANILFYVVG
	1	1	LRNTLTRIRKWIEHSKLREINFKIVEFNPMGLKGKIRPDSSRPE
ļ		1	LLQPLNFVRFYLPLLIHQHEKVIYLDDDVIVQGDIQELYDTTLA
1	1	l	LGHAAAFSDDCDLPSAQDINRLVGLQNTYMGYLDYRKKAIKDLG ISPSTCSFNPGVIVANMTEWKHQRITKQLEKWMQKNVEENLYSS
			SLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFL
ł	}	!	QEAKLLHWNGRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS
6556	241	1449	ASLCKGCFFVTHVLVIILPSLQSPPTFGFLLDIDGVLVRGHRVI
	1	1	PAALKAFRRLVNSQGQLRVPVVFVTNAGNILOHSKAOELSALLG
į.			CEVDADQVILSHSPMKLFSEYHEKRMLVSGQGPVMENAQGLGFR
!			NVVTVDELRMAFPLLDMVDLERRLKTTPLPRNDFPRIEGVLLLG
ì	1		EPVRWETSLQLIMDVLLSNGSPGAGLATPPYPHLPVLASNMDLL
	j	ļ	WMAEAKMPRFGHGTFLLCLETIYQKVTGKBLRYEGLMGKPSILT
ĺ	ĺ	ĺ	YQYAEDLIRRQAERRGWAAPIRKLYAVGDNPMSDVYGANLFHQY
ì			LQKATHDGAPELGAGGTRQQQPSASQSCISILVCTGVYNPRNPQ
	}		STEPVLGGGEPPFHGHRDLCFSPGLMEASHVVNDVNEAVQLVFR
CE CE			KEGWALE
6557	2598	1534	RMCGRTSCHLPRDVLTRACAYQDRRGQQRLPEWRDPDKYCPSYN
}			KSPQSNSPVLLSRLHFEKDADSSERIIAPMRWGLVPSWFKESDP
ŀ			SKLQFNTTNCRSDTVMEKRSFKVPLGKGRRCVVLADGFYEWQRC
]	}		QGTNQRQPYFIYFPQIKTEKSGSIGAADSPENWEKVWDNWRLLT MAGIFDCWEPPEGGDVLYSYTIITVDSCKGLSDIHHRMPAILDG
l	1		EEAVSKWLDFGEVSTQEALKLIHPTENITFHAVSSVVNNSRNNT
1			PECLAPVDLVVKKELRASGSSQRMLQWLATKSPKKEDSKTPQKE
1	1		ESDVPQWSSQFLQKSPLPTKRGTAGLLEQWLKREKEEEPVAKRP
1	<u> </u>		YSQ
6558	21	1138	FHGRRRGGRKMELGSCLEGGREAAEEEGEPEVKKRRLLCVEFAS
1			VASCDAAVAQCFLAENDWEMERALNSYFEPPVEESALERRPETI
			SEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWNID
1		•	GLDLNNLSERARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSS
]			NYEIITGHEEGYFTAIMLKKSRVKLKSQEIIPFPSTKMMRNLLC
j			VHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEAPES
1			ATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWD
			TOMNSNLGITAACKLRFDRIFFRAAAEEGHIIPRSLDLLGLEKL
L			DCGRFPSDHWGLLCNLDIIL
6559	3	364	GPELSGLPTRPKKLKANQTPIAMDCCASRSCSVPTGPATTICSS
1			DKSCRCGVCLPSTCPHTVWLLEPTCCDNCPPPCHIPQPCVPTCF
6560		7,475	LLNSCQPTPGLETLNLTTFTQPCCEPCLPRGC
0360	3	1435	TATSGGIWLRRKWRCHWPRPLPQSCVGTEGGLQVRDTSSRIAKG
1			GVDHTKMSLHGASGGHERSRDRRRSSDRSRDSSHERTESQLTPC
			IRNVTSPTRQHHVEREKDHSSSRPSSPRPQKASPNGSISSAGNS
			SRNSSQSSSDGSCKTAGEMVFVYENAKEGARNIRTSERVTLIVD
			NTRFVVDPSIFTAQPNTMLGRMFGSGREHNFTRPNEKGEYEVAE GIGSTVFRAILDYYKTGIIRCPDGISIPELREACDYLCISFEYS
			TIKCRDLSALMHELSNDGARROFEFYLEEMILPLMVASAOSGER
			ECHIVALTODDVVDWDEEYPPQMGEEYSQIIYSTKLYRFFKYIE
	Ļ <u>.</u>		TATABATTE G. CONSTRUCTION TO THE TATE

SEO	Predicted	1 8 - 33 3	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
Ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	1
ļ	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	1	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ĺ			NRDVAKSVLKERGLKKIRLGIEGYPTYKEKVKKRPGGRPBVIYN
!			YVQRPFIRMSWEKEEGKSRHVDFQCVKSKSITNLAAAAADIPQD
			QLVVMHPTPQVDELDILPIHPPSGNSDLDPDAQNPML
6561	3	1086	PGRRFRRKESSSSRWFPADCLLGLRGPASSLLSPEPSPSWPSHS
1			PCPMAALTDLSFMYRWFKNCNLVGNLSEKYVFITGCDSGFGNLL
{	1	!	AKQLVDRGMQVLAACFTEEGSQKLQRDTSYRLQTTLLDVTKSES
İ	ļ		IKAAAQWVRDKVGEQGLWALVNNAGVGLPSGPNEWLTKDDFVKV
	{		INVNLVGLIEVTLHMLPMVKRARGRVVNMSSSGGRVAVIGGGYC
ĺ	i		VSKFGVEAFSDSIRRELYYFGVKVCIIEPGNYRTAILGKENLES
1			RMRKLWERLPQETRDSYGEDYFRIYTDKLKNIMQVAFPRVRDVI
			NSMEHAIVSRSPRIRYNPGLDAKLLYIPLAKLPTPVTDFILSRY
			LPRPADSV
6562	1	1562	MSTLYDIRAHKAQLLRFFASSDSNKALBQRRTLHTPKLEHLDRV
1			LYEWFLGKRSEGVPVSGPMLIEKAKDFYEQMQLTBPCVFSGGWL
			WRFKARHGIKKLDASSEKQSADHQAAEQFCAFFRSLAAEHGLSA
ł			EQVYNADETGLFWRCLPNPTPEGGAVPGPKQGKDRLTVLMCANA
1	ŀ		TGSHRLKPLAIGKCSGPRAFKGIQHLPVAYKAQGNAWVDKEIFS
l	İ	i	DWFHHIFVPSVREHFRTIGLPEDSKAVLLLDSSRAHPQEAELVS
į	ļ		SNVFTIFLPASVASLVQPMEQGIRRDFMRNFINPPVPLQGPHAR
l	ł ·		YNMNDAIFSVACAWNAVPSHVFRRAWRKLWPSVAFAEGSSSEEE
	ļ		LEAECFPVKPHNKSFAHILELVKEGSSCPGQLRQRQAASWGVAG
			REAEGGRPPAATSPAEVVWSSEKTPKADQDGRGDPGEGEEVAWE
Ì			QAAVAFDAVLRFAERQPCFSAQEVGQLRALRAVFRSQQQVRRRR
			GALGAVVKVEALQEGPGGCGATAQSPLPCSSTAGDN
6563	1319	2694	LARPAQPVLLREPEGAGPPVPAGHLVHHLQGGHLRERAHPDLEA
	ĺ		HEHPLPCDQMFWRQMGGHLRMVEANSRGVVWGIGYDHTAWVYTG
			GYGGGCFQGLASSTSNIYTQSDVKCVHIYENQRWNPVTGYTSRG
			LPTDRYMWSDASGLQECTKAGTKPPSLQWAWVSDWFVDFSVPGG
			TDQEGWQYASDFPASYHGSKTMKDFVRRRCWARKCKLVTSGPWL
			EVPPIALRDVSIIPESPGAEGSGHSIALWAVSDKGDVLCRLGVS
1			ELNPAGSSWLHVGTDQPFASISIGACYQVWAVARDGSAFYRGSV
	·		YPSQPAGDCWYHIPSPPRQRLKQVSAGQTSVYALDENGNLWYRQ
1			GITPSYPQGSSWEHVSNNVCRVSVGPLDQVWVIANKVQGSHSLS
į			RGTVCHRTGVQPHEPKGHGWDYGIGGGWDHISVRANATRAPRSS
L			SQEQEPSAPPEAHGPVCC
6564	1	975	APGSCALWSYCGRGWSRAMRGCQLLGLRSSWPGDLLSARLLSQE
]	:	1	KRAAETHFGFETVSEEEKGGKVYQVFESVAKKYDVMNDMMSLGI
1			HRVWKDLLLWKMHPLPGTQLLDVAGGTGDIAFRFLNYVQSQHQR
J			KOKROLRAQONLSWEEIAKEYONEEDSLGGSRVVVCDINKEMLK
			VGKQKALAQGYRAGLAWVLGDAEELPFDDDKFDIYTIAFGIRNV
i			THIDQALQEAHRVLKPGGRFLCLEFSQVNNPLISRLYDLYSFQV
			IPVLGEVIAGDWKSYQYLVESIRRFPSQEEFKDMIEDAGFHKVT
			YESLTSGIVAIHSGFKL
6565	1464	999	RSAVANGLTKRRMGLKLNGRYISLILAVQIAYLVQAVRAAGKCD
			AVFKGFSDCLLKLGDSMANYPQGLDDKTNIKTVCTYWEDFHSCT
			VTALTDCQEGAKDMWDKLRKESKNLNIQGSLFELCGSGNGAAGS
<u> </u>			LLPAFPVLLVSLSAALATWLSF
6566	3	1385	KYESAQPGGTQPEPGLGARMAIHKALVMCLGLPLFLFPGAWAQG
<u> </u>			HVPPGCSQGLNPLYYNLCDRSGAWGIVLEAVAGAGIVTTFVLTI
}			ILVASLPFVQDTKKRSLLGTQVFFLLGTLGLFCLVFACVEKPDF
!			STCASRRFLFGVLFAICFSCLAAHVFALNFLARKNHGPRGWVIF
1			TVALLLTLVEVIINTEWLIITLVRGSGEGGPQGNSSAGWAVASP
<i>[</i>]			CAIANMDFVMALIYVMLLLLGAFLGAWPALCGRYKRWRKHGVFV
			LLTTATSVAIWVVWIVMYTYGNKQHNSPTWDDPTLAIALAANAW
			AFVLFYVIPEVSQVTKSSPEQSYQGDMYPTRGVGYETILKEQKG
L			QSMFVENKAFSMDEPVAAKRPVSPYSGYNGQLLTSVYQPTEMAL

SEQ	Predicted	Dradiated and	1 Amino agid gogment gontaining signal weekida
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location		
ł	1	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	1	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
!	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			MHKVPSEGAYDIILPRATANSQVMGSANSTLRAEDMYSAQSHQA
			ATPPKDGKNSQVFRNPYVWD
6567	125	863	TKRSNLKAYACSIHHIRTMSYVFVNDSSQTNVPLLQACIDGDFN
		1	YSKRLLESGFDPNIRDSRGRTGLHLAAARGNVDICQLLHKFGAD
1	1	1	LLATDYQGNTALHLCGHVDTIQFLVSNGLKIDICNHQGATPLVL
	1		AKRRGVNKDVIRLLESLEEQEVKGFNRGTHSKLETMQTAESESA
ĺ		1	MESHSLLNPNLQQGEGVLSSFRTTWQEFVEDLGFWRVLLLIFVI
			ALLSLGIAYYVSGVLPFVENQPELVH
6568	3	1183	HASDRLLVLPDNYSHFSQASANLQGPSRTTELFHPTLASISSPM
			LEGAELYFNVDHGYLEGLVRGCKASLLTQQDYINLVQCETLEDL
l			KIHLQTTDYGNFLANHTNPLTVSKIDTEMRKRLCGEFEYFRNHS
			LEPLSTFLTYMTCSYMIDNVILLMNGALOKKSVKEILGKCHPLG
	Ì		RFTEMEAVNIAETPSDLFNAILIETPLAPFFODCMSENALDELN
1			IELLRNKLYKSYLEAFYKFCKNHGDVTAEVMCPILEFEADRRAF
l	1		
Ì			IITLNSFGTELSKEDRETLYPTFGKLYPEGLRLLAQAEDFDQMK
Į.			NVADHYGVYKPLFEAVGGSGGKTLEDVFYEREVQMNVLAFNRQF
6560			HYGVFYAYVKLKEQEIRNIVWIAECISQRHRTKINSYIPIL
6569	205	1532	RRRGPORLGHGRPTPLLCRWRTAGPSHWEKQARAFQGLRPVDPR
	i	l	RMSWLFPLTKSASSSAAGSPGGLTSLQQQKQRLIESLRNSHSSI
j		}	AEIQKDVEYRLPFTINNLTININILLPPQFPQEKPVISVYPPIR
!	1		HHLMDKQGVYVTSPLVNNFTMHSDLGKIIQSLLDEFWKNPPVLA
i	1	1	PTSTAFPYLYSNPSGMSPYASQGFPFLPPYPPQEANRSITSLSV
J	ļ	ļ	ADTVSSSTTSHTTAKPAAPSFGVLSNLPLPIPTVDASIPTSONG
	[FGYKMPDVPDAFPELSELSVSQLTDMNEQEEVLLEQFLTLPQLK
1			QIITDKDDLVKSIEELARKNLLLEPSLFAKRQTVLDKYELLTQM
Ì	1		KSTFEKKMQRQHELSESCSASALQARLKVAAHEAEEESDNIAED
j		ĺ	FLEGKMEIDDFLSSFMEKRTICHCRRAKEEKLQQAIAMHSQFHA
1			PL
6570	330	1304	ARLPRLTFLREGFLYVLLSHWVFVGAPRPPASDSWKKGLVPSAP
		ł	PASRKMGSKALPAPIPLHPSLQLTNYSFLQAVNTFPATVDHLQG
1			LYGLSAVQTMHMNHWTLGYPNVHEITRSTITEMAAAQGI.VDARF
l	j	i	PFPALPFTTHLFHPKQGAIAHVLPALHKDRPRFDFANLAVAATQ
ļ			EDPPKMGDLSKLSPGLGSPISGLSKLTPDRKPSRGRLPSKTKKE
1	1	į	FICKFCGRHFTKSYNLLIHERTHTDERPYTCDICHKAFRRODHL
	1		RDHRYIHSKEKPFKCOECGKGFCOSRTLAVHKTLHMOTSSPTAA
1	1		SSAAKCSGETVICGGT
6571	169	656	APDMNRKKLOKLTDTLTKNCKHLFRGFDXDNDGCVNVLEWIHGL
}			SLFLRGSLEEKMKYCFEVFDLNGDGFISKEEMFHMLKNSLLKQP
			SEEDPDEGIKDLVEITLKKMDHDHDGKLSFADYELAVREETLLL
	1		EAFGPCLPDPKSOMEFEAOVFKDPNEFNDM
6572	49	1646	
33,12	""	1040	TPERAQPGALLGAAGCCVCGGRWPRSHERGYFSSAKMGSKRRN
ł			LSCSERHQKLVDBNYCKKLHVQALKNVNSQIRNQMVQNENDNRV
1			QRKQFLRLLQNEQFELDMEEAIQKAEENKRLKELQLKQEEKLAM
	1		ELAKLKHESLKDEKMRQQVRENSIELRELEKKLKAAYMNKERAA
[QIAEKDAIKYEQMKRDAEIAKTMMEEHKRIIKEENAAEDKRNKA
[KAQYYLDLEKQLEEQEKKKQBAYEQLLKEKLMIDEIVRKIYEED
			QLEKQQKLEKMNAMRRYIEEFQKEQALWRKKKREEMEEENRKII
!	1	1	EFANMQQQREEDRMAKVQENEEKRLQLQNALTQKLBEMLRQRED
l			LEQVRQELYQEEQAEIYKSKLKEEAEKKLRKQKEMKQDFEEQMA
	ļ		LKELVLQAAKEEEENFRKTMLAKFAEDDRIELMNAQKQRMKQLE
	}	į.	HRRAVEKLIEERRQQFLADKQRELEEWQLQQRRQGFINAIIEEE
			RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI
			CEEK
6573	767	275	GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK
			LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL
		1	TRKLSORPTVEELRERKILIRFSDYVEVADAQDYDRRADKPWTR
			

SEQ	Predicted	Predicted end	l Amino agid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	50400.00	\=possible nucleotide insertion)
	Dequeine		LTAADKVSRGECWRVGGRTVCWVSLGSPLGSV
6574	204	1159	LESSVPVSVGVFWACGVSWTGAAGLODGALSDTMARNAEKAMTA
05,12	, 201	1177	LARFRQAQLEEGKVKERRPFLASECTELPKAEKWRRQIIGEISK
1	ĺ		KVAQIQNAGLGEFRIRDLNDEINKLLREKGHWEVRIKELGGPDY
			GKVGPKMLDHEGKEVPGNRGYKYFGAAKDLPGVRELFEKEPLPP
1			PRKTRAELMKAIDFEYYGYLDEDDGVIVPLEQEYEKKLRAELVE
			KWKAEREARLARGEKEEEEEEEEINIYAVTEEESDEEGSOEKG
	i		GDDSQQKFIAHVPVPSQQEIEEALVRRKKMELLQKYASETLQAQ
			SEEARRLLGY
6575	117	820	
53,3	1 ***	020	SPALASQSGGITEEKMLEPQENGVIDLPDYEHVEDETFPPFPPP ASPERQDGEGTEPDEESGNGAPVPVPPKRTVKRNIPKLDAQRLI
]		SERGLPALRHVFDKAKFKGKGHEAEDLKMLIRHMEHWAHRLFPK
1			LQFEDFIDRVEYLGSKKEVOTCLKRIRLDLPILHEDFVSNNDEV
ſ	1		AENNEHDVTSTELDPFLTNLSESEMFASELSISLTEEOOORIER
1			NKQLALERROAKLP
6576	1,	1060	PEPQALVGQKRGALRLLVARLVLTVSAPAEVRRRVLRPVLSWMD
1	_	1300	RETRALADSHFRGLGVDVPGVGQAPGRVAFVSEPGAFSYADFVR
			GFLLPNLPCVFSSAFTQGWGSRRRWVTPAGRPDFDHLLRTYGDV
į			VVPVANCGVQEYNSNPKEHMTLRDYITYWKEYIQAGYSSPRGCL
1			YLKDWHLCRDFPVEDVFTLPVYFSSDWLNEFWDALDVDDYRFVY
]		AGPAGSWSPFHADIPRSFSWSVNVCGRKKWLLFPPGOEEALRDR
1			HGNLPYDVTSPALCDTHLHPRNQLAGPPLEITQEAGEMVFVPSG
1			WHHQVHNLVMCCFSCPLSGAFLQEDGSTTSPLSQPELGWNGVAH
1			G
6577	2271	987	SDRMASDDFDIVIEAMLEAPYKKEEDEOORKEVKKDYPSNTTSS
}			TSNSGNETSGSSTIGETSNRSRDRDRYRRRNSRSRSPGRQCRHR
i			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF
	i		REKSPVREPVDNLSPEERDARTVFCMQLAARIRPRDLEDFFSAV
1			GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG
1			VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED
			MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL
1			EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG
1			RFQLMAKLAEGAGIQLPSTAAAAAAAAAAQAAALQLNGAVPLGA
L			LNPAALTALSPALNLASQCLQLSSLFTPQTM
6578	377	1489	PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA
1			LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL
1			VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG
1			MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA
1			LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI
1			YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLLGELQALRDF
1			AQLGSAHFWGMMTLGGLFGFAIGYVTGLQIKFTSPLTHNVSGTA
1			KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK
L			KTPEEPSPKDSEKSAMGV
6579	2	711	RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT
			IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI
}			EDIPKEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM
			DVGQIGFHRQKDVKIVTVEKKVNEILNRLEKTKVERFPDLAAEK
	į		ECRDREERNEKKAQIQEMKKREKEEMKKKREMDELRSYSSLMKV
			ENMSSNQDGNDSDEFM
6580	62	1571	LVALKNWKPKGTNIPAPQSPVFGEAVSGVYMMTKVLGMAPVLGP
1	ĺ		RPPQEQVGPLMVKVEEKEEKGKYLPSLEMFRQRFRQFGYHDTPG
Į i			PREALSQLRVLCCEWLRPEIHTKEQILELLVLEQFLTILPQELQ
]			AWVQEHCPESAEEAVTLLEDLERELDEPGHQVSTPPNEQKPVWE
[]	į		KISSSGTAKESPSSMQPQPLETSHKYESWGPLYIQESGEEQEFA
			QDPRKVRDCRLSTQHEESADEQKGSEAEGLKGDIISVIIANKPE
L			ASLERQCVNLENEKGTKPPLQEAGSKKGRESVPTKPTPGERRYI

SEQ	Predicted	Predicted end	1 2-1-10
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
-	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Í	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
1			CAECGKAFSNSSNLTKHRRTHTGEKPYVCTKCGKAFSHSSNLTL
i	J		HYRTHLVDRPYDCKCGKAFGQSSDLLKHQRMHTEEAPYQCKDCG
ł	ł	1	KAFSGKGSLIRHYRIHTGEKPYQCNECGKSFSOHAGLSSHORLH
			TGEKPYKCKECGKAFNHSSNFNKHHRIHTGEKPYWCHHCGKTFC
6581	222		SKSNLSKHQRVHTGEGEAP
6201	228	476	RVFLKDLSSTPMASNNTASIAQARKLVEQLKMEANIDRIKVSKA
6582	1428	<u> </u>	AADLMAYCEAHAKEDPLLTPVPASENPFREKKFFCAIL
0302	1428	718	CFTTKTHCSPVSVPYLSPLVLRKELESLLENEGDQVIHTSSFIN
	1		QHPIIFWTLVWYFRRLDLPSNLPGLILTSEHCNEGVQLPLSSLS
ł	1		QDSKLVYIQLLWDNINLHQEPREPLYVSWRNFNSEKKSSLLSEE
1	}		QQETSTLVETIRQSIQHNNVLKPINLLSQQMKPGMKRQRSLYRE
			ILFLSLVSLGRENIDIEAFDNEYGIAYNSLSSEILERLQKIDAP PSASVEWCRKCFGAPLI
6583	487	41	RIFSMTSGRLRWRCTWRPATALWSASLRLGTSSMHPSPRSISLP
1	1		LSMMLSPLPSNTRGLSPTALFRSPDSEHATSCPRLHLWRCRAPL
1			RSPSPLGRLQVLPRSPLHVHTHNSGKEVLGLQVQRSRSGTGPAC
L			SQAGSGAVQGGNWCIF
6584	189	1750	PLPMAALGPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFAT
ļ		•	WNQARLERDLSNKKIYQEEEMPESGAGSEFNRKLREBARRKKYG
ì			IVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTO
			CPDGAFEAFPVHNWYNFTPLARHRTLTAEEAEEEWERRNKVLNH
1			FSIMQQRRLKDQDQDEDEEEKEKRGRRKASELRIHDLEDDLEMS
			SDASDASGEEGGRVPKAKKKAPLAKGGRKKKKKKGSDDEAFEDS
			DDGDFEGQEVDYMSDGSSSSQEEPESKAKAPQQEEGPKGVDEQS
1			DSSEESEEKPPEEDKEEEEEKKAPTPQEKKRRKDSSEESDSSE
1			ESDIDSEASSAFFMAKKTPPKRERKPSGGSSRGNSRPGTPSAE
			GGSTSSTLRAAASKLEQGKRVSEMPAAKRLRLDTGPQSLSGKST
	1		PQPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK TGLSSEQTVNVLAQILKRLNPERKMINDKMHFSLKE
6585	. 3	1678	GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDOMO
1			HWKEQRAAQKADVI.TTGAGNPVGDKLNVITVGPRGPLLVQDVVF
1 ,			TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE
1 1	,		HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL
	į		VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLR
[]			PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCK
1 1	.		FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW
j	ì		TFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRN
	Ì		PVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHR
1 1	ļ		LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF
!	1		GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE
1 1	Ī	i	EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL
6586	32	804	DKYNAEKPKNAIHTFVQSGSHLAAREKANL
		004	PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMELTGGGQESSGL
ļ †		}	NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP
			DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE
			TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA
	į	ľ	YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFOMPKV
6587	75	1117	RVPSLGXMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY
			HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF
	1	ĺ	PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA
		ļ	LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH
		İ	LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD
! !	i i	İ	INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT
		1	FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS
		i	RTASLTSASSVDGSRPQACTHSESSEGLGQVNHTMEVSC

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	M. Termtonian W. Managine W. W.
	amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į	sequence	sequence	Codon, /=possible nucleotide deletion,
6500			\=possible nucleotide insertion)
6588	137	501	LGLQAQLLELRINNYQLSDELRKNGVELTSLRQKVAYLDKEFSK
ļ]	AQKALSKSKKAQEVEVLLSENEMLQAKLHSQEEDFRLQNSTLMA
		<u> </u>	EFSKLCSQMEQLEQENQQLKEGAAGAGVAQAGP
6589	2	1405	RPWGSAMATFSRQEFFQQLLQGCLLPTAQQGLDQIWLLLAICLA
i	1	ļ	CRLLWRLGLPSYLKHASTVAGGFFSLYHFFQLHMVWVVLLSLLC
	İ		YLVLFLCRHSSHRGVFLSVTILIYLLMGEMHMVDTVTWHKMRGA
1	1	l	QMIVAMKAVSLGFDLDRGEVGTVPSPVEFMGYLYFVGTIVFGPW
1		<u> </u>	ISFHSYLQAVQGRPLSCRWLQKVARSLALALLCLVLSTCVGPYL
1	1	i	FPYFIPLNGDRLLRNKKRKARGTMVRWLRAYESAVSFHFSNYFV
i	1	l	GFLSEATATLAGAGFTEEKDHLEWDLTVSKPLNVELPRSMVEVV
t	1		TSWNLPMSYWLNNYVFKNALRLGTFSAVLVTYAASALLHGFSFH
1	i e		LAAVLLSLAFITYVEHVLRKRLARILSACVLSKRCPPDCSHOHR
l .			LGLGVRALNLLFGALAIFHLAYLGSLFDVDVDDTTEEQGYGMAY
1			TVHKWSELSWASHWVTFGCWIFYRLIG
6590	2177	656	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR
	}		GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTTMEGAMLPNY
i			GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY
}	}		VDFFEDPSSERKEKKERIPVFCIDVERNDRRAVGHEPEHWSVYR
	i .		RYLEFYVLESKLTEFHGAFPDAQLPSKRIIGPKNYEFLKSKREE
			FQEYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG
İ			KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL
1			SPTSENNKKLFNDLFKNNANRAENTERKQNQNYFMEVMTVEGVY
1		·	DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLQCKL
1	ļ		EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM
İ	(MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI
			VIQELFPELNKVQKEVTSVTSWM
6591	2177	656	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR
	i		GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTTMEGAMLPNY
			GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY
1			VDFFEDPSSERKEKKERIPVFCIDVERNDRRAVGHEPEHWSVYR
			RYLEFYVLESKLTEFHGAFPDAQLPSKRIIGPKNYEFLKSKREE
1			FQEYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG
	1	•	KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL
i I	ĺ		SPTSENNKKLFNDLFKNNANRAENTERKONONYFMEVMTVEGVY
1			DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLOCKL
i i	l		EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM
ŀ			MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKOLTYVLLDI
			VIQELFPELNKVQKEVTSVTSWM
6592	3	1861	APEFLGSTISSGSMIDANLKLLQEAEQRLKAIVAEKFAIATKEG
1			DLPQVERFFKIFPLLGLHEEGLRKFSEYLCKOVASKAERNLLMV
			LGTDMSDRRAAVIFADTLTLLFEGIARIVETHQPIVETYYGPGR
			LYTLIKYLQVECDRQVEKVVDKFIKQRDYHQQFRHVQNNLMRNS
] 1			TTEKIEPRELDPILTEVTLMNARSELYLRFLKKRISSDFEVGDS
			MASEEVKQEHQKCLDKLLNNCLLSCTMQELIGLYVTMEEYFMRE
]			TVNKAVALDTYEKGQLTSSMVDDVFYIVKKCIGRALSSSSIDCL
Į 1			CAMINLATTELESDFRDVLCNKLRMGFPATTFQDIQRGVTSAVN
1 1			IMHSSLOOGKPDTKGIESTDEAKMSFLVTLANVEVCSENISTLK
	l	l	KTLESDCTKLFSQGIGGEQAQAKFDSCLSDLAAVSNKFRDLLQE
	Į.		GLTELNSTAIKPQVQPWINSFFSVSHNIEEEEFNDYEANDPWVQ
	1	ļ	QFILNLEQQMAEFKASLSPVIYDSLTGLMTSLVAVELEKVVLKS
			TFNRLGGLQFDKELRSLIAYLTTVTTWTIRDKFARLSQMATILN
	i		
{	Ī		LERVTEILDYWGPNSGPLTWRLTPAEVRQVLALRIDFRSEDIKR
6593		1837	PARSACEPPECIAL OPOUL COLCOVERCEPPECELL VILLEY
	-	1021	EAFSAGSRRRGLALQRGVLGGLGGYCPCCCRRRGRLLVLLLLVR RGGEGGGRGRGDKRRRRQARRQRRRPEPAEARGGKMADVLSVL
	j		RQYNIQKKEIVVKGDEVIFGEFSWPKNVKTNYVVWGTGKEGOPR
			"KK-COTA A WODER A TE GET ONE WAS A WELGE OF A MOTOVE OF K

SEQ Predicted predicted and beginning nucleotide nucleotide nucleotide location corresponding to first amino acid residue of amino acid sequence se
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence codon, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide insertion) EYYTLDSILFLLNNVHLSHPVYVRRAATENIPVVRRPDRKDLI IKAKIMAKKRSTIKTDLDDDITALKQRSFVDAEVDVTRDIVSE RVWRTRTTILOSTGKNFSKNIFAILQSVKAREEGRAPEQRPAI AAPVDPTLRTKQPIPAAYNRYDQERFKGKEETEGFKIDTMGTY GMTLKSVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRTIIIPAATTSLTTMLNAKDLLQDLKFVPSDEKKKQGCQRENET IQRRKDQMQPGGTAISVTVPYRVVDQFLKLMPQDWDRVVAVFQ GPAWQFKGWPWLLPPGSPVDIFAKKAFHLKYDEVRLDPNVQK GPAWQFKGWPWLLPPGSPVDIFAKKAFHLKYDEVRLDPNVQK GPAWQFKGWPWLLPPGSPVDIFAKKAFHLKYDEVRLDPNVQK GPAWQFKGWPWLLPPGSPVDIFAKKAFHLKYDEVRLDPNVQK GPAWQFKGWPWLLPPGSPVDIFAKKAFHLKYDEVRLDPNVQK GPAWQFKGWPWLLPPGSPVDIFAKKAFHLKYDEVRLDPNVQK GPAWQFKGWPWLLPPGSPVDIFAKKAFHLKYDEVRLDPNVQK GPAWQFKGWPWLLPPGSPVDIFAKKAFHLKYDEVRLDPNVQK GPAWQFKGWPWLLPPGSPVDIFAKKAFHLKYDEVRLDPNVQK GPAWQFKGSPSPLCATCGPALLRAPTRAAMTRSLFKGNPWS DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIEERYGKDI
location corresponding to first amino acid amino acid residue of amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide insertion) EYYTLDSILFLLNNVHLSHPVYVRRAATENIPVVRRPDRKDLI YLNGEASTSASIDRSAPLEIGLQRSTQVKRAADEVLAEAKKPR EDEECVRLDERLARKEGIVQTEQIRSLSEAMSVEKIA IKAKIMAKKRSTIKTDLDDDITALKQRSFVDAEVDVTRDIVSE RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRPAI IIIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENET IQRRKDQMQPGGTAISVTVPRVDQWDVTVVPV GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQW DVTVLELSYHKRHLDRPVFLRVWETLDRYWVKHKSHLFF 1096 EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNFWS DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIBERYGKDI
corresponding to first amino acid residue of amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide insertion) EYYTLDSILFILNNVHLSHPVYVRRAATENIPVVRRPDRKDLI YLNGEASTSASIDRSAPLEIGLQRSTQVKRAADEVLAFAKKPR EDEECVRLDKERLAARLEGHKEGIVQTEQIRSLSEAMSVEKIA IKAKIMAKKRSTIKTDLDDDITALKQRSFVDAEVDVTRDIVSE RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRPAE AAPVDPTLRTKQPIPAAYNRYDQERFKGKEETEGFKIDTMSTY GMTLKSVTEGASARKQTPAAQPVPRPVSQARPPPNQKKGSRT IIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENET QRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFV GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQM DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF 6594 1 1096 EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNPWS DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIEERYGKDI
to first amino acid residue of amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, amino acid sequence Codon, /=possible nucleotide deletion, \ EYYTLDSILFLLNNVHLSHPVYVRRATENIPVVRRPDRKDLI YLNGEASTSASIDRSAPLEIGLQRSTQVKRAADEVLAEAKKPR EDEECVRLDKERLAARLEGHKEGIVQTEQIRSLSEAMSVEKIA IKAKIMAKKRSTIKTDLDDDITALKQRSFVDAEVDVTRDIVSE RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRPAI AAPVDPTLRTKQPIPAAYNRYDQERFKGKEETEGFKIDTMGTY GMTLKSVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRTIIIPAATTSLITMLNAKDLLQDLKFVSDEKKKQGCQRENET IQRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFV GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQMDVVVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF EFPGRRFRGSQASFLCATCGPALLRAPTRAAMTRSLFKGNPWSDILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIEERYGKDI
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \
residue of amino acid sequence
amino acid sequence Codon, /=possible nucleotide deletion,
=possible rucleotide insertion
EYYTLDSILFLLNNVHLSHPVYVRRAATENIPVVRRPDRKDLI YLNGEASTSASIDRSAPLEIGLQRSTQVKRAADEVLAEAKKPR EDEECVRLDKERLAARLEGHKEGIVQTEQIRSLSEAMSVEKIA IKAKIMAKKRSTIKTDLDDDITALKQRSFVDAEVDVTRDIVSE RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRPAI AAPVDPTLRKQPIPAAYNRYDQERFKGKEETEGFKIDTMGTY GMTLKSVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRT IIIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENET IQRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFV GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQN DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF 6594 1 1096 EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNPWS DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIEERYGKDI
YLNGEASTSASIDRSAPLEIGLQRSTQVKRAADEVLAEAKKPR EDEECVRLDKERLAARLEGHKEGIVQTEQIRSLSEAMSVEKIA IKAKIMAKKRSTIKTDLDDDITALKQRSFVDAEVDVTRDIVSE RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRPAE AAPVDPTLRTKQPIPAAYNRYDQERFKGKEETEGFKIDTMGTY GMTLKSVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRT IIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENET IQRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFV GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQM DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF 6594 1 1096 EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNPWS DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIEERYGKDI
EDEECVRLDKERLAARLEGHKEGIVQTEQIRSLSEAMSVEKIA IKAKIMAKKRSTIKTDLDDDITALKQRSFVDAEVDVTRDIVSE RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRPAE AAPVDPTLRTKQPIPAAYNRYDQERFKGKEETEGFKIDTMGTY GMTLKSVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRT IIIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENET IQRRKDQMQ>GGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFV GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQN DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF 6594 1 1096 EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNPWS DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIEERYGKDI
IKAKIMAKKRSTIKTDLDDDITALKQRSFVDAEVDVTRDIVSE RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRPAE AAPVDPTLRTKQPIPAAYNRYDQERFKGKEETEGFKIDTMGTY GMTLKSVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRT IIIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENET IQRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFV GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQN DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF 6594 1 1096 EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNPWS DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIBERYGKDI
RVWRTRTTILQSTGKNFSKNIFAILQSVKAREEGRAPEQRPAR AAPVDPTLRTKQPIPAAYNRYDQERFKGKEETEGFKIDTMGTY GMTLKSVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRT IIIIPAATTSLITMINAKDLLQDLKFVPSDEKKKQGCQRENET IQRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFV GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQN DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF 6594 1 1096 EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNFWS DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIBERYGKDI
AAPVDPTLRTKQPIPAAYNRYDQERFKGKEETEGFKIDTMGTY GMTLKSVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRT IIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENET IQRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFV GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQN DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF 6594 1 1096 EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNFWS DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIBERYGKDI
GMTLKSVTEGASARKTQTPAAQPVPRPVSQARPPPNQKKGSRT IIIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENET IQRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFV GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQN DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF 6594 1 1096 EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNFWS DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIEERYGKDI
IIIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENET IQRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFV GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQN DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF 6594 1 1096 EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNFWS DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIEERYGKDI
IQRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFV GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQN DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF 6594 1 1096 EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNFWS DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIBERYGKDI
GPAWQFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVQN DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF 6594 1 1096 EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNFWS DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIEERYGKDI
DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF 6594 1 1096 EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNPWS DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIBERYGKDI
6594 1 1096 EFPGRRFRGSQASPLCATCGPALLRAPTRAAMTRSLFKGNFWS DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIBERYGKDI
DILSTIGYDNIJQHLNNGRKNCKEFEDFLKERAAIEERYGKDI
]
ARKMEEPREKQKLQRKKTELIMDAIHKQKSLQFKKTMDAKKNY
OKCRDKDEAEOAVSRSANLVNPKQOEKLFVKLATSKTAVEDSI
AYMLHIGTLDKVREEWQSEHIKACEAFEAQECERINFFRNALW
HVNQLSQQCVTSDEMYEQVRKSLEMCSIQRDIEYFVNQRKTGQ
PPAPIMYENFYSSOKNAVPAGKATGPNLARRGPLPIPKSSPDI
NYSLVDDYSLLYO
6595 57 781 PLGTMSDSDLGEDEGLLSLAGKRKRRGNLPKESVKILRDWLYI
RYNAYPSEOEKLSLSGOTNLSVI.OICNWFINARRLLPDMLR
GKDPNOFTISRRGGKASDVALPRGSSPSVLAVSVPAPTNVLSI
VCSMPLHSGQGEKPAAPFPRGELESPKPLVTPGSTLTLLTRAE
GSPTGGLFNTPPPTPPEQDKEDFSSFQLLVEVALQRAAEMELC
QQDPSLPLLHTPIPIVSENPQ
6596 2 1026 PRLPVRRYHGRRILGGRSRGHMAEGDAGSDORONEEIEAMAAI
GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTF
PIYOLNAPWLKGOERADLSNSLEEIYIONIGESILYLWVEKIR
VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACOPESSVKAI
FDISETRTEVEVEELPPIDHGIPITDRRSTFOAHLAPVVCPKO
KMVLSKLYENKKIASATHNIYAYRIYCEDKOTFLODCEDDGET
AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCAF
ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH
6597 2 1026 PRLPVRRYHGRRRLOGRSRGHMAEGDAGSDORONEEIEAMAA1
GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLOVMLPNEYPGTA
PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIR
VLIQKSQMTEPGPDVKKKTEEEDVBCEDDLILACQPESSVKAI
FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKC
KMVLSKLYENKKIASATHNIYAYRIYCEDKOTFLODCEDDGET
AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCAF
ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH
6598 1099 419 PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCS
VLSFCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIOIVLE
LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNS
FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITV
DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPF
SKGLOS
6599 164 1593 KMAALTTLFKYIDENODRYIKKLAKWVAIQSVSAWPEKRGEIR
MMEVAAADVKOLGGSVELVDIGKOKLPDGSEIPLPPILLGRIG
DPOKKTVCIYGHLDVOPAALEDGWDSEPFTLVERDGKLHGRGS
DDKGPVAGWINALEAYOKTGQEIPVNVRFCLEGMEESGSEGLI
· · · · · · · · · · · · · · · · · · ·
LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFI
VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGI
EAVAAVTEEHKLYDDIDFDIEEFAKDVGAQILLHSHKKDILM
RWRYPSLSLHGIEGAFSGSGAKTVIPRKVVGKFSIRLVPNMTE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ĺ			L=Leucine, M=Methionine, N=Asparagine,
l	corresponding	to first	
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			VVGEQVTSYLTKKFAELRSPNEFKVYMGHGGKPWVSDFSHPHYL
ļ	\	ļ	AGRRAMKTVFGVEPDLTREGGSIPVTLTFQEATGKNVMLLPVGS
1	ì		ADDGAHSONEKLNRYNYIEGTKMLAAYLYBVSQLKD
6600	2	934	PGRLFRVAAMESAGLEOLLRELLLPDTERIRRATEOLOIVLRAP
0000	1 -	1	AALSALCDLLASAADPQIRQFAAVLTRRRLNTRWRRLAAEQRES
1			LKSLILTALORETEHCVSLSLAOLSATIFRKEGLEAWPOLLOLL
	1		
ì	1	1	QHSTHSPHSPEREMGLLLLSVVVTSRPEAFQPHHRELLRLLNET
<u> </u>	}	ł	LGEVGSPGLLFYSLRTLTTMAPYLSTEDVPLARMLVPKLIMAMQ
!	1	l	TLIPIDEAKACEALEALDELLESEVPVITPYLSEVLTFCLEVAR
1		Ĭ	NVALGNAIRIRILCCLTFLVKVKSKALLKNRLLATLAAHPFPHC
1		1	GC
6601	529	1420	PRAAARAPPPAVLRRDRRAATAPGAGEMTLHGPLAQRYFLNHIE
l .		1	KITTWQDPRKAMNQPLNHMNLHPAVSSTPVPQRSMAVSQPNLVM
,		1	NHQHQQCMAPSTLSQQNHPTQNPPAGLMSMPNALTTQQQQQQKL
		1	RLORIOMERERIRMRQEELMRQBAALCRQLPMEAETLAPVQAAV
}	Ì	}	NPPTMTPDMRSITNNSSDPFLNGGPYHSREQSTDSGLGLGCYSV
ł		l	PTTPEDFLSNVDEMDTGENAGQTPMNINPQQTRFPDFLDCLPGT
l		1	NVDLGTLESEDLIPLFNDVESALNKSEPFLTWL
- 6600		617	LLDFPALPKFVLAOSPKAGKPSTMTSMTQSLREVIKAMTKARNF
6602	127	61,	** * * * * * * * * * * * * * * * * *
ļ		1	ERVLGKITLVSAAPGKVICEMKVEEEHTNAIGTLHGGLTATLVD
1			NISTMALLCTERGAPGVSVDMNITYMSPAKLGEDIVITAHVLKQ
		<u> </u>	GKTLAFTSVDLTNKATGKLIAQGRHTKHLGN
6603	79	660	PVGPSSLAARTGLGHLPFLHRLASSRGLDMDLLQFLAFLFVLLL
·			SGMGATGTLRTSLDPSLEIYKKMFEVKRREQLLALKNLAQLNDI
1	1	1	HQQYKILDVMLKGLFKVLEDSRTVLTAADVLPDGPFPQDEKLKD
		l .	AFSHVVENTAFFGDVVLRFPRIVHYYFDHNSNWNLLIRWGISFC
	l		NCTGVFNQGPHSPILSLM
6604	3	688	TSTAQRQGGERMSFRGGGRGGFNRGGGGGGFNRGGSSNHFRGGG
	1	1	GGGGGNFRGGGRGGFGRGGGRGGFNKGQDQGPPERVVLLGEFL
ł	1		HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDE1FGQLR
f			DFYFSVKLSENMKASSFKKLQKFYIDPYKLLPLQRFLPRPPGEK
			GPPRGGGRGGGRGGGRGGGRGGGFRGGRG
	1	1	GGFRGRGH
F.C.0.5	7	848	SGSRRGAMRAAGVGLVDCHCHLSAPDFDRDLDDVLEKAKKANVV
6605	1	848	
Į			ALVAVAEHSGEFEKIMQLSERYNGFVLPCLGVHPVQGLPPEDQR
!			SVTLKDLDVALPIIENYKDRLLAIGEVGLDFSPRFAGTGEQKEE
1	1	1	QRQVLIRQIQLAKRLNLPVNVHSRSAGRPTINLLQEQGAEKVLL
			HAFDGRPSVAMEGVRAGYFFSIPPSIIRSGQQKLVKQLPLTSIC
1		Į.	LETDSPALGPEKQVRNEPWNISISABYIAQVKGISVEEVIEVTT
			QNALKLFPKLRHLLQK
6606	2	1682	FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS
			KSLGLIEGYGGRGKGGLPATLSPAEEEKAKGPHEKYGYNSYLSE
i			KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR
			SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLBEYVHKRYPGL
}			VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP
1			
1			VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM
			YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG
Į.		1	MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI
1			GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER
1			RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC
1			LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP
Į			DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG
1		1	RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK
6607	137	986	VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT
0307	13'	700	GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD
I	1		ALEDEL DWANTOND DEGLECT BY CONTEMADEL UNITADES AND AND AND AND AND AND AND AND AND AND
1	1	I	KIEDELEMTMVCHRPEGLEQLEAQTNFTKRELQVLYRGFKNECP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
!	sequence		\=possible nucleotide insertion)
	 		SGVVNEDTFKQIYAQFFPHGDASTYAHYLFNAFDTTQTGSVKFE
Ī			DFVTALSILLRGTVHEKLRWTFNLYDINKDGYINQEEMMDIVKA
į	1	l	IYDMMGKYTYPVLKEDTPRQHVDVFFQKMDKNKDGIVTLDEFLE
			SCOEDDNIMRSLOLFONVM
6608	224	1140	RPCFSSPTGLCPRLSYPMILLQHAVLPPPKOPSPSPPMSVATRS
	1		TGTLQLPPQKPFGQEASLPLAGEELSKGGEQDCALEELCKPLY
	1		CKLCNVTLNSAQQAQAHYQGKNHGKKLRNYYAANSCPPPARMSN
1			VVEPAATPVVPVPPCMGSFKPGGRVILATENDYCKLCDASFSSP
1	1		AVAQAHYQGKNHAKRLRLAEAQSNSFSESSELGQRRARKEGNEF
			KMMPNRRNMYTVQNNSGPYFNPRSRQRIPRDLAMCVTFSGQFYC
<u>L</u>			SMCNVGAGEEMEFRQHLESKQHKSKVSEQRYRNEMENLGYV
6609	1	443	FRLRCRRFRVAGGRLAGAGLRESRVPAPEQRLSALTLLSWSAVT
			PAAEPGNFQLSPAEPRGPLASPVRAAPRAPCPAAEMSELNTKTS
1			PATNQAAGQEEKGKAGNVKKAEEEEEIDIDLTAPETEKAALAIQ
			GKFRRFQKRKKDPSS
6610	319	881	GRKSLCNLHIFIRFPLTYPDMYMGMMCTAKKCGIRFQPPAIILI
Į.			YESEIKGKIRQRIMPVRNFSKFSDCTRAAEQLKNNPRHKSYLEQ
j			VSLRQLEKLFSFLRGYLSGQSLAETMEQIQRETTIDPEEDLNKL
			DDKELAKRKSIMDELFEKNQKKKDDPNFVYDIEVEFPQDDQLQS
			CGWDTESADEF
6611	978	212	PGCSGAGSRVWWLPALRHLAMGSTESSEGRRVSFGVDEBERVRV
]		LOGVRLSENVVNRMKEPSSPPPAPTSSTFGLQDGNLRAPHKEST
i	ľ		LPRSGSSGGQQPSGMKEGVKRYEQEHAAIQDKLFQVAKREREAA
1	<u> </u>		TKHSKASLPTGEGSISHEEQKSVRLARELESREAELRRRDTFYK
	1		EQLERIERKNAEMYKLSSEQFHEAASKMESTIKPRRVEPVCSGL
6612	1724	992	QAQILHCYRDRPHEVILLCSDLVKAYQRCVSAAHKG VSTHASALSRTQGQPQRQPRAAASGAGAGTAGGGGSGGAEGSKM
1	1	7,72	STEAQRVDDSPSTSGGSSDGDQRESVQQEPEREQVQPKKKEGKI
1] !		SSKTAAKLSTSAKRIQKELAEITLDPPPNCSAGPKGDNIYEWRS
	i l		TILGPPGSVYEGGVFFLDITFSPDYPFKPPKVTFRTRIYHCNIN
1	l i		SQGVICLDILKDNWSPALTISKVLLSICSLLTDCNPADPLVGSI
	1		ATQYMTNRAEHDRMARQWTKRYAT
6613	130	748	ELELSSNMPEQSNDYRVAVFGAGGVGKSSLVLRFVKGTFRESYI
i]		PTVEDTYRQVISCDKSICTLQITDTTGSHQFPAMQRLSISKGHA
į			FILVYSITSRQSLEELKPIYEQICEIKGDVESIPIMLVGNKCDE
			SPSREVQSSEABALARTWKCAFMETSAKLNHNVKELFQELLNLE
			KRRTVSLQIDGKKSKQQKRKEKLKGKCVIM
6614	3	1191	SSAAEAMRVLVRRCWGPPLAHGARRGRPSPQWRALARLGWEDCR
			DSRVREKPPWRVLFFGTDQFAREALRALHAARENKEEELIDKLE
1			VVTMPSPSPKGLPVKQYAVQSQLPVYEWPDVGSGEYDVGVVASF
1)		GRLLNEALILKFPYGILNVHPSCLPRWRGPAPVIHTVLHGDTVT
1			GVTIMQIRPKRFDVGPILKQETVPVPPKSTAKELBAVLSRLGAN
1	İ		MLISVLKNLPESLSNGRQQPMEGATYAPKISAGTSCIKWEEQTS
1			EQIFRLYRAIGNIIPLOTLWMANTIKLLDLVEVNSSVLADPKLT
			GQALIPGSVIYHKQSQILLVYCKDGWIGVRSVMLKKSLTATDFY
L-53-5			NGYLHPWYQKNSQAQPSQCRFQTLRLPTKKKQKKTVAMQQCIE
6615	832	35	GRVGAGASAMSELPGDVRAFLREHPSLRLQTDARKVRCILTGHE
}			LPCRLPELOVYTRGKKYORLVRASPAFDYAEFEPHIVPSTKNPH
	1	1	QLFCKLTLRHINKCPEHVLRHTQGRRYQRALCKYBECQKQGVEY
1			VPACLVHRRRREDQMDGDGPRPREAFWEPTSSDEGGAASDDSM
1			TDLYPPELFTRKDLGSTEDGDGTDDFLTDKEDEKAKPPREKATD
1			EGRRETTVYRGLVQKRGKKQLGSLKKKFKSHHRKPKSFSSCKQS
6616	342	1000	G
0010	347	1886	LLPPCQGARPLSSPPHASEDNLFLFWNCILCAFPHPSPQPLQYP
			VWPLLLVITQIPAPRHLRNRPFSFSRGGLDSFSGSLSTPSICRS

			
SEQ	Predicted	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	beginning nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Í	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			PAWVKMAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSP
Ì	}	Ì	PPQPHPCHTCRGLVDSFNKGLERTIRDNFGGGNTAWEEENLSKY
1	•		KDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQQEA
1	ļ		PDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEG
1			EGTRGGSGHCDCQAGYGGEACGQCGLGYFEAERNASHLVCSACF
ì	j		GPCARCSGPEESNCLQCKKGWALHHLKCVDIDECGTEGANCGAD
1	ł		QFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKC
1	1	1	LDVDECETEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQ
1			IPESAGFFSEMTEDELVVLQQMFFGIIICALATLAAKGDLVFTA
			IFIGAVAAMTGYWLSERSDRVLEGFIKGR
6617	118	673	VWMAWQVSLLELEDRLQCPICLEVFKESLMLQCGHSYCKGCLVS
1			LSYHLDTKVRCPMCWQAVDGSSSLPNVSLAWVIEALRLPGDPEP KVCVHHRNPLSLFCEKDQELICGLCGLLGSHQHHPVTPISTVCS
			RMKEELAALFSELKQEQKKVDELIAKLVKNRTRIDGSAPSLCPC
	ł		LGPATFTFL
6618	548	136	DGKVARRAPNSPAFONDIYPLVSAPRATTAESPWSKVLQNTQCR
1 0010	340	133	NVPKMTSERSRIPCLSAAAAEGTGKKOOEGRAMATLDRKVPSPE
ł			AFLGKPWSSWIDAAKLHCSDNVDLEEAGKEGGKSREVMRLNKEA
1	1	İ	WKYGT
6619	246	842	PASSEVLTAAVMFLLLNCIVAVSQNMGIGKNGDLPRPPLRNEFR
			YFORMTTTSSVEGKONLVIMGRKTWFSIPEKNRPLKDRINLVLS
1	1		RELKEPPQGAHFLARSLDDALKLTERPELANKVDMIWIVGGSSV
1	1	ļ	YKEAMNHLGHLKLFVTRIMQDFESDTFFSEIDLEKYKLLPEYPG
ĺ			ILSDVQEGKHIKYKFEVCEKDD
6620	3	1879	NSRVDDFVARARMAAENEASQESALGAYSPVDYMSITSFPRLPE
1		ļ	DEPAPAAPLRGRKDEDAFLGDPDTDPDSFLKSARLQRLPSSSSE
1	Į.	1	MGSQDGSPLRETRKDPFSAAAAECSCRQDGLTVIVTACLTFATG
	1		VTVALVMQIYFGDPQIFQQGAVVTDAARCTSLGIEVLSKQGSSV
1			DAAVAAALCLGIVAPHSSGLGGGGVMLVHDIRRNESHLIDFRES
1	l		APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHQLYGRLPWS OVLAFAAAVAQDGFNVTHDLARALABQLPPNMSERFRETFLPSG
1 .		1	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ
1	1	j	HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI
1			SALNILEGFNLTSLVSREOALHWVAETLKIALALASRLGDPVYD
1	1	ł	STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT
	1		AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS
		1	WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA
l			LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV
		1	SIPHAANMG .
6621	1	662	VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP
	1	1	AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT
1		1	SVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG
1	1 .	1	KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK
	<u></u>		LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL
6622	2	319	GRASGAQEETENGGPERARAMEANMPKRKEPGRSLRIKVISMGN
1	1		AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN
	<u> </u>		IFDMAGHPFFYEVRKPF
6623	1886	189	KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA
	1	-	LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF
1	1	1	VSIYGLTCLYTLYWLFYRSLREYSFEYVRQETGFDDIPDVKNDF
}	1	1	AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL
1	1		ROKLOTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM
1	}		IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKI
1	1		LSIKSNVSKIPQAVVDVSSHLQKMCIHNDGTKLVMLNNLKKMTN
1	1		LTELELVHCDLERIPHAVFSLLSLQELDLKENNLKSIEEIVSFQ
L	.		PARTICULE TELEVALOURD DE MENTANCE DE LA SE

SEQ	Predicted	Predicted end	Amino agid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
		 	ULDELTE MUCIEOTIGE INSERTION)
1		1	HLRKLTVLKLWHNSITYIPEHIKKLTSLERLSFSHNKIEVLPSH
j	ł		LFLCNKIRYLDLSYNDIRFIPPEIGVLQSLQYFSITCNKVESLP
1		1	DELYFCKKLKTLKIGKNSLSVLSPKIGNLLFLSYLDGKGNHFEI
6624	218	1786	LPPELGDCRALKRAGLVVEDALFETLPSDVREQMKTE
		1,00	GSRRGGGSRIPAVSTHVAPGRSVLRPFASGALRLRSLVKALGGC
			RGRPSGLAHLSQETSHWRAKRSGRACLGDFPGEILRSFIMKCTA
		ļ	REWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIA
		Ì	KQRGKRAITDNDMQSILDLHNKLRSQVYPTASNMEYMTWDVELE
			RSAESWAESCLWEHGPASLLPSIGQNLGAHWGRYRPPTFHVQSW
į.	1		YDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGC
1			AINLCHNMNIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCS
1	1		ACPPSFGGGCRENLCYKEGSDRYYPPREEETNEIERQQSQVHDT
			HVRTRSDDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTCNRYEC
	1		PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITR
i			QGRKHYFIKSNRNGIQTIGKYQSANSFTVSKVTVQAVTCETTVE
6625	1124	543	QLCPFHKPASHCPRVYCPRKLYASKSTLCSCNWNSSLF
1 3323	1124	543	PGPRGGGGSLLSTKALGRSRGLGMHPGPSSGGTEGGVPTALRPP
İ	j		GPLVPSTSDDNLLKNIELFDKLALRFHGRLLFLKDVLGDEICCW
ĺ	1		SFYGQGRKINEVCCTSIVYNTEKKQTKVEFPEARIPEETLNILI
i	1		YETPRGPDPALLEATGGAAGAGGAGRGEDEENREHRVRRIHVRR
6626	3		HITHDERPHGQQIVFKD
1 0020	1 3	1498	SAVEFVYTDRFHLILGISVEFLCSLRSDATMESITACLHALQAL
1	1		LDVPWPRSKIGSDQDSGIELLNVLHRVILTRESPSIQLASLEVV
İ	j i		RQIICAAQEHVKEKRRSAEVDDGAAEKETLPEFGEGKDTGGLVP
1			GKSLVFATLELCVCILVRQLPELNPKLTGSPGVKATKPQILLED
1			GSRLVSAALVILSELPAVCSPEGSISILPTILYLTIGVLRETAV
}			KLPGGQLSSTVAASLQALKGILSSPMARAEKSRTAWTDLLRSAL
			TTILDCWDPVDETHQELDEVSLLTAITVFILSTSPEVTTIPCLQ
1			KRCIDKFKATLEIKDPVVQIKTYQLLHSIFQYPNPAVSYPYIYS
	1		LASCIMEKLQEIDKRKPENTAELEIFQEGIKVLETLVTVAEEHH
i	1		RAQLVACLLPILISFLLDENSLGSATSIMRNLHDFALQNLMQIG
]]		PQYSSVFKSLVASSPALKARLEAAIKGNQESVKVKIPTSKYTKS
6627	 		PGKNSSIQLKTSFL
"""	1	697	GIPHLSSRDMTGTPGAVATRDGEAPERSPPCSPSYDLTGKVMLL
1	1		GDTGVGKTCFLIQFKDGAFLSGTFIATVGIDFRNKVVTVDGVRV
1	1		KLQIWDTAGQERFRSVTHAYYRDAQALLLLYDITNKSSFDNIRA
	1		WLTEIHEYAQRDVVIMLLGNKADMSSERVIRSEDGETLAREYGV
1			PFLETSAKTGMNVELAFLAIAKELKYRAGHQADEPSFQIRDYVE
6628			SQKKRSSCCSFM
1	1	1861	QCAEFGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
ł			KEFGDSLSLEILQIIKESQQQHGLRHGDFQRYRGYCSRRQRRLR
l	1		KTLNFKMGNRHKFTGKKVTEELLTDNRYLLLVLMDAERAWSYAM
]			QLKQEANTEPRKRFHLLSRLRKAVKHAEELERLCESNRVDAKTK
1			LEAQAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIYEKLASAFTE
[ı	EQAVLYNQRVEEISPNIRYCAYNIGDQSAINELMOMRLRSGGTE
(i			GLLAEKLEALITQTRAKQAATMSEVEWRGRTVPVKIDKVRIFLL
			GLADNEAAIVQAESEETKERLFESMLSECRDAIQVVREELKPDO
			KORDYILEGEDGKVENLOYLHSYLTYIKLSTAIKRNENMAKGLO
			RALLQQQPEDDSKRSPRPQDLIRLYDIILQNLVELLQLPGLEED
	ľ		KAFQKEIGLKTLVFKAYRCFFIAQSYVLVKKWSEALVLYDRVLK
			YANEVNSDAGAFKNSLKDLPDVQELITQVRSEKCSLQAAAILDA
j l	ļ į		NDAHQTETSSSQVKDNKPLVERFETFCLDPSLVTKQANLVHFPP
}	1	l	GFQPIPCKPLFFDLALNHVAFPPLEDKLEQKTKSGLTGYIKGIF
		[GFRS
6629	5653	4549	GATPLGSVGGRTGKMDAATLTYDTLRFAEFEDFPETSEPVWILG
			RKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGC
_			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	Bequence	\=possible nucleotide insertion)
	Bequence		MLRCGOMIFAQALVCRHLGRDWRWTORKROPDSYFSVLNAFIDR
Į.	}	•	KDSYYSIHQIAQMGVGEGKSIGQWYGPNTVAQVLKKLAVFDTWS
1	1		SLAVHIAMDNTVVMEEIRRLCRTSVPCAGATAFPADSDRHCNGF
l .	Ĭ	1	PAGAEVINRPSPWRPLVLLIPLRLGLTDINEAYVETLKHCFMMP
1			OSLGVIGGKPNSAHYFIGYVGEELIYLDPHTTQPAVEPTDGCFI
İ			PDESFHCOHPPCRMSIAELDPSIAVVRGGHLSTOAFGAECCLGM
}	l		TRKTFGFLRFFFSMLG
6630		423	LVOCGGIRRSAWGAMPGRHVSRVRALYKRVLOLHRVLPPDLKS
6630	2	423	LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANENRQ
}	1	Ì	
1	1	1	NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFSI SBSMKPKF
H-66-3-	 		
6631	2	423	LVQCGGTRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLKS
1		1	LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANENRQ
1		1	NSTGKACFGTFL2EEKLNDFRDEQIGQLQELMQEATKPNRQFSI
L		<u> </u>	SESMKPKF WNSRGRTQRGAAPLAPAAAMKAVVQRVTRASVTVGGEQISAIGR
6632	1273	588	
1			GICVLLGISLEDTQKELEHMVRKILNLRVFEDESGKHWSKSVMD KOYEILCVSOFTLOCVLKGNKPDFHLAMPTEQAEGFYNSFLEQL
1	1		
1	•		RKTYRPELIKDGKFGAYMQVHIQNDGPVTIELESPAPGTATSDP
			KQLSKLEKQQQRKEKTRAKGPSESSKERNTPRKEDRSASSGAEG
	1		DVSSEREP
6633	1145	617	ATGRHEGVPTLEGIIQQLVNGIITPATIPSLGPWGVLHSNPMDY AWGANGLDAIITQLLNQFENTGPPPADKEKIQALPTVPVTEEHV
1		1	
	1		GSGLECPVCKDDYALGERVRQLPCNHLFHDGCIVPWLEQHDSCP
			VCRKSLTGQNTATNPPGLTGVSFSSSSSSSSSSSSSSSNENATSNS
6634	1	1134	CGGIPRKGSGPRRLPMARLRDCLPRLMLTLRSLLFWSLVYCYC
	1	}	GLCASIHLLKLLWSLGKGPAQTFRRPAREHPPACLSDPSLGTHC YVRIKDSGLRFHYVAAGERGKPLMLLLHGFPEFWYSWRYQLREF
			KSEYRVVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLGY
		1	SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINFPHPNVFTEYI
1			LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHSTG
ł			IGRKGCOLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCLPLKH
i	ł		HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEASH
l .			WLQQDQPDIVNKLIWTFLKEETRKKD
6635 .	1420	470	EMRAGQOLASMLRWTRAWRLPREGLGPHGPSFARVPVAPSSSSG
0032.	1420	1 70	GRGGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK
1			ILAOOTGRRVLTVDARNHGDSPHSPDMSYEIMSQDLQDLLPQLG
1	ļ		LVPCVVVGHSMGGKTAMLLALORPELVERLIAVDISPVESTGVS
1	1	1	HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL
{		1	LTNLVEVDGRFVWRVNLDALTOHLDKILAFPOROESYLGPTLFL
ļ	1	1	LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI
1		1	-
1	1614	1000	AAIRGFLV SFCMFSHKODSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE
6636	1514	1801	-
1		1	QPIVRQCLQRPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD
	 		DGGDGVF
6637	2	1501	CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI
1			KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT
Í		1	VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD
	1	1	LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG
1		1	DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS
j		1	CIPICGKIENITAPKTQGLRWPWQAAIYRTSGVHDGSLHKGAW
1	1	}	FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR
		1	DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS
1		1	TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL
1		1	RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC
	l .	l .	TAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAF

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide defection,
	sequence		
			TKVLPFKDWIERNMK
6638	1391	224	GGIPQAGGKMAAPWWRAALCECRRWRGFSTSAVLGRRTPPLGPM
ĺ		<u> </u>	PNSDIDLSNLERLEKYRSFDRYRRRAEQEAQAPHWWRTYREYFG
ł	ì	1	EKTDPKEKIDIGLPPPKVSRTQQLLERKQAIQELRANVEEERAA
		1	RLRTASVPLDAVRAEWERTCGPYHKQRLAEYYGLYRDLFHGATF
		1	VPRVPLHVAYAVGEDDLMPVYCGNEVTPTEAAQAPEVTYEAEEG
ł .	l .		SLWTLLLTSLDGHLLEPDAEYLHWLLTNIPGNRVAEGQVTCPYL
j	j		PPFPARGSGIHRLAFLLFKQDQPIDFSEDARPSPCYQLAQRTFR
1			TFDFYKKHQETMTPAGLSFFQCRWDDSVTYIFHQLLDMREPVFE
l			FVRPPPYHPKQKRFPHRQPLRYLDRYRDSHEPTYGIY
6639	2046	1268	IGCFIMDGGDDGNLIIKKRFVSEAELDERRKRRQEEWEKVRKPE
			DPEECPEEVYDPRSLYERLQEQKDRKQQEYEEQFKFKNMVRGLD
		1	EDETNFLDEVSRQQELIEKQRREBELKELKEYRNNLKKVGISQE
	1	1	NKKEVEKKLTVKPIETKNKFSQAKLLAGAVKHKSSESGNSVKRL
ļ		,	KPDPEPDDKNQEPSSCKSLGNTSLSGPSIHCPSAAVCIGILPGL
ì	}	1	GAYSGSSDSESSSDSEGTINATGKIVSSIFRTNTFLEAP
6640	117	1043	VLEPPDVSMAESEDRSLRIVLVGKTGSGKSATANTILGEEIFDS
3333			RIAAQAVTKNCQKASREWQGRDLLVVDTPGLFDTKESLDTTCKE
	İ	1	ISRCIISSCPGPHAIVLVLLLGRYTEEEQKTVALIKAVFGKSAM
1			KHMVILFTRKEELEGQSFHDFIADADVGLKSIVKECGNRCCAFS
1	3		NSKKTSKAEKESOVOELVELIEKMVQCNEGAYFSDDIYKDTEER
	l l	1	I.KOREEVLRKIYTDOLNEEIKLVEEDKHKSEEKKEKEIKLLKLK
1	1	1	YDRKIKNIREEAERNIFKDVFNRIWKMLSEIWHRFLSKCKFYSS
6641	1	894	SAAVGRRSEVRGCAPRPRLRRSARRMDPVPGTDSAPLAGLAWSS
0011			ASAPPPRGFSAISCTVEGAPASFGKSFAQKSGYFLCLSSLGSLE
ŀ	İ	1	NPQENVVADIQIVVDKSPLPLGFSPVCDPMDSKASVSKKKRMCV
1	1	į.	KLLPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK
	Į.		APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS
1		l	TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF
į.			GDLTIKSLADIEEEYNYGFVVEKTAAARLPPSVS
6642	22	1296	PLEERMMTKMDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTE
		1	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV
	1	1	HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP
ł		1	NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN
	l l	1	KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER
ļ			MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG
1	1	1	NRRRQERFWYCRLALNHKVLHYGDLDDNPQGEVTFESLQEKIPV
	1	1	ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF
1	1	1	IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL
		1	LDLENIQIPEAPPPIPKEPSSYDFVYHYG
6643	3049	2265	SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI
	1		DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG
			HDRTMODIVYKLVPGLOBAEMRKQREFYHKLGMEVPGDIKGETC
	1		SAKOHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI
1	1	1	CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL
1	1		DILCNEEILGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL
6644	1489	290	PRPLATEPRGSSPVOLVSSTMSVRTLPLLFLNLGGEMLYILDQR
1	1		LRAONIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR
			TVYERLAHASIMKLNOASMDKLYDLMTMAFKYQVLLCPRPKDVL
1			LATENHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ
Į			LIROTLLIFFODLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT
-			EVPGI.TRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL
1	1		KIGTNMYSVNOPVETHVSGSSKNLASWTQESIAPNPLAKEELNF
1	}		LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY
1			EVINTOATODOORSEELARIMGEFEITEOPRLSTSKGDDLLAMM
i			
			KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEEL LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEEL EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLA DEL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID .	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6645	6530	4646	FVEGLAGYVYKAASEGKVLTLAALLLNRSESDIRYLLGYVSQQG
i]		GQRSTPLIIAARNGHAKVVRLLLEHYRVQTQQTGTVRFDGYVID
	1	1	GATALWCAAGAGHFEVVKLLVSHGANVNHTTVTNSTPLRAACFD
	į	1	GRLDIVKYLVENNANISIANKYDNTCLMIAAYKGHTDVVRYLLE
i	1		QRADPNAKAHCGATALHFAAEAGHIDIVKELIKWRAAIVVNGHG
1			MTPLKVAAESCKADVVELLLSHADCDRRSRIEALELLGASFAND
ļ	1		RENYDIIKTYHYLYLAMLERFQDGDNILEKEVLPPIHAYGNRTE
l			CRNPQELESIRQDRDALHMEGLIVRERILGADNIDVSHPIIYRG
1	l .		AVYADNMEFEQCIKLWLHALHLRQKGNRNTHKDLLRFAQVFSQM
ļ	1	}	IHLNETVKAPDIECVLRCSVLEIEQSMNRVKNISDADVHNAMDN
	1		YECNLYTFLYLVCISTKTQCSEEDQCKINKQIYNLIHLDPRTRE
1	1	1	GFTLLHLAVNSNTPVDDFHTNDVCSFPNALVTKLLLDCGAEVNA
1	1		VDNEGNSALHIIVQYNRPISDFLTLHSIIISLVEAGAHTDMTNK
1			QNKTPLDKSTTGVSEILLKTQMKMSLKCLAARAVRANDINYQDQ
1			IPRTLEEFVGFH
6646	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY
1	Į.		EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTL
			EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL
1	1		TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLD
l .			FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA
Į.	1		GSEEAEEKQDSEKPLLEL
6647	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY
	Į.		EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTL
[EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL
			TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLD
		1	FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA
L		I	GSEEAEEKQDSEKPLLEL
6648	413	897	RNCWNCFTKYFNSPPEDIDHKDSYLITRSIMAEPDYIEDDNPEL
l	Ì	1	IRPQKLINPVKTSRNHQDLHRELLMNQKRGLAPQNKPBLQKVME
	1		KRKRDQVIKQKEEEAQKKKSDLEIELLKRQQKLEQLELEKQKLQ
			EEQENAPEFVKVKGNLRRTGQEVAQAQES
6649	1357	832	WIPRAAGIRHEVKWDVKEIMSQHNIYVDALLKEFEQFNRRLNEV
İ			SKRVRIPLPVSNILWEHCIRLANRTIVEGYANVKKCSNEGRALM
		1	QLDFQQFLMKLEKLTDIRPIPDKEFVETYIKAYYLTENDMERWI
		L	KEHREYSTKQLTNLVNVCLGSHINKKARQKLLAAIDDIDRPKR
6650	32	765	LVPLVFSLLVQSCKQVYRSIAMKFVPCLLLVTLSCLGTLGQAPR
		l	QKQGSTGEEFHFQTGGRDSCTMRPSSLGQGAGEVWLRVDCRNTD
1		i	QTYWCEYRGQPSMCQAFAADPKSYWNQALQELRRLHHACQGAPV
		[LRPSVCREAGPQAHMQQVTSSLKGSPEPNQQPEAGTPSLRPKAT
1	1	1	VKLTEATQLGKDSMEELGKAKPTTRPTAKPTQPGPRPGGNEEAK
			KKAWEHCWKPFQALCAFLISFFRG
6651	3425	1353	AKELLKVGDFSLCAGPYQNTADTMENLSKEPLASFVSESFDISA
ļ		1	CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSDMHYELSG
		1	DSDLDLLGDCRNPRLDLEDSYTLRGSYTRKKDVPTDGYESSLNF
	1		HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCVPPYVQIR
1			DLHGILRTYANFSITKELKDTMRTSHGLRRHPSFSANCGLPSSW
		1	TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGDSQHSASSANV
1		1	FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP
		1	RPQGQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL
	-		NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN
		1	DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA
		}	CKSTFLFYLVETEDKSFFVRTKNLLRKGGHTEIEPQHFCQAFHR
		1	ENDTLIIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV
			LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG
			RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFQSANIIELLH
	•		YHQCDSRSSTKAEILKCLLNLQIQHIDARFAVLLTDKPTIPREV

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NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			FENNGILVTDVNNFIENIEKIAAPFRSSYW
6652	2	1343	1PGSTISCSCHSRRLRGGSPAPRLSLGAASPRPRPPSLPLPLPL
1	ļ		PFPLFLPTRPAERAWIRSRRASEWVGKMEVPRLDHALNSPTSPC
	İ		EEVIKNLSLEAIQLCDRDGNKSQDSGIAEMEELPVPHNIKISNI
1	}	ļ	TCDSFKISWEMDSKSKDRITHYFIDLNKKENKNSNKFKHKDVPT
ŀ	1		KLVAKAVPLPMTVRGHWFLSPRTEYTVAVQTASKQVDGDYVVSE
			WSEIIEFCTADYSKVHLTQLLEKAEVIAGRMLKFSVFYRNQHKE
ŀ			YFDYVREHHGNAMQPSVKDNSGSHGSPISGKLEGIFFSCSTEFN
į			TGKPPQDSPYGRYRFEIAAEKLFNPNTNLYFGDFYCMYTAYHYV
1			ILVIAPVGSPGDEFCKQRLPQLNSKDNKFLTCTEEDGVLVYHHA
			QDVILEVIYTDPVDLSLGTVAEITGHQLMSLSTANAKKDPSCKT
6653			CNISVGR
6653	170	1910	FFLEPRLRPFPASRARFVPARTRPSPLHPCCFCFEGGGSMLSPQ
1	ł		RVAAAASRGADDAMESSKPGPVQVVLVQKDQHSFELDEKALASI
1]		LLQDHIRDLDVVVVSVAGAFRKGKSFILDFMLRYLYSQKESGHS
	i		NWLGDPEEPLTGFSWRGGSDPETTGIQIWSEVFTVEKPGGKKVA
			VVLMDTQGAFDSQSTVKDCATIFALSTMTSSVQIYNLSQNIQED
			DLQQLQLFTEYGRLAMDEIFQKPFQTLMPLVRDWSFPYEYSYGL
1			QGGMAFLDKRLQVKEHQHEEIQNVRNHIHSCFSDVTCFLLPHPG
1			LQVATSPDFDGKLKDIAGEFKEQLQALIPYVLNPSKLMEKEING
			SKVTCRGLLEYFKAYIKIYOGEDLPHPKSMLQATAEAYNLAAAA SAKDIYYNNMEEVCGGEKPYLSPDILEEKHCEFKQLALDHFKKT
			KKMGGKDFSFRYQQELEEEIKELYENFCKHNGSKNVFSTFRTPA
f 1			VLFTGIVALYIASGLTGFIGLEVVAQLFNCMVGLLLIALLTWGY
			IRYSGQYRELGGAIDFGAAYVLEQASSHIGNSTQATVRDAVVGR
1 1			PSMDKKAO
6654	1	705	RTSLSPSQCSSFNLAMASAGMQILGVVLTLLGWVNGLVSCALPM
1 1			WKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQMQCKVYDSLLAL
			PQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARL
1			VLTSGIVFVISGVLTLIPVCWTAHAVIRDFYNPLVAEAOKRELG
1	i		ASLYLGWAASGLLLLGGGLLCCTCPSGGSQGPSHYMARYSTSAP
			AISRGPSEYPTKNYV
6655	341	16	KDAYMFKKGLLALALVFSLPVFAAEHWIDVRVPEQYQQEHVQGA
1 1			INIPLKEVKERIATAVPDKNDTVKVYCNAGRQSGQAKEILSEMG
			YTHVENAGGLKDIAMPKVKG
6656	2	1212	TELPPRPANLAIQPPLSPLRALAPLPEKPGAVPPPQKRMAKVAK
1			DLNPGVKKMSLGQLQSARGVACLGCKGTCSGFEPHSWRKICKSC
]]			KCSQEDHCLTSDLEDDRKIGRLLMDSKYSTLTARVKGGDGIRIY
[]			KRNRMIMTNPIATGKDPTFDTITYEWAPPGVTQKLGLQYMELIP
1			KEKQPVTGTEGAFYRRQLMHQLPIYDQDPSRCRGLLENELKLM
1 1	. 1	i	EEFVKQYKSEALGVGEVALPGQGGLPKEEGKQQEKPEGAETTAA
	İ		TTNGSLSDPSKEVEYVCELCKGAAPPDSPVVYSDRAGYNKQWHP
	1	İ	TCFVCAKCSEPLVDLIYFWKDGAPWCGRHYCESLRPRCSGCDEI
j	1	į	IFAEDYQRVEDLAWHRKHFVCEGCEQLLSGRAYIVTKGQLLCPT CSKSKRS
6657	830	2120	
		4120	LLTCQERAGDCLLSASTMKEVVYWSPKKVADWLLENAMPEYCEP
1	İ		LEHFTGQDLINLTQEDFKKPPLCRVSSDNGQRLLDMIETLKMEH HLEAHKNGHANGHLNIGVDIPTPDGSFSIKIKPNGMPNGYRKEM
	j		
]	j		IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL
) [1	
		!	LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL
			TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV
]		1	AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK
		j	NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT
6658	35	855	HCCALGAPGSPYRGLYFSSAAPCTAPRKAKHQSTLEGLTKRMLM
			"COLIMON GOT INGUITABAMECIMERIMANNOSIDEGUIKKMUM

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	Doguesioo	\=possible nucleotide insertion)
			FDPVPVKQEAMDPVSVSYPSNYMESMKPNKYGVIYSTPLPEKFF
Ì			QTPEGLSHGIQMEPVDLTVNKRSSPPSAGNSPSSLKFPSSHRRA
1		1	SPGLSMPSSSPPIKKYSPPSPGVQPFGVPLSMPPVMAAALSRHG
l .	ļ	!	IRSPGILPVIQPVVVQPVPFMYTSHLQQPLMVSLSEEMENSSSS
1	i	İ	MQVPVIESYEKPISQKKIKIEPGIEPQRTDYYPEEMSPPLMNSV
ļ	1		SPPOALLOE
6659	18	523	EPORGDCETWFQNCSLPKFVCFFCWGFWLWRAHSMSNLHSLPGL
		1	RGLTSISRNQLQCTNAMRVINNYQRRWKNQNTFLLATFANVVNV
Ĭ.	1	[CGNPTITCPHNRTLNNCHHSGVQVPLMYCNLTTPSPQNISNCRY
1			AQTPANMFYIVACDNRDQRRDPPQYPVVPVHLHTII
6660	514	1707	CAASLDCRHHLCEPDMKLVWPSAKLLQAAAGASARACDSVTSNV
]			LPLLLEQFHKHSQSSQRRTILEMLLGFLKLQQKWSYEDKDQRPL
1	t		NGFKDQLCSLVFMALTDPSTQLQLVGIRTLTVLGAQPDLLSYED
}			LELAVGHLYRLSFLKEDSQSCRVAALEASGTLAALYPVAFSSHL
			VPKLAEELRVGESNLTNGDEPTQCSRHLCCLQALSAVSTHPSIV
1			KETLPLLLQHLWQVNRGNMVAQSSDVIAVCQSLRQMAEKCQQDP
1		1	ESCWYFHQTAIPCLLALAVQASMPEKEPSVLRKVLLEDEVLAAM
1	į		VSVIGTATTHLSPELAAQSVTHIVPLFLDGNVSFLPENSFPSRF
1			QPFQDGSSGQRRLIALLMAFVCSLPRNVSEHIWEVLLFNLDKVT
1			PG
6661	179	430	GVHAASGTLSATWLAEAKMFDSLAKAGKYLGQAAKLMIGMPDYD
l	1		NYVEHMRVNHPDQTPMTYEEFFRERQDARYGGKGGARCC
6662	185	423	RSLPKPAPAQPASIHCARFSGVTPPTAKTAMSDGNTAFNALMYC
			GPKADDGNIFSACAPASSAVKASVSVAQPGQAVIP
6663	3	1005	RPVLSSRVDDFVPPLPETSGRRKKLERMYSVDRVSDDIPIRTWF
ł		l	PKENLFSFQTASTTMQAISNFRKHLRMVGSRRVKAQTFAERRER
1			SFSRSWSDPTPMKADTSHDSRDSSDLQSSHCTLDEAFEDLDWDT
·	1		EKGLEAVACDTEGFVPPKVMLISSKVPKAEYIPTIIRRDDPSII
		İ	PILYDHEHATFEDILEEIERKLNVYHKGAKIWKMLIFCQGGPGH
ŀ		1	LYLLKNKVATFAKVEKEEDMIHFWKRLSRLMSKVNPEPNVIHIM
1	ļ		GCYILGNPNGEKLFQNLRTLMTPYRVTFESPLELSAQGKQMIET
-			YFDFRLYRLWKSRQHSKLLDFDDVL
6664	58	968	PRILITIPRSVVVMDSPWDELALAFSRTSMFPFFDIAHYLVSVMA
I		}	VKRQPGAAALAWKNPISSWFTAMLHCFGGGILSCLLLAEPPLKF
			LANHTNILLASSIWYITFFCPHDLVSQGYSYLPVQLLASGMKEV
1		ļ	TRTWKIVGGVTHANSYYKNGWIVMIAIGWARGAGGTIITNFERL VKGDWKPEGDEWLKMSYPAKVTLLGSVIFTFOHTOHLAISKHNL
1	1		
1	1	İ	MPLYTIFIVATKITMMTTQTSTMTFAPFEDTLSWMLFGWQQPFS SCEKKSEAKSPSNGVGSLASKPVDVASDNVKKKHTKKNE
6665	171	1278	DERRLACROVVTQQRSELYPGFQKRQRFLPKAGEEAAAQGGRHL
""	1 -/-	12/6	PGRWLGPGCTONPCSVHTATGPEPRKLPLLPPDSPNSGYPKEPA
1	1		ALCPGIPSPCRMTHQDLSITAKLINGGVAGLVGVTCVFPIDLAK
1	1		TRLONOHGKAMYKGMIDCLMKTARAEGFFGMYRGAAVNLTLVTP
1	1		EKAIKLAANDFFRRLLMEDGMQRNLKMEMLAGCGAGMCQVVVTC
			PMEMLKIOLODAGRLAVHHOGSASAPSTSRSYTTGSASTHRRPS
1	1	ļ	ATLIAWELLRTOGLAGLYRGLGATLLRDIPFSIIYFPLFANLNN
[LGFNELAGKASFAHSFVSGCVAGSIAAVAVTPLDVLKTRIOTLK
1			KGLGEDMYSGITDCAR
6666	498	2868	MTTFLPVPOMMAGFSFGTFGNPPMESPSAWOTIHOPFIVSCLTL
		2000	WSPGCWPOPIOKEGVGLWDIRKPOSSLLRYGGNLSLQSAMSVRF
			NSNGTQLLALRRRLPPVLYDIHSRLPVFQFDNQVYFNSCTMKSC
			CFAGDRDOYILSGSDDFNLYMWRIPADPEAGGIGRVVNGAFMVL
1	1		KGHRSIVNQVRFNPHTYMICSSGVEKIIKIWSPYKQPGCTGDLD
			GRIEDDSRCLYTHEEYISLVLNSGSGLSHDYANQSVQEDPRMMA
ŀ			FFDSLVRREIEGWSSDSDSDLSESTILQLHAGVSERSGYTDSES
i			SASLPRSPPPTVDESADNAFHLGPLRVTTTNTVASTPPTPTCED
L	1	L	GUODERGEET ANE SWINGER BRANCH AND LEEL BICED

No. Destining location corresponding to first amino acid amino acid sequence coation corresponding to first amino acid amino acid sequence coation corresponding to first amino acid sequence coation coatio				
No. location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence sequenc	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Corresponding Corresponding Corresponding Corresponding Corresponding Control Cont	i .			(A=Alanine, C=Cysteine, D=Aspartic Acid. E=
corresponding to first anino acid residue of residue of anino acid residue of anino acid residue of anino acid sequence solvent anino acid sequence solvent anino acid sequence solvent anino acid sequence solvent seq	NO:	. —		Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of sequence sequence sequence Assectie, T. *Threonine, V.*Valine, wathytophan, V=Tyrosine, X=Unknown, *-Stop codon, /=possible nucleotide deletion, logical sequence Assectie, T. *Threonine, V.*Valine, sequence Assectie, T. *Threonine, X=Unknown, *-Stop codon, /=possible nucleotide insertion logical sequence Assectie, T. *Threonine, V.*Unknown, *-Stop codon, /=possible nucleotide insertion TREDRESAPRIPTOTESURGNINSSSEEMUCEVELDIPDIPE PRESPREDESSSSSSSSSSEDEREINERRATWORMARBROOT TREDRESAPRIPTYTIGENDYPTOTUKDOLSPISTSPERST TREDRESAPRIPTYTIGENDYPTOTUKDOLSPISTSPERST STLEIOPSRAPPTSDIESURGNITALATURGNINGONIGGLE BCCSKDTYKEETPOTPSNGCHEHSIAMAEVPECTSGOTMAN SURPPETKIKINGKALISSRAEDEPSPPVEKASGSINGS SURPPETKIKINGKALISSRAEDEPSPPVEKASGSINGS SURPPETKIKINGKALISSRAEDEPSPPVEKASGSINGSSINGSSINGS SURPPETKIKINGKALISSRAEDEPSPPVEKASGSINGS SURPPETKIKINGKALISSRAEDEPSPPVEKASGSINGS SURPPETKIKINGKALISSRAEDEPSPPVEKASGSINGS SURPPETKIKINGKALISSRAEDEPSPPVEKASGSINGS SURPPETKIKINGKALISSRAEDEPSPPVEKASGSINGS SURPPETKIKINGKALISSRAEDEPSPPVEKASGSINGS SURPPETKIKINGKALISSRAEDEPSPPVEKASGSINGS SURPPETKIKINGKALISSRAEDEPSPPVEKASGSINGSSINGSSINGSSINGSSINGSSINGSSINGSSI		1		H=Histidine, I=Isoleucine, K=Lysine,
Contract				L=Leucine, M=Methionine, N=Asparagine,
amino acid residue of amino acid sequence solver the status of amino acid sequence solver the sequence solver the sequence sequence solver the sequence solver the sequence sequence solver the sequence sequence solver the sequenc				P=Proline, Q=Glutamine, R=Arginine,
residue of amino acid sequence Aspace of codon, /-possible nucleotide deletion, codon, /-possible nucleotide deletion, codon, /-possible nucleotide deletionsertion) Aspace of codon, /-possible nucleotide deletionsertion Aspace of codon, /-possible nucleotide deletionsertion Aspace of codon, /-possible nucleotide insertion in recodor insertion in the nucleotide insertion in the nucleotide i			residue of	S=Serine, T=Threonine, V=Valine,
Sequence			amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Apossible nucleotide insertion		amino acid	sequence	Codon, /=possible nucleotide deletion.
AASROCRISALRIYODVRILLALISMISDEREVICEVELIDTÜLFER FRSPSPSPSEDESSSSSSSSEDEELINERRASTKORMANTROCH TREDKPSAPIKPITTYTIGEDRYDYPOLIKUDLSSSSTSSPST STLEIOPSRSSSSSSSSSERKTYKAYKWEKTYSYNKUGE TSUNTGEADEGRACTSHKUNDAPSSSKRACUNTAMAQRNOOLPP BCCSKUTPREEDPTPSSNOOPGERISSHAACUNTAMAQRNOOLPP BCCSKUTPREEDPTPSSNOOPGERISSHAACUNTAMAQRNOOLPP BCCSKUTPREEDPTPSSNOOPGERISSHAACUNTAMAQRNOOLPP BCCSKUTPREEDPTPSSNOOPGERISSHAACUNTAMAQRNOOLPP BCCSKUTPREEDPTPSSNOOPGERISSHAACUNTAMAQRNOOLPP BCCSKUTPREEDPTPSSNOOPGERISSHAACUNTAMAQRNOOLPP BCCSKUTPREEDSLETICANNINGRIHPPRPHEASGINESGNOOP BTOSDDSEERSLETICANNINGRIHPPRHEASGINESGNOOP BTOSDDSEERSLETICANNINGRIHPPRHEASGNOOPGERISH AXSSPORTURALISSIACUNTAMACHACUNTAMACHACONIGHIEFDRAGRE AXSSPORTURALISSIACUNTAMACHACONIGHIEFDRAGRE AXSSPORTURALISSIACUNTAMACHACONIGHIEFDRAGRE AXSSPORTURALISSIACUNTAMACHACONIGHIEFDRAGRE AXSSPORTURALISSIACUNTAMACHACONIGHIEFDRAGRE AXSSPORTURALISSIACUNTAMACHACONIGHIEFDRAGRE AXSSPORTURALISSIACUNTAMACHACONIGHIEFDRAGRE AXSSPORTURALISSIACUNTAMACHACONIGHIEFDRAGRE AXIOANACHACHACONIGHIEFDRAGREACHACON		sequence		\=possible nucleotide insertion)
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DIMDEPPDGAPVKLSPELPPKKWNICMPUGGDLSUS SYTAQKSGQQCVAGHHTVULSQIQHGLQYGSHQGLLPSTGSU JPMHPSGCRMIDELNKTLAMTMQRLESSEQRVPCSTSYHSSGLHS GDGYTKAGPMGLPSIRQVPTVVIECDDINKENVPHSSDYSDSSCL YTREEEBEBBDDDSSLYTSSLAMKVCRKDSLAILSPENRPSKR ELEEKNILPROTDERHLELRQOIGTKL 6668 714 358 TLAUATGPAITLECHVCTSSINSLAMKVCRKDSLAILSPENRPSKR ELEEKNILPROTDERHLELRQOIGTKL LIGHLVKKDCAESCTPSYTLQGOVSSGTSSTQCCQEDLCNEKLH NAAPTRTALAHSALSLALASLAVILAPPL CALSVEQFFSWMSYNKALSYLATVPKYRIQATEIAKQGLLK KAKKEKSKNKKSKESERDEBENIKII IKSKINIKGGYGKPGLC LILPGIILAPPHLCSYTUWYCRWIYMFNIKGKGYGKPGLC LILLPGIILAPPHLCSYTUWYCRWIYMFNIKGKGYGKPGLC LILLPGIILAPPHLCSYTUWYCRWIYMFNIKGKGYGKPGLC LILLPGIILAPPHLCSYTUWYCRWIYMFNIKGKGYGKPGLC LILLPGIILAPPHLCSYTUWYCRWIYMFNIKGKGYGKPGLEELK KSMKNSKGOFDSLEDHOKETPLAFLEEKSGAPPTFGRSSPA VMQPPPGMPLDPPADIGPPPYPPGGPTAFLLEEKSGAPPTFGRSSPA VMQPPPGMPLDPADIGPPPYPPGGPTAFLLEEKSGAPPTFGRSSPA VMQPPPGMPLDPADIGPPPYPPGGPTAFLLEEKSGAPPTFGRSSPA TTVTV 6671 1 763 LPAEKPRSAPNMAGGRCGPQLTALLAAWTAAVAATAGPEEAALP PEQSAVQPMTASKMTLVMGCEWMLKPTAPWCDSCQOTDSEWEAF YRGPGIPEDLQNYILEKKMGSVSPFLTGWRSPASLTMSGMAGLFS AKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFPHAKDGIFRR YRGPGIPEDLQNYILEKKMGSVSPFLTGWRSPASLTMSGMAGLFS LIGHKWHLMYPTYTTGJIPAWGSVYPTVATLVFGLSMDLVL*V ISQCMWDPYRHVS*/RPSTNLGVHTAHTSEHLRL 6672 304 1089 APGSKVVQTVIGTLALSSYSTHLLLTCAGIAGIRAYEQLGQRAFG PAGKVVVATVICLINVGAMSSYLFIIKSELPLVIGTFLYMPEGE UVFLKGMLLILLCIALLSSYSIHLLLTCAGIAGIRAYEQLGQRAFG PAGKVVVATVICLINVGAMSSYLFIIKSELPLVIGTFLYMPEGE UVFLKGMLLILVSVLIILPLALMKHGVLGYTGGLSILTAVAKAN MFHS*LTGVLTGWP INAFAFVCHPGGAGFSITELCRAFOAGO WFHS*LTGVLTGWP INAFAFVCHPGGAGFSITELCRAFOAGO WFHS*LTGVLTGWP INAFAFVCHPGGAGFSITELCRAFOAGO WFHS*LTGVLTGWP INAFAFVCHPGGAGFSITELCRAFOAGO WFHS*LTGVLTGWP INAFAFVCHPGGAGFSITELCRAFOAGO SFSRV/SGSKGKMLIPRQLM*ARTNICCQGSSMAPAFSQ SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEGG*G*GLIND NAVPR*QG*KVWPSGOGRGS\WVLPLPYGEPLKLPGLIPG*NK SFSRV/SGSKGKMLIPRQLM*ARTNICCQGSSSSLGCPCVTQHPRFSDTGW ITWH*SAPTPPLKACPAPRSSDPCSSCLSCPCVTQHPRFSDTGW FGSAPCHSSCDFTRKGAAGGGPG WLPPGSPCHKLPGLGGAFSITELTHYPPT LTWH*SAPTPPLKACPAPRSSDPCSSCLSCPCVTQHPRFSDTGW LEFTYHANG				
SYTACKSGQGVAQHHHTVLPSQIQHGLQYGSHGQHLPSTTSSLH BMHPSGCRMIDELMKTLAMTQALSSEQRVPCSTSYHSSGLH GDGVTKAGPMGLPEIRQVPTVVIECDDNKENVPHESDYEDSSCL YTREEBERBEBDDDDSSLTSSLAMKVCKROSLAIKPSMCPSSCL YTREEBERBEBDDDDSSLTSSLAMKVCKROSLAIKPSMCPSKR ELEEKNILPRQTDEERLELRQQIGTKL 6668 714 358 TLAVATGPALTLRCHVCTSSSNCKHSVVCPASSRFCKTTNTVEP LIGKINLVKKDCASCTPSYTLQGVSGTSSTGCCQEDLCNEKLH NAAPTRTALAHSALSLALALSLLAVILAPSL 6669 459 1207 KDETTRKDYDYMLDHPEEYYSHYYHYYSRLAPKVDVRVVILVS KOMETRKDYDYMLDHPEEYYSHYYHYYSRLAPKVDVRVVILVS KOMETRKDYDYMLDHPEEYYSHYYHYYSRLAPKVDVRVVILVS KOMETRKDYDYMLDHPEEYYSHYYHYYSRLAPKVDVRVVILVS KAKKGKKNKKKKEEIRDBEENIIKNIIKSKIDIKGGYQKPQICD LLLPGIILAPHLCSYLWVCHIVSHNIKKSKYGEERHYIIR KSMKMSKSQFDSLEDHGKETFLKRELMIKENYEVYKQEQEELK KKLANDPRNKRYRRWMKNREGPGRITTVDD 6670 184 594 VART*GEARMSSEPPPPYPGGTTAFLLEEKSGAPPTFGRSSPA VMQPPFGMPLPPADIGPPYEPPGGTTAFLLEEKSGAPPTFGRSSPA VMQPPPGMPLPPADIGPPYEPPGGTTAFLLEEKSGAPPTFGRSSPA VMQPPFDMPLPPADIGPPYEPPGGTTAFLLEEKSGAPPTFGRSSPA TTVTV 1 763 LPAEKPRSAPNMAGGRCGPQITALLAAWIAAVAATAGPEEAALP PEQSRVQPMTASNWTLVMECEMMLKFYAPWCSCQQTDSEWEAF AKNGEILQISUGKVDVIQEPGLSGRPFVTLPAPFHAKNGIFRR YRGFGIFEDLONIILEKKMGSVEPLTGWKSPASJIMSGMAGLFS ISGKIWHLHNYFTVTLGIPAWCSYVPFVLATILVFGLSMDLVL*V ISQCNWDPYRHVS*/RPSTNLGWTHAHTSEHIRL GVIFFLALLCIALLSYSIHLLLTCAGIAGIRAYEGIGGRAFG PAGKVVATVICIALINGAMSSYIHIKSSELIVIGTFTLYMBGE DWFLKGNLLIILVSVLIILPLAMKHLGYIGYTSGLSITCMLFF LVSVIYKKFQLGLCYRATMKQQWSSEALVGTPQORAFG DWFLKGNLLIILVSVLIILPLAMKHLGYLGYTSGLSITCMLFF LVSVIYKKFQLGLCYRATMKQQWSSEALVGTPQORAFG ONFLKGNLLIILVSVLIILPLAMKHLGYLGYTSGLSITCMLFF LVSVIYKKFQLGLCYRATMKQQWSSEALVGTPQORAFG ONFLKGNLLIILVSVLIILPLAMKSHGNGGG*G*GINV WLCPCVAFHEGARPQAEEGGARWISLVSSPWIPPNP*HSSIGAE NAVPRP*QG*KVMPSGOERGSWVLPLPGEPLKLBGLE*NK SFSRV/SGSKGKMLIPRQLM*AS*R\TVFFFFGTWVFITM/PL ITWH*SAPTPLKACPAPRESDPCSSCLSCPCVTQHFFFSDTGW FGSAPCHSSCDFTRKGAAGGGG*GSSLACPCTGVVPTITM/PL ITWH*SAPTPTLKACPGDPGITKKGADGGG*G*GINV WLCPCVAFHEGARPQAEEGGARWISLVSSPWIPPNP*HSSIGAE NAVPRP*QG*KVABSGOERGSWVLPLEVGEPLKLBGLE*NK SFSRV/SGSKGKALIPRQLM*AS*R\TVFFFFGTWWPITM/PL ITWH*SAPTPTLKACPAPRESDPCSSCLSCPCVTQHFFFSDTGW FGSAPCHSSCDFTRTKGAAGGGG*G*GNAPFS				SWEEDSTEINGQSESSSQESEPALSEMEPVPMPRDPCSYEVLQPS
PMHPSGCRMIDELNKTLAMTMORLESSEGRVPCSTSYHSSGLHS GGGVTKAGPMGLPEIRQVPTVVIGCDDNKENVPHESDYEDSSCL YTREEEEEEBDDDDSSLYTSSLAMKVCKROSLAIKPSNRPSKR ELEKKNILPRGTDERRLEIRQQIGTKL 6668 714 358 TLAVATGPAITLECHVCTSSINCKHSVVCPASSRFCKTTNTVEP LRGNLVKKDCAESCTPSYTLQGVSSGTSSTQCCQEDLCNEKLH NAAPTRTALAHSALSLGLALSLLAVILAPSL 6669 459 1207 KDEETRKDYDYMLDHPESYYSHYYHYYSRRLAPKVDVRVVILVS VCAISVPCFFSWMSYNKAISYLATVPKYRIQATEIAKQQGLIK KAKKKKKNKKKSKESEIRDEENIKNIIKSHVAIVAKYRIQATEIAKQQGLIK KAKKKKKNKKKSKESEIRDEENIKNIIKSHVENYEVYKQGEEELK KKLANDPRWKKYRRWMKNEGPGRLITFVDD 6670 184 594 VARI*GEAAKWSSEPPPPYPGGPTAPILEEKSGAPFTGRSSPA VMQPPOMPLPPADAIGPPPYPGEPMPQDGGTIPPMSAGGTSPA VMQPPOMPLPPADAIGPPYPGEPMPQDGGTIPPMSAGGAT FFGSVVDWTASKWTLWEGEWMLKFYAPWCPSCQOTDSEWEAF AKNGELIQISVGRVDVICEGEMIKFYAPWCPSCQOTDSEWEAF AKNGELIQISVGRVDVICEGEMIKFYAPWCPSCQOTDSEWEAF AKNGELIQISVGRVDVICEGEMIKFYAPWCPSCQOTDSEWEAF AKNGELIQISVGRVDVICEGEMIKFYAPWCPSCQOTDSEWEAF AKNGELIQISVGRVDVICEGEMIKFYAPWCPSCQOTDSEWEAF AKNGELIQISVGRVDVICEGEMIKFYAPWCPSCQOTDSEWEAF AKNGELIQISVGRVDVICEGEMIKFYAPWCPSCQOTDSEWEAF AKNGELIQISVGRVDVICEGEMIKFYAPWCPSCQOTDSEWEAF AKNGELIQISVGRVDVICEGEMIKFYAPWCPSCQOTDSEWEAF AKNGELIQISVGRVDVICEGEMIKFYAPWCPSCQOTDSEWEAF AKNGELIQISVGRVDVICEGEMIKFYAPWCPSCQOTDSEWEAF AKNGELIQISVGRVDVICHANGAMSSYLFIIKSELBLUIGTFLYMPDEG DWFLKGNILLIIVSVLIILPLAMKHLGYLGYTTSGLSLTCHLFF LVSVIYKRFQLGLCYAFMKQDSERALVGTPOPBDSTTAAVKAQ MFHS*LTGVLTQWPIMAFAFVCHPGGAGPSITELCRAFOAQD 6673 1116 1963 LQTQTHHTHIGARVTHLGSHQLLANAGTHLCRQGSSSMAPAFSQ SVTCGSPCVRKQCSATKCLHIGACGSDLWARGRQG*G*GNN WLCPCVAFHRGARPQAEGGARNNSLVSSBWTPPBP*HSSIGAE NAVPBPPQ*G*VAPVGCSATKCLHIGACGSDLWARGRQG*G*GNN WLCPCVAFHRGARPQAEGGARNNSLVSSBWTPPBP*HSSIGAE NAVPBPPQ*G*VAPVGSATKCLHIGACGSDLWARGRQG*G*GNN WLCPCVAFHRGARPQAEGGARNNSLVSSBWTPPBP*HSSIGAE NAVPBPPQ*G*VAPVGCORCS*WVPLTHY*PPL TTH*SAPTPFLKACPAPRESDPCSSCLSCPCVTQHPRFSDTGW FGSGMCHSSCDFTRKGAAGGGG*GSNWVPLTHY*PPL TTH*SSAPTPFLKACPAPRESDPCSSCLSCPCVTQHPRFSDTGW FGSGMCHSSCDFTRKGAAGGGG*GNN WPLTHSGSPCHAGCHSCBCHVERORPPAPIQSIGSSL HVLFHSDGSKNPGGFG*TKKCGDPC*MVPITN*PPAY			1	DIMDGPDPGAPVKLPCLPVKLSPPLPPKKVMICMPVGGPDLSLV
GGGVTKAGFMGLPEIRQQVTVVIELDDKENVPHSEDVEDSSCL TTREEBEEBEDDDDDSSLYTSSLAMKVCRKDSLAIKPSNRPSKR ELEEKNILPRQTDEERLELRQQIGTKL TLAVATOPALTIRCHVCTSSSNCKHESVCPASSRFCKTTNTVEP LRGMIVKROLGSCTPSYTLQGQVSSGTSSTQCCCGDLCNEKLH NAAPTRTALARSALSIGLALSLLAVILAPSL CARRIGKNAKSCASCTPSYTLQGQVSSGTSTQCCCGDLCNEKLH NAAPTRTALARSALSIGLALSLLAVILAPSL VCAISVPQFFSWWNSYNKAISYLATVPRYRTQATEIAKQQCLK KAKEKGKKKKSKEEIRDEEENIINIKSKIDIKGGYQKPQICD LLLPQIILAPPHICSYIVWYWINFNIKGEVGEEBELVIIR KSMKNSKSQFDSLEDHQKETFIKRELWIKENYEVYKQEQEEELK KKLANDPRNKRYRRMKNEGPGRITFVDD VMQPPFGMPLPPADIGPPFYBPPGHPMPQPGFIPPHMSADGTYM VMQPPFGMPLPPADIGPPFYBPPGHPMPQPGFIPPHMSADGTYM PPGFYPPPGPIPPMSYYPPGPYTFGPYFGFGGHTATVLVPSGAA TTVTV TJVTV AFAKEKGINIKANTLVMEGEWMLKFYAPWCPSCQTDSEMEAF AKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHANGIFRR FGGIFEDLQNYILEKKGVEPLIGKRSPSITMSGMAGLFS ISGKIWHLMNYFTVTLGIPAWCSYVPFVIATLVEGLSMDLVL*V ISQCNWDPYSHVS*/RPSIUSVFNIANINGSGILGLAYAWAHT GVIFFLALLCIALLSSYSIHLLITAGAIAGIRAYEQLGQRAFG PAGKVVVATVICLHNVGAMSSYLFIIKSELPLVIGTFILVMPBEG DWFIKGKILIIIVSVIIILPLALMKHLGYLGYTSGLSLTCMLFF DWFIKGKILIIIVSVIIILPLALMKHLGYLGYTSGLSLTCMLFF LVSVIYKKFQLGLCYRATMKQQWESEALVGTPQPRDSTAAVKAQ MFHS*LTGVUTQWPIMAFAFVCHPGGAGPSITELCRAFQAQD AFGSKPVQTHTHGSRQTLAMAGTMLCTQGSSSMAPAFSQ SVTCGSSFCVVAFPREARPCCHPGGAGPSITELCRAFQAQD AFGSKVVATVATVCLHNVGAMSSYLFIIKSELPLVIGTFILVMPBEG SVTCGSSFCVVAFPREARPCCHPGGAGPSITELCRAFQAQD AFGSKFVQTHRHGGRAPQAEGGARWSLUSSPWIPPNP*KSSIGAE NAVPRP*QQ*KVNPSGOERGS*WVLPLPPVPCEPLKLEGLEG*CN WLCPCVAFHRGARPQAEGGGARWSLUSSPWIPPNP*KSSIGAE NAVPRP*QQ*KVNPSGOERGS*WVLPLPPVPCEPLKLEGLEG*CN WLCPCVAFHRGARPQAEGGGARWSLUSSPWIPPNP*HSSIGAE NAVPRP*QQ*KVNPSGOERGS*WVLPLPPVPCEPLKLEGLEG*CN FGSGVCCSCFTKGGAGGGTTKSCLSCCCVTQHPRFSDTGW FGSGCCFTKGGAGGCTTKACAGGGTTKACAGGG*CN FGSGCCFTTKGGAGGGTTKTCAGGGTTKACAGGG*CNSCLSCCCCVTQHPRFSDTGW FGGGCCFTTKGGAGGGTTTKACAGGGTTKACAGGGTTTKACAGGTTTKACAGGTTTKACAGGTTTKACAGGTTTCACTTTTTTTTTT		1	1	SITAQKSGQQGVAQHHHTVLPSQTQHQLQYGSHGQHLPSTTGSL
### TREEEBEEDDDDSSLYTSSLANKVCRKDSLAIKDSNRPSKR ELERNILIPROTDERRIELRQQIGTKL 6668 714 358 TLAVATGPALTLRCHVCTSSSNCKHSVVCPASSRFCKTTNTVEP LRGNLVKKDCAESCTPSYTLQQQVSSGTSSTQCCQEDLCNEKIH NAAPTRTALARSALSLIALSLAIVLAPSI 6669 459 1207 KDEETRKDYDVMLDBPEEYYSHYXHYYSRRLAPKVDVRVVILUS VCALSVPQFFSWWNSYNKAISYLATVPKYRIQATEIAKQQGLLK KAKKKGKNKKSKEEIRDBEENIIKNIIKSKTUKGEYGGEERLYTIR KSMKNSKSGFDSDLEDHQKETTLKRELWIKENIEVKYRQQGEEK KKLANDPRWKRYRRWKNEGPGRLTFVDD 184 594 VARI*GEAAKWSSEPPPFYPGGPTAFLLEEKSGAPPTGRSSPA VQCPPPGWPLPPADIGPPPYEPPGGPTAFLLEEKSGAPPTGRSSPA VQCPPPGWPLPPADIGPPPYEPPGGPTAFLLEEKSGAPPTGRSSPA YQCPPPGWPLPPADIGPPYEPPGPYTPGGPTAFLLEEKSGAPTGRSSPA YQCPPPGWPLPPADIGPPYEPPGFPTAFLLEEKSGAPTGRSSPA AKNGEILGISKGKUDVICPGGLGRFFVTTLPAPFHAKDGIFRR YRGGGIFPDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFS ISGKIWHLHNYFTVTLGIPARCSVYFVIATLVRGLSKDLVI-V ISQCNWDPYKHVS*/RSTNLGVHTAHTSEHLRL GVIPFLALLLCIALLSSYSIHLLTCAGLAGIRAYPAPHT GVIPFLALLLCIALLSSYSIHLLTCAGLAGIRAYPAPHT LVSVIYKKFQLGLCYNATWAGNSSYLFIIKSELJLUIGTFIYMDPEG DWFLKGNLLIIIVSVLIILPLALMKHGYLGYTSGLSLTCNLFF LVSVIYKKFQLGLCYNATWAGNSSPALTHLGYGSSMAPAFSQ WICCPCVAFHRGARPABEGGRRWNSLVSSPWIPPNP*RSSIGAE SVTCGFSPCVKQESATKCLHIGACGSDLWARGWEQG*G*GINN WLCPCVAFHRGARPABEGGRRWNSLVSSPWIPPNP*RSSIGAE SVTCGFSPCVKRGSSATKLHIGACGSDLWARGWEQG*G*G*SINN NAVPPP*OG*kVNPSCOROG*NO*WILDLEVPDGEPLKLPGLPO*NK SFSRV/SGSKGKWILPRQLM*AS*R\TPRPVPGTQWFFIT*/PL ITHH*SAPTPPLKACPAPRESDPCSCLSCPCVTQHPRFSDTGW SFSRV/SGSKGKWILPRQLM*AS*R\TPRPVPGTQWFFIT*/PL ITHH*SAPTPPLKACPAPRESDPCSCLSCPCVTQHPRFSDTGW FGAGHCHSSCD-FTRKGAAGGFG 6674 1 440 LEFDYMCQYDYVEVRDGDNRDGQIIKRVCGRRPAPIQSIGSSL HVLFFSUSSNNFDGFMAIYEEITACSSPCFHDGTVLLDKAGSSV KCACLAGYTGQCFCNLLEERERNCSDPG/WPSQWVEENRREPPAYQ KCACLAGYTGQCFCNLLEERERNCSDPG/WPSQWVEENRREPPAYQ KCACLAGYTGQCCFCNLLEERERNCSDPG/WPSQWVEENRREPPAYQ KCACLAGYTGQCCFCNLLEERERNCSDPG/WPSQWVEENRREPPAYQ KCACLAGYTGQCCFCNLLEERERNCSDPG/WPSQWVEENRREPPAYQ				PMHPSGCRMIDELNKTLAMTMQRLESSEQRVPCSTSYHSSGLHS
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VMQPPPGMPLPPADIGPPPYEPPGHPMPQPGFIPPHSADGTYM PPGFYPPPGPHPPMGYYPPGPYTPGPYPGGGHTATVLVPSGAA TTVTV LPAEKPRSAPNMAGGRCGPQLTALLAAWIAAVAATAGPEEAALP PEQSRVQPMTASNWTLVWEGEWMLKFYAPWCPSCQQTDSEWEAF AKNGEILQISVGKVDVIQEPGLSGRPFVTTLPAPPHAKDGIFRR YRGPGIFEDLQNYILEKKWQSVEPLTGWKSFASLITMSGMAGLFS ISGKIWHLHNYFTVLGIPAWCSYVFFVIATLVFGLSMDLVL*V ISQCNWDPPYRHVS*/RPSTNLGVHTAHTSEHLRL 6672 304 1089 APGSKPVQFMDFEGKTSFGMSVFNLSNAIMGSGILGLAYAMAHT GVIFFLALLLCTALLSSYSIHLLLTCAGIAGIRAYEQLGQRAFG PAGKVVVATVLCHNVGAMSSYLFIIKSELPLVIGTFLYMDPEG DWFLKGNLLIIVSVLIILPLALMKHLGYLGYTSGLSLTCMLFF LVSVIYKKFQLGLCYRATMKQQWESEALVGTPOPDSTAAVKAQ MFHS*-LTGVLTQWPIMAFAFVCHPGGAGFSITELCRAFQAQD 6673 1116 1963 LQIQTHHTHHGARVTHLGSHQLLANAGTMLCRQQSSMAPAFSQ SVTCGFSPCVKKQESATKCLHIGACGSDLWARGWEGC*G*GLNV WLCPCVAFHRGARPQAEGGGARWNSLVSSPWIPPNP*HSSIGAE NAVPRP*QG*KVNPSGGEROS.WVLPLPVEGEPLKLPGLPG**NK SFFSKV/SGSKCKWILPRQLM*AS*R\TPRFVPGTQWVPITW/PL ITWH*SAPTPPLKACPAPRESDPCSSCLSCPCVTQHPRFSDTGW FGAGHCHSSCDFTRKGAAGGPG 6674 1 440 LEFDYMCQYDYVEVRDGDNRDGQITKRVCGNERPAPIQSIGSSL HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY KCACLAGYTQQRCENLLEERNCSDPG/WPSQWVPENNRGPWAYQ	6670	184	594	
PPGFYPPPGPHPPMGYYPPGPYTPGPYPGPGGHTATVLVPSGAA TTVTV LPAEKPRSAPNMAGGRCGPQLTALLAAWIAAVAATAGPEEAALP PEQSRVQPMTASAWTLVMGGEWMLKFYAPWCPSCQQTDSEWEAF AKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFPHAKDGIFRR YRGPGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFS ISGKIWHLHNYFTVTLGIPAWCSYVFFVIATLVFGLSMDLVL*V ISQCNNDPPYRHVS*/RPSTNLGVHTAHTSEHLRL 6672 304 1089 APGSKPVQFMDFEGKTSFGMSVPNLSNAIMGSGILGLAYAMAHT GVIFFLALLCIALLSSYSIHLLLTCAGIAGIRAYPQLGQRAFG PAGKVVVATVICLHNVGAMSSYLFIIKSELPLVIGTFLYMDPEG DWFLKGNLLIIIVSVLIILPLAMKHLGYLGYTSGLSLTCMLFF LVSVIYKKFQLGLCYRATMKQQWESEALVGTPQDRDSTAAVKAQ MFHS*LTGVLTQWPIMAFAFVCHPGGAGPSITELCRAFQAQD MFHS*LTGVLTQWPIMAFAFVCHPGGAGPSITELCRAFQAQD MCCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPNP*HSSIGAE SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEGG*G*GLNV WLCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPNP*HSSIGAE NAVPRP*QG*KVNPSGOEROS\WVLPLPVPGEPLKLPGLPG*NK SFSRV/SGSKGKWILPRQLM*AS*R\TPRFVPGTQWVPITW/PL ITWH*SAPTPPLKACPAPRPSDPCSSCLSCPCVTQHPRFSDTGW FGAGHCHSSCDFTRKGAAGGPG 6674 1 440 LEFPYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY KCACLAGYTGQRCENLLEERNCSDPG/WPSQWVPENNRGPWAYQ		1	354	
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6673 1116 1963 LQIQTHHTHHGARVTHLGSHQLLANAGTMLCRQQSSSMAPAFSQ SVTCGFSPCVRKQESATKCLHIGACGSDLWARGWEQG+G*GLNV WLCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPNP*HSSIGAE NAVPRP*QG*KVNPSGOEROS\WVLPLPVPGEPLKLPGLPG*NK SFSRV/SGSKGKWILPRQLM*AS*R\TPRFVPGTQWVPITW/PL ITWH*SAPTPPLKACPAPRESDPCSSCLSCPCVTQHPRFSDTGW FGAGHCHSSCDFTRKGAAGGPG 1 440 LEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY KCACLAGYTGQRCENLLEERNCSDPG/WPSQWVPENNRGPWAYQ				DWFLKGHLLIIIVSVLIILPLALMKHLGYLGYTSGLSLTCMLFF
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SVTCGPSPCVRKQESATKCLHIGACGSDLWARGWEQG+G+GLNV WLCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPND+HSSIGAE NAVPRP+QG+KVNPSGOEROS\WVLPLPVPGEPLKLPGLPG+NK SFSRV/SGSKGKWILPRQLM+AS+R\TPRFVPGTQWVPITW/PL ITWH+SAPTPPLKACPAPRESDPCSSCLSCPCVTQHPRFSDTGW FGAGHCHSSCDFTRKGAAGGPG 6674 1 440 LEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY KCACLAGYTGQRCENLLEERNCSDPG/WPSQWVPENNRGPWAYQ	6677	1116	1035	mrhs-ligvliqwpimafafvchpggagpsitelcrafqaqd
WLCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPNP*HSSIGAE NAVPRP*QC*KVNPSGOEROS\WVLPLPVPGEPLKLPGLPG*NK SFSRV/SGSKGKWILPRQLM*AS*R\TPRFVPGTQWVPITW/PL ITWH*SAPTPPLKACPAPRESDPCSSCLSCPCVTQHPRFSDTGW FGAGHCHSSCDFTRKGAAGGPG 1 440 LEFDYMCQYDVVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY KCACLAGYTGQRCENLLEERNCSDPG/WPSQWVPENNRGPWAYQ	00/3		1263	LQIQIHHTHHGARVTHLGSHQLLANAGTMLCRQQSSSMAPAFSQ
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itwh*saptpplkacpapresdpcssclscpcvtqhprfsdtgw fgaghchsscdftrkgaaggpg 6674 1 440 LEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY KCACLAGYTGQRCENLLEERNCSDPG/WPSQWVPENNRGPWAYQ		·		SFSRV/SGSKGKWILPRQLM*AS*R\TPRFVPGTQWVPITW/PL
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HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY KCACLAGYTGQRCENLLEERNCSDPG/WPSQWVPENNRGPWAYQ				FGAGHCHSSCDFTRKGAAGGPG
KCACLAGYTGQRCENLLEERNCSDPG/WPSQWVPENNRGPWAYQ	6674	1	440	LEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL
I none a recommendation of the second				
PTPC*IGTRVAFFLT				PTPC*IGTRVAFFLT

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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Ì		amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	to first		S=Serine, T=Threonine, V=Valine,
}	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	residue of	amino acid	W=Tryptopnan, Y=Tyrosine, X=Onkhown,Scop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	1 -	\=possible nucleotide insertion)
	277	1678	GNWPTERMAFLDNPTIILAHIROSHVTSDDTGMCEMVLIDHDVD
6675	2"	1 10,0	LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR
ì			RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE
•	}	l	KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV
ĺ		1	KKSLKERPTSGRQSTLSVRLEQCPLQDRAFTNLTGRC BORGHT
1	1	1	GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ
1	1		YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF
İ	1	1	GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
Į.	1	1	KEILI.KAVKRRKGSOKVSGSRADGVFEEDSQIDIATVQDMLSSH
Į.	i	1	HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
ļ	1	1	ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ
1	1	1	KASTKFWIKQKPISIDSDLLCAC\DLAEE
l .			KASIAFWIAQAYISIDSDDDCAC DDAGAGOMAT TOURING
6676	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
1		1	LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR
l	1		RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE
			KKSLKEKPPISGKOSILSVRLEOCPLQLNNPFNEYSKFDGKGHV
1			GTTATKKIDVYLPLHSSODRLLPMTVVTMASARVQDLIGLICWQ
1]	1	YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF
1	1		GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
	1		KEILLKAVKRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH
	1	i	KEILLKAVKRKGSQKVSGSKADGVFEEDSQIDIII VQDII DVDADUDCI DBC
Į.	1	ł	HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
1	1	1	ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ
1	i	1	KASTKFWIKQKPISIDSDLLCAC\DLAEE
6677	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
00//	2,,	1	T.EKTHPPSMPGDSGSETOGSNGETOGYVYAQSVDITSSWDFGIR
1	1	1	RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE
		\	KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV
ì	ļ		GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ
i	l .	I	YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF
ĺ	1		YTSEGREPKLNDNVSAYCLHTAEDDGEVDTDFFFEDSANT TIME
	1	1	GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
	i	1	KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH
1	1	i	HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
i ·	1		ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ
1	1	l l	KASTKEWIKOKPISIDSDLLCAC\DLAEE
<u> </u>			GPSNQSSGSLSLIVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR
6678	221	865	PFPCSQLPMSQGCLWHLDCCCPWVPYIPGQQWRKGRQRMRN*QS
1	1	ļ	LLGSDQESVGLEDLCVFVNFLLHVLLGLFP*PHELFLLPVVDLG
1			PEGSDOES AGREDICAL AND THE ARMADIS EN LINE TARRESTE AND THE ARMADIS EN LINE TO SERVICE OF THE ARMADIS EN LIN
Į.	1	1	FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN
1	1	1.	HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP
6679		786	LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL
1 30,7	1		CCVCNKEUVNKENI, FNSI, NYD/SCSOEEKEGHAE*QNQNS \DFH
1	1		OEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAILDSRRFNYVV
1		i	RLLELIAKSQLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR
1		i	ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN
1		j.	EPPÖ LPILOPOT OBBOCCOT PEDECOMBODERADOLER COT'S
-			NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF
6680	1498	2951	PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVGSISEE
		Ī	P\RKNEPDTHCPRGEARPEV*HLPKPHSPGSEGAEIQTSA*ALP
ļ		}	/NOVSDPODM*GAEENGDORGGKEEAGEELHRSSSGLTAAPGF?
1		1	FUNDAL OTERGI.PSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS
1		l	MODSOAGI.PGWEAGI.VESPTHHIPALRPSGTNATGEAFPSTTCS
}			SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD
i			SGF \PAPPGFTGERFGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
l	1	1	POSOGRGPTOGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS
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	1	(ACCCPPGACCWGSOPRGSORCPRTYTHSPLGHGRAPCPRRCWH*
1			
	- }	į	WODDBCGDBTCCLBGTDAROAVSAPRTRSRPGIRTGRAAYGFIR
			WODPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR FOGGGGG

Predicted Predicted Amino acid segment containing signal peptide Notation Nota	SEO	Predicted	T =	<u> </u>
No:	_	beginning	Predicted end	
Cocation Corresponding Coffice Corresponding Coffice Corresponding Coffice Coffi		puglectide		Managaria Cacysteine Dalanartic laid n
to first amino acid serious cid amino acid amino acid sequence seq	"""	location		Grucamic Acid, Fephenvisianing Consists
to first and acid are did residue of and acid				n=nistidine. I=Isoleucine V-1,
residue of amino acid sequence some control of an acid sequence some control of an acid sequence some control of acid sequence	1	to first		Labeucine, Mamethionine Nabsparaging
residue of amino acid sequence Samino acid	1			F=FLO11Ne, O=Giutamine P=Argining
amino acid sequence 6681 1169 511 1169 511 1177YROGORA, Y-PYSTOEINE, X-UNKNOWN, *-SSCD Acodon, /-possible nucleotide deletion, -\ -\ -\ -\ -\ -\ -\ -\ -\ -\ -\ -\ -\				S=Serine, T=Threonine V-Valina
Sequence	1			W=Tryptophan, Y=Tyrosine, X=Unknown + Sh
This This			sequence	Codon, /=possible mucleotide deletion
### AUTOVITOTY OPENS REGISTA SKOLDEN SKOLPET AND SKOLP	6681			\=possible nucleotide insertion\
LOQUADELTARONAMISPHA VVITLINYSHE HIARALTRY LLOQRADELTARONAMISPHA VVITLINYSHE HIARALTRY TILLCENHKYI EVSNY / LANGAGRAPHCVITLIKYSHE HIARALTRY TILLCENHKYI EVSNY / LANGAGRAPHCVITLIKYSHE SPAPVITL SRPHLERID + TSVANGLYJVGOGGYAPHCVITLKYSHE SPAPVITL VARRIELIODFEMPTVCTITKYSHOOQYILLATGYVGRVUCVDT VARRIELIODFEMPTVCTITKYSHOOQYILLATGYVGRVUCVDT VOLSLKERE CLUSEVVYTER LISDYSKIV PLENDYSKIV PLENDYSKY PL		1 2209	211	INYIYYNQQQRAFHELK\EKLMSAPALGLPDLTKLFTLHVSERE
LUCIONINITE INSURITIVE CHILD TO SERVICE SERVICE STRATEGY TO TELCHEN PLANT ELLIPSE STRATEGY TO THE CONTROL OF TH	1	l .		MAINGVLTQTVGPWSRPGAYISKOLDGVSVGWDDCDDALAADAL
SEPNILADIP TSTUDELLIVESSYNTHENCESTRAPUTER S SEPNILADIP TSTUDELLIVESSYNTHENCESTRAPUTER S TULGGAMQUSSINEVKIYSLSGGKSLEWILSDRKKGRALOKKUVO VERRIELIOPEMPTVCTITKVSKOGYILATGYRKFRALOKKUVO VERRIELIOPEMPTVCTITKVSKOGYILATGYRKFRALOKKUVO VERRIELIOPEMPTVCTITKVSKOGYILATGYRKFRALOKKUVO VERRIELIOPEMPTVCTITKVSKOGYILATGYRKFRALOKKUVO VERRIELIOPEMPTVCTITKVSKOGYILATGYRKFRALOKKUVO PLOTDAABNIVCDINSVIRSPROBLILADISTRIVENDENTEHISOSC FYYKTRIPKGROFSYHPSCOLIFKVSHOOGALILATGYRKGALIVKOMINK NGKIFTSLEPEHDINDVCLYPKSGMLITANETTROVLLY DLASDKPLLVKOHOYGUP HISVEROGOYILATGYRKGRIVYTOVL VOLSLKFERCIDESVYTFEILIDDYSKIVTHOKOTILADISRIVKOMINK NGKIFTSLEPEHDINDVCLYPKSGMLITANETTROVLLY VOLSLKFERCIDESVYTFEILIDDYSKIVTHINDRYIEFHSGSC FYYKTRIPKFRODFSYHYPSCOLIFVUASSEVYKHALOKKOVD VOLSLKFERCIDESVYTFEILIDDYSKIVTHINDRYIEFHSGSC FYYKTRIPKFRODFSYHYPSCOLIFVUASSEVYKHALOKGOYIL DLASPORTOSTHIVSKOHOYGUP HISVEROGOYILATGYRKGRUCKOND VOLSLKFERCIDESVYTFEILIDDYSKIVTHINDRYIEFHSGSC FYYKTRIPKFRODFSYHYPSCOLIFVUASSEVYKHALOKGOYIL DLASPORTOSTHIVSKOHOYGUP HISVEROGOPOPOPOPORORIERRAP VOLSKAFTSLEPEHDINDVCLIFVUAGFCOSPCOPOPOPORORIERRAP DLASPORTOSTHIVSKOHOYGUP HISVEROMETHSOGGENERAP PLAGTITA PRA*MUGGGGGGGGGENERAP PLAGTITA PRA*MUGGGGGGGGGGENERAP PLAGTITA PRA*MUGGGGGGGGGGENERAP PLAGTITA PRA*MUGGGGGGGGGGGGGGGENERAP PLAGTITA PRA*MUGGGGGGGGGGGGGGGGAGENERAP PLAGTITA PRA*MUGGGGGGGGGGGGGGGGGGGAGENERAP RIVONNY KLIGDPFFSCHNIKELISDENGSNS*GSFINFDLIFTELET BCAVVUGSLANGTENNVKSLDCHI PALLOGLISPICTILKT BCAVVUGSLANGTENNVKSLDCHI PALLOGLISPICVITIL BCAVVUGSLANGTENNVKSLDCHI PALLOGLISPICVITIL BCAVVUGSLANGTENNVKSLDCHI PALLOGLISPICVITIL BCAVVUGSLANGTENNVKSLDCHI PALLOGLISPICVITIL BCAVVUGSLANGTENNVKSLDCHI PALLOGLISPICVITIL BCAVVUGSLANGTENNVKSLDCHI PALLOGLISPICVITIL BCAVVUGSLANGTENNVKSLDCHI PALLOGLISPICVITIL BCAVVUGSLANGTENNVKSLDCHI PALLOGLISPICVITIL BCAVVUGSLANGTENNVKSLDCHI PALLOGLISPICVITIL BCAVVUGSLANGTENNVKSLDCHI PALLOGLISPICVITIL BCAVVUGSLANGTENNVKSLDCHI PALLOGLISPICVITIL BCAVVUGSLANGTENNVKSLDCHI PALLOGLISPICVITIL BCAVTUGSLANGTENNICH PARRONICH PARRONICH PARRONICH BCAVTUGSLANGTENNICH PARRONICH PARRONICH PARRONICH BCAVTUGSLANGTENN	1			LAQUADELTLRONLNRKSPHA\VVTI.TNTVCUU+T TNART TOVO
1238	1	1	1	ILLCENPHETIEVSNT/LNPATIJI/PTPQDIPVINCE PRO DOLOGO
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TURISHMUSSINSVISISCKSIPPELISDRKRRALOKKOUD VRRHELIODPEMPTVCTTIKVSKOOYILARGYTYKRPKRCYDT VQLSLKFERCIDSEVVTFEILSDDYSKIVPLHNDRYIEFHSQSG FYYKTRIPKFGREDFSYHYPSCDLYPYGASSEVYRLNLEGGRYLN PLQTDAAENNVCDINSVHGLFATGTIEGRVEKOMPBIRTRKVGLL D\AP*TVSQQIQR*TSLPTISALKEN\GAITMAVGTTIGQVLLIV DLRSDKPLLVKAMCHYGGPILSDRSLVTHALDGRYLN NSGRIFTSLEFEHDLANDVCLYPNSGMLLTANETFKMGIYYIPVL GPAPRWCSFLDNITHELLEEMPSKAMGIYYIPVL GPAPRWCSFLDNITHELLEEMPSKAMGIYYIPVL GPAPRWCSFLDNITHELLEEMPSTFVTDPRNLLLSGAQLEAS RNIVQNYR 6685 258 1473 GLRGGTSRGRAGREPEFAAGULCVVAGFCQSPCPPGGRGRAPA PP\SGRRHA*RPA*WLGGPGGDSGGREEGG/GELQRAMESKMG ELPLDINIQEPRWDQSTFLGARFFTVTDPRNLLLSGAQLEAS RNIVQNYR KLLGDWFEGFCNKFELSDSSMS*QSPL\FDRLFDPDPQKVL GGVIDMKNAVIGNNKQKAMLIVLGAVPRLLYLLQGTSSTELKT ECAVVLGSLAMGTENNVKSLLDCHIIPALLGGLLSPDLKFIRA ECAVVLGSLAMGTENNVKSLLDCHIIPALLGGLLSPDLKFIRA ECAVVLGSLAMGTENNVKSLLDCHIIPALLGGLLSPDLKFIRA CLCLTYHTFTSPTVPEELLYTDATUPHLMALLGSRAYTDGYICQ IFSHCCKGPDHQTILFMRAVQNIAHLLTSLSYKVRMQALKCFS VLAFFENPQUSMTLVNVLVDGBLLPQIFVRHAQRKBILGERFWGA ETLAYLIEBDVSLQRIASITDHLIAMLADVFKYPSSVSAITDIK RDHDLKHAHELRQAFKLYASLGANDEDIRKKVSLGGRPPVL TASRGGVTST 6686 310 927 DSVTPDLAVDFTPKEWTLLDPTQRNLYRUMLENYKNLATVGY OLFKPSLISWLEGESRTVQRGDFQASEWKVQLKTKELALQODV LGEPTSSGIQMIGSINGGEVDVKQCGDVSSEHSCLKTHVNTQN VCOKNRCTRKKAP*LQLTLGKSFH*SIHT LGETSNRSRDRDRYRRNSSSSSGROVSSHVKYCKSNPSSSSSTT SSGMRREDRVHYRSPPLATGEPVNLSPERSKBRRHGSESS SRDHREDFFSLVKYGDFLTLKKKTSTSSTSSGNGTSSSSTT SSGMRREDRVHYRSPPLATGEPVNLSPERSKRIAPVPFCMQLAR INPROLEDFFSAGLGKVKVRDVRIISSTSTSSSSNORTSSSGSTTS SEPGLPR/SATARMATAAAPNNSIDLPSGSMGFISPAGGSL LYVGSLHFNTEDMIRGIFFFFISSSSTIPSLSLAPISFSISSSVSVSSSGTTS STVGSVVAAPTSSSSSTNINDAGLDFSTVITSVSGSLVPSRE VAVICOSKGRAGASGSASCSSRAKTIRATAASSMPGSTSSPSTC TMSLELEFLISJESPSLISSSSTNINDAGLDFSTVITSVSGSLVPSRE VAVICOSKGRAGASGSASCSSRAKKTRATAASSMPGSTSSPSTC TMSLELEFLISJESPSLISSSSTNINDAGDSPSDTGBLS TMSLELEFLISJESPSPLISKLIFTSGSSTAHCCONGRSDSPSDTBLS	6683	109	1228	GPAPRWCSFLDNLTEELEENPESNE
FYTKTRIPKFGRDFSYHTPSCDLYFVGASSEVTRILEGGRYLN PLQTDAABNNVCDINSVIGLEATGIEGRVECWDPRIRNRVGLL D\AP+TVSQQIQT*TSLPTISALKFN\GALTMAVGTTTGGVLLY DLRSDKPLLVKDRGYGLP IKSVHFQDSLDLILSADSRIVKMNKK NSGKIFTSLEFEHDLINDVCLYPNSGMLITANETTRWGIVLIV GPAPRWCSFLDNLTEELEBPESNE 6684 111 527 GLRGGTSRGRAGREPEFAAGVLCVVAGFCQSPCPPGGRGRAPA PP\SGRHA*PRA*WLGCPGGDSGGREEGGS\GELQRAMESKMG ELPLDINIQEPRWDQSTFLGRARRFFTVTDPRILLSGAQLEAS RNIVQNYR 6685 258 1473 KLLGDWFEGFCNKFELSDSENGSNS*QSPL\FDRLFDDPQKVL GGVIDMKNAVIGNNKQKANLIVIGAVPRLLYLLQGETSSTELKT ECAVULGSLAMGTENNVKSILDCHITPALLQCLLSPDLKFIEAC LRCLRTIFTSPVTPEELLYTAVIPHLMALLSERSYTOPSYLQ IFSHCCKGDHQTILRHGAVQNIAHLISLSSRYVGWADALKCFS KLLTYMCRAGA IRTDDNCIVLKTLPCLVRMCSKERLLEERVEGA ETLAYLIEPDVELQRTASITDHLIAMLADYFKYPSSVSAITDIK RLDHDLKHAHELRQAFKLYASIGANDEDIRKKVSLGEGRPPVL TASRGGVTST 181 927 DSVTPDLAVDFTPKENTLDPTQRNLYRDVMLENYKNLATVGY OLFKPSLISWLEQEESRTVQRGFGASEWKVQLKTKELALQQDV LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN SENTFECTLYGYDFITLHKRTGEQRSVFSHVWKKPSSLNPDV VQQKNRCTRKKKAF*LQLTLGKSFH*SIHT LAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST IGETSNSRDRDRYRRRNSGSSPGQCRHRSRSWDRRHGSESR SRDHREDRVHYRSPPLATGEPUNLISPERDATVVCMQLAAR IRPRDLEFFFSKAVGKNDVII ISDRNSRRSKGIAYVEFCEIQSV PLAIGLTGQRLLGVFIIVQASQAEKNRLAAMANNLOKGNGGPWR LYVGSLHFNITEDMLRGIFEPFGKV SEPCLIPK\SATARMATAAAPPNSSIDLPSDSCMGFISPAGSLD LPVSGCTGFFSLAGDSSSTRLSSLAFISFELSSEVSGSAGTTS STSVGSVVAAPTSSSSSTRIBDVAGLDFSTVITSVSGSLVTGRE VAVICGSKGAGAASGSASCSSRAGKTTEATAASSMPSGTSSFSFC TMSELELFSLIFSPAPLLISKLYTSGSIAYCDRSGLSC VAVICGSKGAGAASGSASCSSRAGKTTEATAASSMPSGTSSFSFC TMSELELFSLIFSPAPLLISKLYTSGSIAYCDRSGLSC VAVICGSKGAGAASGSASCSSRAGKTTEATAASSMPSGTSSFSFC TMSELELFSLIFSPAPLLISKLYTSGSIAYCDRSGLSC TMSELELFSLIFSPAPLLISKLYTSGSIAYCDRSGLSC TMSELELFSLIFSPAPLLISKLYTSGSIAYCDRSGLSC TMSELELFSLIFSPAPLLISKLYTSGSIAYCDRSGLSC TMSELELFSLIFSPAPLLISKLYTSGSIAYCDRSGRSFSFFC TMSELELFSLIFSPAPLLISKLYTSGSIAYCDRSGRSFSFFTC	j		1230	VDDDTHY
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DAP*TYSQUQIQR*TSLPIALKEN\CALITMAVGITTGQVLLY DAP*TYSQUQIQR*TSLPIALKEN\CALITMAVGITTGQVLLY DLRSDKPLLVKDHQYGLPIKSVHFQDSLDLILSADSRIVKMNNK NSKIFTSLEPEDLINDVCLYPINSKMLLTANETPKMGIYYIPVL GPAPRWCSFLDNLTEELEENPESNE GPAPRWCSFLDNLTEELEENPESNE GPAPRWCSFLDNLTEELEENPESNE GPAPRWCSFLDNLTEELEENPESNE GPAPRWCSFLDNLTEELEENPESNE EPLDINIQEPRWQGSTCVAGFCQSPCPPGGGREAPA PP\SGRRHA*RPA*WLGGPGGGGGEGGGGEGGGGGGAGARAESKMG ELPLDINIQEPRWQGSTFLGGRAEGGFEGGGGEGGAGAGAEASKMG ELPLDINIQEPRWQGSTFLGGRAEGGFEGGG/GELQRAMESKMG ELPLDINIQEPRWQGSTFLGGRAEGGFEGGG/GELQRAMESKMG ELPLDINIQEPRWQGSTFLGGRAEFFTVTDPPDPDFQKVL GGVIDMKNAVIGNKQKANLIVLGAVPPLLYILQQETSSTELKT ECAVULGSLAMGTERNVKSLLDCHIIPALLGGLLSPDLKFIEAC LRCLRTIFTSPVTPEELLYDATVIPHLMALLSRSRYTQSYICQ IFSHCCKGPDHQTILFNHGAVQNIAHLITSLSYKVMQALKCFS VLAFENPQVSMTLUNVLVUGGLLEQIFVKMLQRDKPIEMQLKFS VLAFENPQVSMTLUNVLVUGGLLEQIFVKMLQRDKPIEMQLKFS VLAFENPQVSMTLUNVLVUGGLLEQIFVKMLQRDKPIEMQLKGS ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSAITDIK RLDHDLKHAHELKQAPKLVASLGANDEDIRKKVSLGEGRPPVL TASRGGVTST DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY QLFKPSLISWLEQEESTVQRGGASEMKVQLKTKELAAQQDV LGEPTSGIQMIGSHNGGEVSHVVKXVSLEHGLKTKHLAAQQDV LGEPTSGIQMIGSHNGGEVSHVVKKYPSNTTSSTSNSGNETSGST LGETSNRSGRDREYTRRNSGSRSGRGCRHRSRSWDRHGSESR SRDHREDEVKKAFF*LQLTLGKFSH*SIHT GETSNRSGRDREYTRRNSGSRSGGCRHRSRSWDRRHGSESR SRDHREDEVKVRSPPLATGEPVONLSPEERDARTVFCMQLAAR LYVGSLHFNITSDMLRGIFEPPGKV LYVGSLHFNITSDMLRGIFEPPGKV LYVGSLHFNITSDMLRGIFEPPGKV SEPCLPR/SATARMATAAAPPNNSIDLPSDSGMGFISPAGDSLD LYSGSLHVBKSGSLAFISFSLSSVSVGSSAGTTS SEPCLPR/SATARMATAAAPPNNSIDLPSDSGMGFISPAGDSLD LYSGSLHVBKSGLAGASGSASCSSRAGKTTAATAASSMPSGTSSFSTC TMSSLEELFSJEPPAPLUSKJEFTSTSTSTC TMSSLEELFSJEPPAPLUSKJEFTSTSTSTC TMSSLEELFSJEPPAPLUSKJEFTSTSTSTC TMSSLEELFSJEPPAPLUSKJEFTSTSTSTC TMSSLEELFSJEPPAPLUSKJEFTSTSTSTC TMSSLEELFSJEPPAPLUSKJEFTSTSTSTC TMSSLEELFSJEPPAPLUSKJEFTSTSTSTC TMSSLEELFSJEPPAPLUSKJEFTSTSTSTC TMSSLEELFSJEPPAPLUSKJEFTSTSTSTC TMSSLEELFSJEPPAPLUSKJEFTE TATATATATATATATATASSMPSGTSSFSTFTC TMSSLEELFSJEPAPLUSKJEFT	1			FYVERTERSET
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ABBIRPLIV KONCYGIPIKSYHPOSEJOLI LISADSRI VKMNNK NSGRIFTSLEPEIDLINVCLYPHSGMLLTANETPKMGIYYI PVI GPAPRWCSFLDNI.TEBLEENPESNE 6684 111 527 GLRGGTSRGAGREPEFAACVLCVAGFCOSPCPFGGREAPA PPI\SGRRHA*RPA*WLGPGGDSGGREGGG /GELQRAMESKMG ELPLDINIQEPRWDQSTFLGRARHFFTVTDPRNLLLSGAQLEAS RNIVONYR 6685 258 1473 KLLGDNFEGFCNKFELSDSENGSNS*OSPL\FDRLPDPDPQKVL OGVIDMKNAVIGNNKQKANLIVIGAVPRLLYLLQGETSSTELKT ECAVVLGSLAMGTENNVKSLDCHIIPALLQGLSPDLKFIEAC LRCLRTIFTSPVTPEELLYTDATVIPHLMALLSRSRYTOBYICQ IFSHCCKGPDHQTILFNHGAVONIAHLLTSLSYKVRMQALKCFS VLAFENPQVSMTLVNVLVOGBELLPQIFVKNGSKERLEMEVEGA KCLTYMCRAGAIRTDDNCIVLKTLPCLVRMCSKERLEMEVEGA ETLAYLIEPDVELORIASITDHLIAMLADYFKYPSSVSAITDIK RIDDHDLKHAHELRQAAFKLYASIGANDEDIRKKVSLGEGRPPVL TASRQGVTST DSVTFDDLAVDFTKEWTLLDPTORNLYRDVMLENYKNLATVGY OLFKPSLISKLEQEESRTVQRGDFQASEWKVQLKTKELALQODV LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVTTON SENTFECYLYGVDFLITLHKKTSTEGRSVFSHWKKPSSLNPDV VQXMNCTKRKKAF*LQITLKKSTSTEGRSVFSHWKKPSSLNPDV VQCNNCTKRKKAF*LDITLGKSFH*SIHT 181 915 EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST IGETSNRSRDRDRYRRRNSRSRSPGRQCHHSRSRUDRRHGSESR SRDHREEDRYHYRSPDLATGEPVONLSPERDARTVFCMQLAR IRPROLEDFFSAVGKVRDVRIISDRNSRSKGIATVEFCEIGSV PLAIGLTGCRLLUVFIIVQASQARKRIAAAMANNLQKGNGGPMR LYVGSLHFNITEBMLKGIFEPFGKV LYVGSLHFNITEBMLKGIFEPFGKV AEVPHYPRVFHKCPDSCWRFKFQPIOLOPYILLSFSSEKPPISF SEPGLPR/SATARMATAAAPNSIDLPSDSGMGFISPAGBLD LPSDCGTGFFSLAGDSSTFLLSSLAFIFSELSSVSVGSSAGTTS STSUGSVVAAPTSSSSSSTRIDVAGLDFSTVITTSVGGSLVPSRE VAVICGSKGAGASGSASCSSRACKTTEATAASSMPSGTSSFPTC TMSSLEELFSLFSPSPATLISKLFTSSGSILVCONSGEPDTVBLIS	1			D\AP*TUSCOTOP+TICLEDTIEGRVECWDPRTRNRVGLL
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KLIGDNFEGFCNKFILISDSENGSNS*QSPL\FDRIFDPDPQKVL QGVIDMKNAVIGNIKQKANLIVIGAVPRILIYILQQETSSTELKT ECAVVLGSLAMGTENNVKSLLDCHI PALLQGLISPDLKFIEAC LRCLRTIFTSPVTPEELLYTDATVIPHLMALLSRSRYTQEYICQ IFSHCCKGPDHQTILIFNHGAVONIAHLLTSLSYKVRMQALKCFS VLAFENPQVSMTLVNVLVDGELLPQIFVKMLQRKPIEMQLTSA KCLTYMCRAGAIRTDDNCIVLKTIPCLVRMCSKERLLEERVEGA ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSAITDIK RLDHDLKHAHELRQAAFKLYASIGANDEDIRKKVSLGEGRPPVL TASRQGYTST DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY OLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV VCQKNRCTRKKAAF*LQLTLGKSFH*SIHT EAMLEAPYKKEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST IGETSNRSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRRHGSESR SRDHRREDRVHYRSPPLATGEPVDNLSPERDARTVFCMQLAAR IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV PLAIGLTGQRLLGVPIIVQASQAEKNRLAAMANNUQKGNGGPMR LYVGSLHFNITEDMLRGIFEPFGKV AEVPNYFNVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKDPISF SEPCLPR/SATARMATAAAPNSIDLPSDSGMGFISPAGDSLD LPSDGGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS STSVGSVVAAFTSSSSSSTINRDVAGLDFSTVITSVSGSLVPSRE VAVICGSKGAQASGSSASCSSRAGKTTEATAASSNPSGTSSFSTC TMSELEELFSLFSPAPILISKLFTSSGSIAICCONSGSPTSPILS				RNIVONYR
GGATUMRAN TIGNIKOKANLIVIGAVPRILIYLLQQETSSTELKT ECAVVIGSLAMGTENNVKSLLDCHI IPALLQGLISPILKFIEAC LRCLRTIFTSPVTPEELLYTDATVIPHLMALLSRSRYTOBYICQ IFSHCCKGPDHQTILFNHGAVQNIAHLLTSLSYKVRMQALKCFS VLAFENPQVSMTLVWVLVDGELLPQIFVKMLQRDKFIEMQLTSA KCLTYMCRAGAIRTDDNCIVLKTLPQLVRMCSKERLLEERVEGA KCLTYMCRAGAIRTDDNCIVLKTLPQLVRMCSKERLLEERVEGA KCLTYMCRAGAIRTDDNCIVLKTLPQLVRMCSKERLLEERVEGA KCLTYMCRAGAIRTDDNCIVLKTLPQLVRMCSKERLLEERVEGA KCLTYMCRAGAIRTDDNCIVLKTLPQLVRMCSKERLLEERVEGA KCLTYMCRAGAIRTDDNCIVLKTLPQLVRMCSKERLLEERVEGA KCLTYMCRAGAIRTDDNCIVLKTLPQLVRMCSKERLLEERVEGA KCLTYMCRAGAIRTDDNCIVLKTLPQLVRMCKSKELLEERVEGA KCLTYMCRAGAIRTDDNCIVLKTLPQLVRMCKVSLGEGRPPVL TASRQGVTST TASRQGVTST DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY QLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST IGETSNRSRDRDRYRRRNSRSRSGRQCCRHRSRSWDRRHGSESR SRDHRREDRVHYRSPPLATGEPVDNLSPEERDATTVFCMQLAAR IRPROLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV PLAIGLTGQRLLGVFIIVQASQAEKNRLAAMANNLQKGNGGPMR LYVGSLHFNITEDMLRGIFEPFGKV AEVPNYPRVFHKKPDSCWRFKFQPIQLQPYILLSFSSEKPPISF SEPCLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD LPSDGGTGFFSLAGDSSSTRLSSLAFISFSLSSVVGSSAGTTS STSVGSVVAAPTSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE VAVICGSKGAGASGSSSSCSSRAGKTTEATAASSMPSGTSSFSTC TMSELEELFSLIFSPAPLLSKLFTSSGSIAICCODSGPSDTGPLS	6685	258	1473	KLLGDNFEGFCNKFELSDSENGSNS*OSDI \ EDDI BODDO
LECAVIGSLAMGTERNVKSLLDCHITPALLQGLLSPDLKFIEAC LECLRTIFTSPVTPEELLYTDATVIPHLMALLSRSRYTQEYICQ IFSHCCKGPDHQTILFNHGAVQNIAHLLTSLSYKVRMQALKCFS VLAFENPQVSMTLVNVLVDGELLPQIFVKNLQRDKPIEMQLTSA KCLTYMCRAGAIRTDDNCIVLKTLPCLVRMCSKERLLEERVEGA ETLAYLIEPDVELQRIASITDHLIAMLADYFKYSSSVSAITDIK RLDHDLKHAHELRQAAFKLYASIGANDEDIRKKVSLGEGRPPVL TASRQGVTST DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY QLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV VCOKNRCTRKKKAF+LQLTLGKSFH*SIHT 1GETSNRSRDRDRYRRRNSRSSPGRQCRHRSRSWDRRIGSSSR SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGLAYVEFCEIQSV PLAIGLTGQRLLGVPIIVQASQAEKNRLAAMANNLQKGNGGPMR LYVGSLHFNITEDMLRGIFEPFGKV AEVENYPVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD LPSDGGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS STSVGSVVAAFTSSSSSTNRDVAGLDFSTVITTSVGGLVPSRE VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSPSTC TMSELEELFSLFSPAPLLSKLFTSSGSIAICCODSGREDTERLS		1		QGVIDMKNAVIGNNKOKANI, TVI GAVERIA VILL CORRECTED VILL
IECCKGPDHQTILFNHMALLSRSRYTQEYICQ IFSHCCKGPDHQTILFNHGAVQNIAHLLTSLSYKVRMQALKCFS VLAFENPQVSMTLVNVLVDGELLPQIFVKMLQRDKPIEMQLTSA KCLTYMCRAGAIRTDDNCIVLKTLPCLVRMCSKERLLEERVEGA ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSAITDIK RLDHDLKHAHBLRQAAFKLYASLGANDEDIRKKVSLGEGRPPVL TASRQGVTST DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY QLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN SENTFECTLYGVDFLTHHKKTSTEGQRSVFSHVWKKPSSLNPDV VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT EAMLEAPYKKEEDEQQRKEVKDYPSNTTSSTSNSGNETSGSST IGETSNRSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRHGSESR SRDHREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAVVEFCEIQSV PLAIGLTGQRLLGVFIIVQASQAEKNRLAAMANNLQKGNGGPMR LYVGSLHFNITEDMLRGIFEPFGKV AEVPNYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD LPSDGGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVGSLVPSRE VAVICGSKGAGASGSASCSSRAGKTTAAASSMPSGTSSFSTC TMSELEELFSLFSPAPLLSKLFTSSGSIAICCODSGPSDTGBLS		1		ECAVVEGSLAMGTENNVKSLLDCHTTPALLOCLLCDDIVETDAG
TISHCKCREPHGTI LFNHGAVQNIAHLLTSLSYKVRMQALKCFS VLAFENPQVSMTLVNVLVDGELLPQIFVKMLQRDKPIEMQLTSA KCLTYMCRAGAIRTDDNCIVLKTLPCLVRMCSKERLLEERVEGA ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSAITDIK RLDHDLKHAHELRQAAFKLYASLGANDEDIRKKVSLGEGRPPVL TASRQGVTST DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY QLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST IGETSNRSRDRDRYRRNSRSRSPGRQCRHRSRSWDRRHGSESR SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR IRPROLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV PLAIGLTGQRLLGVFIIVQASQAEKNRLAAMANNLQKGNGGPMR LYVGSLHFNITEDMLRGIFEPPGKV LYVGSLHFNITEDMLRGIFEPPGKV AEVENYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD LPSCGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS STSVGSVVAAPTSSSSSSTNRDVAGLDFSTVITSVGSLVPSRE VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSFSTC TMSELEELFSLFSPAPLLSKLFTSSGSIAICCODSGPSDTGBLS	1	1		LRCLRTIFTSPVTPEELLYTDATVIDHI.MALI.CDCDVTCDVTCC
KCLTYMCRAGAIRTDDNCIVLKTUPCLVRMCSKERLLEERVEGA ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSAITDIK RLDHDLKHAHELRQAAFKLYASIGANDEDIRKKVSLGEGRPPVL TASRQGVTST DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY QLFKPSLISGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN LGPPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN VCQKNRCTRKKKAF*LQLTIGKSFH*SIHT EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST IGETSNRSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRRHGSESR SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR IRPRDLEDFFSAVGKVRDVRIISDRNSRSKGIAVVEFCEIQSV PLAIGLTGQRLLGVFIIVQASQAEKNRLAAMANNLQKGNGGPMR LYVGSLHFNITEDMLRGIFEPFGKV AEVPNYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD LPSDCGTGFFSLAGDSSTRLSSLAFISFSLSSVSVGSSAGTTS STSVGSVVAAFTSSSSSSTRDVAGLDFSTVITSVSGSLVPSRE VANICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSPSTC TMSELEELFSLFSPAPLLISKLFTSSGSIAICCODSGPSDTYFILS		· i		IF SHCCKGPDHOTILFNHGAVONTAHLLTCLCVVIDMONT VODO
ACITYMCRAGATRTDDNCIVI,KTLPCLVRMCSKERLLEERVEGA ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSAITDIK RLDHDLKHAHELRQAAFKLYASIGANDEDIRKKVSLGEGRPPVL TASRQGVTST DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY QLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV VCQKNRCTKKKAF*LQLTLGKSFH*SIHT EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST IGETSNRSRDRDRYRRNSRSRSPGRQCRHRSRSWDRHGSESR SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV PLAIGLTGQRLLGVFIIVQASQAEKNRLAAMANNLQKGNGGPMR LYVGSLHFNITEDMLRGIFEPFGKV LYVGSLHFNITEDMLRGIFEPFGKV AEVPNYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF SEPGLPR/SATARMATAAAPPNSSIDLPSDSCMGFISPAGDSLD LPSDCGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSFSTC TMSELEELFSLFSPAPLLSKLFTSSGSIATCCODSGPSDTYPLS	- 1	ĺ		VLAFENPQVSMTLVNVLVDGELLDOT FURMI OPDVDTEMOT WOR
6686 310 927 DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY OLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT 6687 181 915 EAMLEAPPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST IGETSNRSRDRDRYRRNRSRSRSPGRQCRHRSRSWDRRHGSESR SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV PLAIGLTGQRLLGVFIIVQASQAEKNRJAAMANNLQKGNGGPMR LYVGSLHFNITEDMLRGIFEPFGKV 1 AEVENYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD LPSDGGTGFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVGGSLVPSRE VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSFSTC TMSELEELFSLFSPAPLLSKLFTSGSIAICCODSGEDTSPLS	į	į		ACLITIMCRAGAIRTDDNCIVI,KTI,PCI,VPMCSKEDI, EPRIMOR
6686 310 927 DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY QLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT EAMLEAPYKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST IGETSNRSRDDRDRYRRRNSRSRSPGQCRHRSRSWDRRHGSESR SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV PLAIGLTGQRLLGVFIIVQASQAEKNRLAAMANNLQKGNGGPMR LYVGSLHFNITEDMLRGIFEPFGKV AEVPNYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD LPSDGGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSFSTC TMSELEELFSLFSPAPLLSKLFTSGSIAICCODSGEDTSPLS				ELLAILLEPDVELORIASITDHTTAMTADVERVERSURATEDTIC
181 915 EAMLEAPYKKEEDEQQRKEVKKQYPSHTWKKNLATVGYV OLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDVV SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDVVCQKNRCTRKKKAF*LQLTLGKSFH*SIHT EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSSTIGETSNSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRRHGSESRSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRRHGSESRSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRRHGSESRSRDRDRYRRRDRDRYRRNSRSKGIAYVEFCEIQSVPLATGLTUQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITEDMLRGIFEPFGKV 1025 1 AEVPNYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISFSECHPYSRAGASGASGASCSSRAGKTEATAASSMPSGTSSFSTCTMSELEELFSLFSLSSSTRLDVAGLDFSTVITSVSGSLVPSREVAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSFSTCTMSELEELFSLFSPAPLLSKLFTSGSIAICCODSGESDTSPLS	ŀ			REDHOLKHAHELRQAAFKLYASLGANDEDIRKKVSLGEGPROVI
DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY QLKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN SENTFECYLYGVDFLITLHKKTSTGEQRSVFSHVWKKPSSLNPDV VCQKNRCTRKKKAF*LQLITLGKSFH*SIHT EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST IGETSNRSRDRDRYRRNSRSRSPGRQCRHRSRSWDRRHGSESR SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV PLAIGLTGCRLLGVPIIVQASQAEKNRLAAMANNLQKGNGGPMR LYVGSLHFNITEDMLRGIFEPFGKV AEVPNYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD LPSDCGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS STSVGSVVAAFTSSSSSSTNLDVAGLDFSTVITSVSGSLVPSRE VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSFSTC TMSELEELFSLFSPAPLLSKLFTSGSIAICCODSGESDTSPLS	6686	310		IASKQGVIST
G688 1025 1 AEVPNYPRVFHKCPDSCWFKFQPIQLOPYILLSFSSEKPPISF SEPGLPR/SLTSWLEQGESRTVQRGDFQASEWKVQLKTKELALQQDV LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST IGETSNRSRDRDRYRRNSRSRSPGRQCRHRSRSWDRRHGSESR SRDHRREDRVHYRS PPLATGEPVDNLSPEERDARTVFCMQLAAR IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV PLAIGLTGQRLLGVPIIVQASQAEKNRLAAMANNLQKGNGGPMR LYVGSLHFNITEDMLRGIFEPFGKV AEVPNYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD LPSDCGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS STSVGSVVAAPTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSSFSTC TMSELEELFSLFSPAPLLSKLFTSGSIAICCODSGEDTSPLS	- 1		927	DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGV
G688 1025 1 AEVENYPRVFHKCPDSCWFKFQPIQLQPYILLSFSSEKPPISF SEPGLER SERVER SUBSCRIPTION LPSDCGTGFFSLAGDSSTRLSSLAFISSSIALCCODSGSDTSPLS SENTFECYLYGVDFLTHKKTSTGEQRSVFSHVWKKPSSLNPDV VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST IGETSNRSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRRHGSESR SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV PLAIGLTGQRLLGVPIIVQASQAEKNRLAAMANNLQKGNGGPMR LYVGSLHFNITEDMLRGIFEPFGKV SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD LPSDCGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS STSVGSVVAAPTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE VAVICGSKGAGASGSASCSSRAGKTTEATAASSMPSGTSFSTC TMSELEELFSLFSPAPLLSKLFTSGSIAICCODSGEDTGPLS	J			ULFRPSLISWLEOEESRTVORGDFOASEWRYOLVTVEL ALCONIC
6687 181 915 EAMLEAPYKKEF*LQLTLGKSFH*SIHT CAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST IGETSNRSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRRHGSESR SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV PLAIGLTGQRLLGVPIIVQASQAEKNRLAAMANNLQKGNGGPMR LYVGSLHFNITEDMLRGIFEPFGKV AEVPNYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD LPSDCGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS STSVGSVVAAPTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE VAVICGSKGAGASGSASCSSRAGKTEATAASSMPSGTSFSTC TMSELEELFSLFSPAPLLSKLFTSGSIAICCODSGEDTGPLS	1	1	l	LGEPTSSGIQMIGSHNGGEVSDVKOCGDVSSEHSCI, KTURDTON
6687 181 915 EAMLEAPYKKEEDEQQKEVKKDYPSNTTSSTSNSGNETSGSST IGETSNRSRDRDRYRRNSRSRSPGRQCRHRSRSWDRRHGSESR SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV PLAIGLTGQRLLGVPIIVQASQABKNRIAAMANNLQKGNGGPMR LYVGSLHFNITEDMLRGIFEPFGKV 1 AEVENYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD LPSDGGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVGGSLVPSRE VAVICGSKGAGASGSASCSSRAGKTEATAASSMPSGTSFSTC TMSELEELFSLFSPAPLLSKLFTSGSIAICCODSGEDTGPLS	1	1	1	DENTI ECIDIGVOE L'ILHKKISTGEORSVESHVWKKDSSI MDDV
EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST IGETSNRSRDRDRYRRRNSRSPSPGQCRHRSRSWDRRHGSESR SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV PLAIGLIGCRLLSVPIIVQASQAEKNRLAAMANNLQKGNGGPMR LYVGSLHFNITEDMLRGIFEPFGKV AEVPNYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD LPSDGGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE VAVICGSKGAGASGSSASCSSRAGKTTEATAASSMPSGTSSFSTC TMSELEELFSLFSPAPLLSKLFTSGSIAICCODSGESDTSPLS	6687	181	015	VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT
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NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP 6696 1 782 PRVRGRVGERWAFLSVPAAMSSEMEPLLLAWSYFRRKFQLCAI LCTQMLEKSPYDQAAWILKARALTEMYVIDEIDVDQEGIAEMM. DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGF RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASM. TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALL LAALSTEHSQYKDWWK/DQIEKCYYRVGMYREAEKQIKSS 6697 3 782 PPLFLRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKD. IPQILTKVIDTLHRHKSEFFEKHGEBGVEAEKKAISLLSKLRN. LQTDKPFIPLVEKFVDTDIWNQYLEYQQSLLNESDGKSRWFYS. WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQE. IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVD. SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRC	1			EVHSLGQILPQDGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA
FRVRGRVGERWAFLSVPAAMSSEMEPLILAWSYFRRKFQLCAL LCTQMLEKSPYDQAAWILKARALTEMVYIDEIDVDQEGIAEMM DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGF RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASM TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALL LAALSTEHSQYKDWWK/DQIEKCYYRVGMYREAEKQIKSS FPLFLRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKD IPQILTKVIDTLHRHKSEFFEKHGEBGVEAEKKAISLLSKLRN LQTDKPFIPLVEKFVDTDIWNQYLEYQQSLLNESDGKSRWFYS WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQE IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVD SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK F698 F68 F54 VGSCACAGSCKCKECKCTSCKKSECRAFP F699 FFRENCH	1	1	1	LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV
FRVRGRVGERWAFLSVPAAMSSEMEPLILAWSYFRRKFQLCAL LCTQMLEKSPYDQAAWILKARALTEMVYIDEIDVDQEGIAEMM DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGF RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASM TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALL LAALSTEHSQYKDWWK/DQIEKCYYRVGMYREAEKQIKSS FPLFLRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKD IPQILTKVIDTLHRHKSEFFEKHGEBGVEAEKKAISLLSKLRN LQTDKPFIPLVEKFVDTDIWNQYLEYQQSLLNESDGKSRWFYS WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQE IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVD SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK F698 F68 F54 VGSCACAGSCKCKECKCTSCKKSECRAFP F699 FFRENCH	1	1		NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
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DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGF RPSTQSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASM TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALI LAALSTEHSQYKDWWK/DQIEKCYYRVGMYREAEKQIKSS 6697 3 782 PPLFLRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKD LPQILTKVIDTLHRHKSEFFEKHGEBGVEAEKKAISLLSKLRN LQTDKPFIPLVEKFVDTDIWNQYLBYQQSLLNESDGKSRWFYS WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQE IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVD SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRC		1		
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782 PPLFLRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKD IPQILTKVIDTLHRHKSEFFEKHGEBGVEAEKKAISLLSKLRN LQTDKPFIPLVEKFVDTDIWNQYLEYQQSLLNESDGKSRWFYS WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQE IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVD SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRC	1	1		
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LQTDKPFIPLVEKFVDTDIWNQYLEYQQSLLNESDGKSRWFYS WLLV\ECYMYRRIHEAI\IQSPPIDYFDVFKESKEQNFYGSQE: IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVD: SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK C6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP C699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVVVTSCKHPRC	009/	1 3	/82	4 ·
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IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVD. SL\SGGESSSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK 6698 668 754 VGSCACAGSCKCKECKCTSCKKSECRAFP 6699 325 492 EGELP/PARRVLPRAMTASAQPRGRRPGVGVVVTSCKHPRC		1		
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		668	754	
	6699	325	492	EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV
	Į.			LLGKRKGSVGAGSFQLPGGHLEFGETWEECAQRETWEEAALHLK
NVHFASVVNSFIEKENYHYVTILMKGEVDVTHDSEPKNVEPEK	I	1		NVHFASVVNSFIEKENYHYVTILMKGEVDVTHDSEPKNVEPEKN

ID beginning nucleotide (A=Alanine, C=Cysteine	
	ntaining signal peptide
	e, D=Aspartic Acid, E= ylalanine, G=Glycine,
location corresponding H=Histidine T=Tsoleug	ylalanine, G=Glycine,
1 1 -	
	ine, X=Unknown, *=Stop
1	
sequence \=possible nucleotide	
ESKRIIYNHAFFFQESKWSGG	
	LECGQGFSQQENGHCMDTNECIQ
;	RTNKKCSRGYEPNEDGTACVERT
LLLGLCNLLGK	
,	SPGLGPTSDKAAAPRTPKRRRLW
RQRQ/HPAMLCYVTRPDAVLMI	E VEVEAKANGEDCLNQVCRRLGI
IEVDYFGLQFTGSKGESLWLNI	LRNRISQQMDGLAPYRLKLRVKF
FVEPHLILQEQTRHIFFLHIKI	BALLAGHLLCSPEQAVELSALLA
QTKFGDYNONTAKYNYEELCAI	KELSSATLNSIVAKHKELEGTSQ
ASAEYQVLQIVSAMENYGIEWI	HSVRDSEGQKLLIGVGPEGISIC
	GKNVYLTVTKESGNSIVLLFKMI
· · · · · · · · · · · · · · · · · · ·	DTVTSAVMMQYSRDLKGHLASLF
t t	VYDHARRALYNAGVVDLVSRNNO
j (LSCOOTRVLOEKLRKLKEAMLCM
	SCAAQLQVGESAAHFCLQPHLSL
LLTGSRSOVLAR	
	FLFYRTCFCSMGLGSSCHLSLPK
	MAEEQEFTOLCKLPAOPSHPHCV
1 1	DSGILFDVVLVVEGRHIEAHRIL
	EEVLIHGVSYNAMCQILHFIYTS
	PEIIHFCCDFLMSWVDEENILDV
	KNFVAFSRTDKYROLPLEKVYSL
	HYSLEQVQADQISLHEPPKLLET
i i	PLRDTVASALMYHRNESLOPSLO
	TPS\MSSATRPKYLNPLLGEWKH
	YLIGGDNNVQGFRAESRCWRYDP
, , ,	
I I	VVGRYIYAVAGRDYHNDLNAVER
6703 45 1244 GVGPRAAMPLELELCPGRWVC	
	GGQHPCFIIAEIGONHQGDLDVA
	LEFKFNRKALERPYTSKHSWGKT
1 1 "	AEEVGIFFTASGMDEMAVEFLHE
	TAK/TRGWHSVLRDVCGVQLNDE
	VLDYSGRPMVISSGMQSMDTMKQ
	PLQPEDVNLRVISEYQKLFPDIP
	KVLERHITLDKTWKGSDHSASLE
1	TKQLLPCEMACNEKLGKSVVAKV
1 1 "	GYPPEDIFNLVGKKVLVTVEEDD
TIMEE	
	TRDPQDPSGRQGELSPVEDQREG
1	SAYTLIAPNINRRNBIQRIAEQE
	RLGGSQSETEVRQKQQLQLMQSK
	LQKMKAIQREKSNKLEEKKRLQE
1	QTEHRIARQKCLSKCCLWPTILN
MGQKLGLQ\DSLKAEENRKLQI	KMKDEQHQKSELLELKRQQQEQE
RAKIHQTEHRRVNNAFLDRLQC	GKSQPGGLEQSGGCWNMNSGNSW
GI	İ
6705 2 786 RLCRNSARVPCGWSASRSLGEG	GAGFIGPLRGPHPRAGGTGTSFT
SYKRKGGIMSTIAAFYGGKSII	LITVATGFLGKELMEKLFRTSPD
: : :	QILDSKLFEKVIEVRPNVHEKIR
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	LSCTNIIFHCAATVRFDDTLRHA
]	EAFIHISTAYSNCNLKHIDEVIY
VOI.NVTATROLIJIMASOMPKIJE	
	IDETTPKI.TRDWPMTYTYTK !
PCPVEPKKIIDSLEW\LDDAII	
PCPVEPKKIIDSLEW\LDDAI3 6706 130 531 PTHSSSHSQEMLGKLNMLRNL	OGHFCDITIRVQDKIFRAHKVVL
PCPVEPKKIIDSLEW\LDDAIJ 6706 130 531 FTHSSSSHSQEMLGKLNMLRNI AACSDFFRTKLVGQAEDENKN	OGHFCDITIRVQDKIFRAHKVVL VLDLHHVTVTGFIPLLEYAYTAT
PCPVEPKKIIDSLEW\LDDAIJ 6706 130 531 FTHSSSSHSQEMLGKLNMLRNI AACSDFFRTKLVGQAEDENKN	OGHFCDITIRVQDKIFRAHKVVL

	Durade at a 2	Predicted end	Thing said goment containing signal wants
SEQ	Predicted	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	location	Glutamic Acid, F=Phonylalanine, G=Glycine,
NO:	nucleotide		
[location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	to first	residue of	S=Serine, T=Threonine, V=Valine,
]	amino acid		
<u> </u>	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6707	2233	1343	YWSGIGYELQHFHWRKFHFEKKGPPSTCQBRLYESRSRWPCIS*
	ļ	i e	GMVVVGWTAVNGSW*GGQLRCVCVCTSHSSDSTRSSQRASKCHS
]	Į.	FFILSQ*KT*SSWENWVFAKYSRIYSYGHSCSKGRGD*DFK*NV
[]	1		SQAR*SRFCGLCNPCGHCGLDINLRGGSSPWTDKHSCVHNNLLC
			NRRVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEH
1]	TD*LPK*GPGYIQHPHCDSNILCILYNISFNLFSYSF*GVARYA
			C*RCHWYFEWLLYNHCGDILVACL*RRQL*SSQ
6708	115	1729	TVGSWSRSGRSPPVGRQLLLTGRGAQAAGSPQGGMALQVELVPT
] .	,	1	GEIIRVVHPHRPCKLALGSDGVRVTMESALTARDRVGVQDFVLL
			ENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDIQIYSR
!	ļ	1	QHMERYRGVSFYEEPPHLLAVADTVYRALRTERRDQAVMISVES
		1	GAGKTDATKRLLQLYAETCPAPQRGGAVRDRLLQSNPVLEAFGN
1	İ	1	AKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKSRVVHQ
		1	NHGERNFHIFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAK
1			VSSINDKSDWKVVRKALTVIDFTEDEVEDLLSIAASVLHLGNIH
ļ			FAANEESNAQVTTENQLKYLTRLLSVEGSTLREALTHRKIIAKG
.l		!	EELLSPLNLEQAAYARDALAKAVYSRTFTWLVGKINRSLASKDV
1			ESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFI
		1	ELTLKSEQEEYEAEGIAWEPVQYFNNKIICDLVEEKFKGII\SI
L		l	LDE\ECLRPGE
6709	3	894	PPHEHLFPSGERGPFSFLVSRRGLGPGKMGKKGKKEKKGRGAEK
į		1	TAAKMEKKVSKRSRKEEEDLEALIAHFQTLDAKRTQTVELPCPP
]			PSPRINASISVHPEKDELILFGGEYFNGQKTFLYNELYVYNIRK
1		1	DTWTKVDIPSPPPRRCAHQAVVVPQGGGQLWVFGGEFASPNGEQ
1			FYHYKDLWVLHLATKTWEQVKSTGGPSGRSGHRMVAWKRQLILF
			GGFHESTRDYIYYNDVYAFNLDTFTWSKLSPSGTGPTPRSGCQ\
			IPSLPRAASSVYGGYSKQRVKKDVDKGTRHSDMF
6710	158	980	RHKMTNYRVESSSGRAARKMRLALMGPAFIAAIGYIDPGNFATN
l			IQAGASFGYQLLWVVVWANLMAMLIQILSAKLGIATGKNLAEQI
		1	RDHYPRPVVWFYWVQABIIAMATDLAEFIGAAIGFKLILGVSLL
1			QGAVLTGIATFLILMLQRRGQKPLEKVIGGLLLFVAAAYIVELI
1		{	FSQPNLAQLGKGMVIPSLPTSEAVFLAAGVL\GATIMPHVI/YI
į.		1	WHSSLTQHLHGGSRQQRYSATKWDVAIAMTIAGFVNLAIMATAA
<u> </u>			SELNFYGHTGVA
6711	3	347	VTECKTMTCKMSQLERNI+TMINTLHHYSVKLGHPDTLIHGEFK
1		1	ELVRTDLHNILMKENKNDQAI*HIMEDLDTNAHMQIIFKELIML
L	 	<u> </u>	MAMLTWSYHDNMHDADYGPGQQHRPG PHGOKRTRYPOVRAPGQOPQAQLAMALCLKQVFAKDKTFRPRKR
6712	118	578	
		,	FEPGTQRFELYKKAQASLKSGLDLRSVVRLPPGENIDDWIAVHV
1			VDFFNRINLIYGTMAERCS*TSCPVMAGGPRYEYRWQDERQYRR PAKLSAPRYMALLMDWIESLI
6713	2485	3	QARGSDSEDGEFEIQAEDDARARKLGPGRPLPTFPTSECTSDVE
1		1	PDTREMVRAQNKKKKKSGGFQSMGLSYPVFKGIMKKGYKVPTPI
1			QRKTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAQTG
1	,		ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF
1		1	AALHENPDIIIATPGRLVHVAVEMSLKLQSVEYVVFDEADRLFE
1	I		MGFAEQLQEIIARI.PGGHQTVLFSATLPKLLVEFARAGLTEPVL
1		4	IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV
1		1	
			VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL
			VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA
			VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA
			VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ
			VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLBASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRLRL
			VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRLRL VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ
			VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA GVDGMLGRVPQSVVDEEDSGLQSTLBASLELRGLARVADNAQQQ YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRLRL

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Segrine, TeThreonine, Wevaline, amino acid amino acid asquence sequence ### ActivityCophan, YeTyrosine, X=Unknown, *=Stop Codon, /=possible nuclectide delction, /=possible nuclectide insertion) LSISGEGGAFEQQAGAVALDAMGEAQUITEGRAQLAMBERKER FVGOSOGENEKKERSERVISSYSKEDLYGAWERQKERPS- FVGOSOGENEKKERSERVISSYSKEDLYGAWERQKERPS- FVGOSOGENEKKERSERVISSYSKEDLYGAWERGKERPS- FVGOSOGENEKKERSERVISSYSKEDLYGAWERGKERPS- FVGOSOGENEKKERSERVISSYSKEDLYGAWERGKERPS- FVGOSOGENEKKERSERVISSYSKEDLYGAWERGKERPS- FVGOSOGENEKKERSERVISSYKEDLYGAWERGKERPS- FVGOSOGENEKKERKERSERVISSYSKEDLYGAWERGKERPS- FVGOSOGENEKKERKERSERVISSYSKEDLYGAWERGKERPS- FVGOSOGENEKKERKERSERVISSYSKEDLYGAWERGKERPS- FVGOSOGENEKKERKERSERVISSYSKEDLYGAWERGKERPS- FVGOSOGENEKKERSERVISSYSKEDLENDER- FVGOSOGENEKKERSERVISSERVISSKEDLENDER- FVGOSOGENEKKERSERVISSER	- 1	1	amino acid	P=Proline, Q=Glutamine, R=Arginine
amino acid sequence decode, "Fryptopham, "FTyptopham, "Ft	1	I '	1	S=Serine, T=Threonine, V=Valine.
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TOTS COGRET PEPDIMPO COPTITICITY COPTOATT PASCOPETY IN FEBLEPLIE BLEIGHNEH I WORTSTATULE KVADGS INNETDLAG PMVFCLAFGATLLLAGKIQ FGYVYGI SAIGCLGMFCLLINLMSMT GVSFGCVAS VLGYCLLEMILLSFAVIFSLQGMVGI LITAGI IG WCSFGASKIFISALAMEGOQLLVAY PCALLIX GVFALIS WF WCSFGASKIFISALAMEGOQLLVAY PCALLIX GVFALIS WF WCSFGASKIFISALAMEGOQLLVAY PCALLIX GVFALIS WF VIFTS ELIGLID PVQRIN LYDVILLS WCHIPF KHOVEL LEKEK KLDIMKTATO LEKEK LIKEK LEKEK LIKUK KLDIMKTATO LIKEK LIKEK LIKEK LIKEK LIKEK LIK	6717	115	896	
FEDEPPLLEELGINFDHIWCRTLTULHPLKVADGSINMETDLAG PMVFCLAFGATLILLAGRIQFGYVYGISAIGCLGMFCLLNLMSMT GVSFGCVASVLGYCLLFMILLSSFAVIFSLQGMVGILLAGNIG GVSFGCVASVLGYCLLFMILLSSFAVIFSLQGMVGILLAGNIG GVSFGCVASVLGYCLLFMILLSSFAVIFSLQGMVGILLAGNIG GVSFGCVASVLGYCLLFMILLSSFAVIFSLGGMVGILLAGNIG CVSFSASKIFISALAMEGQOLLVAYPCALLYGVFALLSVF VIFTFEELGLLDPVQRNLYQDVMLENFRKLLSVGHHEPFKHDVFL LEKEKKLDIMKTATQ 6719 1 691 PTRPEEODREDGECHWARMMPISGNLNCDPIAMSQCSSDHGCET DLDSDDDKIEKPNNFMKDSASQDNGLSRKISRKGVCSSDSDSSL QVVKKSSKARTGLLRITRRCAATAANKIKLMSDVEDVSLRNVHT RSKNGRKKPLHLAGTTAKKKLSDCEGSVNCEVPSEQVACEGKPP DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVAEEAGGTVVPQRGTMPGTKRFQHVIETPEFGKWELTGYEAA VPITEKSMPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQGPUKEPPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLTYTLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFFSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVVPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPP ILRSLTVPFSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADMQAITVALGEAVE LCCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPADPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGGFVAVVWDKSSPVEALKGLIVDKIQALT GREGGRVSVENIKQLLQSAHKESSFDIILSGLTUKGGTTLSRABEIL	1			YDYSQQGRFVPPDMMQPQOPYTGOIYOPTOAYTPASPOPFYCMM
### PMVFCLAFGATLILAGRIQFGYVYGISAIGCLGMFCLINLMSMT GVSFGCVASVLGYCLLFUILLSSPAVIFSLQGMVGIILTAGIIG MCSFSASKIFISALAMEGQQLLVAYPCALLYGVFALISVF 6718 290 599 KQSSTVPGTILPSLKWHINSGLCKFPETGGKMTFKEGLTFKDVA VIFTEEEIGLLDPVQRNLYQDVMLENFRNLLSVGHHPFKHDVFL LEKEKKLDIMKTATQ 6719 1 691 PTRPEGODEEGCKHKWEMBISGNLNCDPIAMSQCSSDHGCET DLDSDDDKIEKPNNFMKDSASQDNGLSRKISRKRVCSSDSDSSL QVVKKSSKARTGLLRITRRCAATAANKIKIMSDVEDVUSLENVHT RSKNGRKKPLHLACTTAKKKISDCEGSVHGEVPSEQYACEGKPP DPDSEGSTKVLSQALNGDSDSEDMINSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVABEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCNNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLIFSM SVVTLISE 6721 3 822 HEVABEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMRGLGGKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPPILSLSLTVPPSLRAPHYQITSLLFSM SVVTLISE 1 390 ENSKRYPQALPMAVLFILLFLCGTPQAADMMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAAPDFCK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW 6723 173 659 VCQYCTARMADFGISAGGFVAVWWDKSSPVEALKGLVDKKQALT GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	1			FEDEPPLLEELGINFDHIWQKTLTVLHPLKVADGSIMNETDLAG
GVSFGCVASVLGYCLLPMILLSSFAVLFSLQGMVGILLTAGIIG WCSFSASKIFISALAMBGQQLLVAYPCALLYGVFALISVF KQSSTVPGTILPSLKWHNSGLCKFPETGKWTTFKEGLTFKDVA VIFTEELGLIDPVQRNLYQDVMLENFRNLLSVGHHPFKHDVFL LEKERKLDIMKTATQ 6719 1 691 PTRPEEQDREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET DLDSDDDKIEKPNNFMNDSASQDNGLSRKISRKRVCSSDSDSSL QVVKKSSKARTGLLRITTRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDSEGSTXVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK RKSSSVTSG 6720 3 822 HEVAREAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFOEGQALSTY QRLYSESILTTMVQAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLYTLLAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGGMDCCMNNTAVFLP VLVGPNYSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAREAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLYTTLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGGMDCCMNNTAVFLP VPTEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGTSGRMAF LMSVSFNQLMKGLGQKPLYTTLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLIFSM SVVTLISE SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LDCDSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWGAVLGOHHNYQNW 6792CTARMADFGISAGGFVAVAVWDKSSFVEALKGLVDKLQALT GNEGRVSVENIKQLLQSAHKESSPDIILSGLVPGSTTLHSAEIL	1	1		PMVFCLAFGATLLLAGKIQFGYVYGISAIGCLGMFCLLNLMSMT
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ACSS TYPET LIPSTEM SELCK PETGGKMTT FKEGLITF KDVA VIFTERELGILIDPVORNLY QDVMLEN FRNIL SVGHHPF KHDVFL LEKEKKLDIMKTATQ 6719 1 691 PTRPEQOREDGKCHKMEMBP ISGNLNCDPIAMSQCSSDHGCET DLDSDDDKIEKPNNFMKDSASQDNGLSRKISK KRVCSSDBSSL QVVKKSSKARTGLIRITRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDSEGSTKVLSQALNGDSDSEDMINSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVABEAGGTVYPQRGTMFGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVELLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLLAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLUGFNPVSMARHFFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVABEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLLAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHFFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSMSKRTWQALPMAVLFLLLFLCGTPQAADNMQATYVALGRAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGOHNNYQNW 659 VCQYCTARMADFGISAGGFVAVVWDKSSPVEALKGLVDKLQALT GNEGGVSVENINGLLGSAHKESSFDIILSGLVPGSTTLHSABIL	6710	300		WCSFSASKIFISALAMEGOOLLVAYPCALLYGVFALISVF
6719 1 691 PTRPESQDREDKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET DLDSDDDKIERPNNFMKDSASQDNGLSRKISRKRVCSSDSDSSL QVVKKSSKARTGLLRITRRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK RKSSVTSSG 6720 3 822 HEVAREAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQBVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLYTYLLAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVLVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG LMSVSFNQLMKGLGQKPLTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADMMQAIYVALGERVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDFGK PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQCHINYONW 6723 173 659 VCQYCTARMADFGISAGQFVAVVWMKSSPVEALKGLVDKLQALT GNBGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	0'10	290	599	KQSSTVPGTILPSLKWHNSGLCKFPETGGKMTTFKEGLTFKDVA
6719 1 691 PTRPEEQDREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET DLDSDDDKIEKPNNFMKDSASQDNGLSRKISRKVCSSDSDSSL QVVKKSSKARTGLRITRRCAATAANKIKLMSDVEDVSLENVHIT RSKNGRKKPHILACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVABEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVABEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRLRLLGNYSLWLEGGSKEEDAGRYWCAVLGCHHNYQNW GRESRLRLLGNYSLWLEGGSKEEDAGRYWCAVLGCHHNYQNW VCQYCTARMADFGISAGQFVAVWWKSSPVEALKGLVDKLQALT GNAGGROSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL]			VIFTEELGLLDPVQRNLYQDVMLENFRNLLSVGHHPFKHDVFL
DLDSDDKLIEKPNNFMKDSASQDNGLSRKISRKRVCSSDSDSL QVVKKSSKARTGLLRITRRCAATAANKIKLMSDVEDVSLENVHT RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK RKSSSVTSSG 6720 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAP LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGGMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6721 3 822 HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM SVVTLISE 6722 1 390 RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQATYVALGEAVE LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK PGRESRRLLGNYSLWLEGSKEEDAGRYWCAVLAGHHNYQNW 6723 173 659 VCQYCTARMADFGISAGQFVAVWDKSSPVEALKGLVDKLQALT GNPGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL	6719		693	
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LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE GRGRLAPQNGGSSDAPAYRTPPSRQGRREWFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPWMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	1	.		AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRORN
GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAYSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	1	1		LGSIKPSSRSTKATSTIMAGDGRRAEAVREGWGVYVTPRADIDE
PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD				GRGRLAPQNGGSSDAPAYRTPPSROGRREVRFSDEPPEVVGDFE
PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD				PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSROPROPR
DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD		1		POETEEMKTRRTTRLOOOHSEOPPLOPSPVMTRRGLRDSHSSRE
YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG DKTTRSSQYIESFW 6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLBEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	1 1	1		DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPT.RVDR
6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWQDLDD		Į		YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDRSG
6733 613 1311 RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPBVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEBVAVHFTWEEWQDLDD				
KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	6733	613	1311	
QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD		ļ		KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDT.T
VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD		i		
LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	1			VLHRDAILAQEKSIGEDVYEKPISELDRLEEKOKETYRRMI.EOI.
LLEQEKAYQARKE 6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD	1 1			
6734 189 551 SAAMFPVFSGCFQELQEKNKSLELVSFERVAVHFTWEEWQDLDD				
	6734	189	551	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
-	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			TLNLRLSGGSKKQVFSGICHRSLVELQEVHLV
6735	280	558	KSRRAGVTKMSNPFLKQVFNKDKTFRPKRKFEPGTQRFELHKKA
ł			QASLNAGLDLRLAVQLPPGEDLNDWVAVHVVDFFNRVNLIYGTI XDGCT
6736	195	808	MNYELNFKREMPNIKSLGLTNLNFLLKRLSSVLPLITDYVYFEN
1			SSSNPYLIRRIEELNKTASGNVEAKVVCFYRRRDISNTLIMLAD
1	}		KHAKEIEBESETTVBADLTDKQKHQLKHRELFLSRQYESLPATH
	1		IRGKCSVALLNETESVLSYLDKEDTFFYSLVYDPSLKTLLADKG
Í			BIRVGPRYQADIPEMLLEGTFFCVFAVL
6737	150	1209	PVIMPLHFSPGDIVRPSCCVSSSPKLRRNAHSRLESYRPDTDLS
Į	1		REDTGCNLQHISDRENIDDLNMEFNPSDHPRASTIFLSKSQTDV
1	1		REKRKSLFINHHPPGQIARKYSSCSTIFLDDSTVSQPNLKYTIK
i	}		CVALAIYYHIKNRDPDGRMLLDIFDENLHPLSKSEVPPDYDKHN
1	1		PEQKQIYRFVRTLFSAAQLTAECAIVTLVYLERLLTYAEIDICP
1			ANWKRIVLGAILLASKVWDDQAVWNVDYCQILKDITVEDMNELE
			ROFLELLOFNINVPSSVYAKYYFDLRSLARANNLSFPLEPLSRE
6738			RAHKLEAISRLCEDKYKDLRRSARKRSASADNLTLPRWSPAIIS
6/38	148	653	CACAEQPARAEVGAATALPVRWASGEMAPSGSLAVPLAVLVLLL
] .		WGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
Ì	,		QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHC
6739	3	631	KDGEFRRYQGPRTKKDFINFISDKEWKSIEPVSSWF
0,35		631	SWPDMAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF
1			VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
İ	ł		REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ
			TABELNASTLMNYCAEIIASHWVSEVEGVNKAL
6740	3	631	SWPDMAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ
1	1		ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF
			VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
			REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ
			TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
6741	141	960	PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA
1			HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM
1			YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI
1			WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW
1			DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
			PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ
6742	141	960	LIPKTKIP
"'""	,**,	300	PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA
1			HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM
			VDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI
j			WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
			PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTO
1			LIPKTKIP
6743	1	412	MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK
Į.			ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN
I			FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL
i			FONIS
6744	95	1343	RTPARNRCAGCEVLSRFSSPNKASSPALQSAGGGLPAVRALRRD
1			RQKVSTVGYGMDEVEQDQHBARLKELFDSFDTTGTGSLGOEELT
1			DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT
			LSNEEHFQEPDCSLBAQPKYVRGGKRYGRRSLPEFQESVEEFPE
1			VTVIEPLDEEARPSHIPAGDCSEHWKTQRSEEYEAEGQLRFWNP
			DDLNASQSGSSPPQDWIEEKLQEVCEDLGITRDGHLNRKKLVSI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			CEQYGLQNVDGBMLEEVFHNLDPDGTMSVEDFFYGLFKNGKSLT
1			PSASTPYRQLKRHLSMQSFDESGRRTTTSSAMTSTIGFRVFSCL
ŀ	ì	1	DDGMGHASVERILDTWQEEGIENSQEILKALDFGLDGNINLTEL
i	· ·	Ì	TLALENELLVTKNSIHQACI
6745	1	588	TFRDQGWAQRRRWLLGCASWESWEAALAAGPGLPSSTARQQNNP
			AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERRRDP
1		i	ELPVTSFDCAVCLEVLHQPVRTRCGHVFCRSCIATSLKNNKWTC
J			PYCRAYLPSEGVPATDVAKRMKSEYKNCAECDTLVCLSEMRAHI
	ŀ	1	RTCOKYIDKYGPLOELEETA
6746	110	492	GATGAMAESAPARHRRKRRSTPLTSSTLPSQATEKSSYFQTTEI
3,40		""	SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCEKMA
ļ	1	ļ	VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN
6747	247	484	EAVTFKDVAVVFTEEELGLLDLAQRKLYRDVMLENFRNLLSVGH
0/4/	24/	101	QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC
6748	201	665	MTTFKEAVTFKDVAVVFTEEELGLLDPAQRKLYRDVMLENFRNL
0/48	1 201	003	LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIQIEMET
1	j	1	VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGDVPC
ĺ	}	İ	OIEARLSISXVQQXPYRCNECKQ
		719	RREVKGGDGVCPRARGSPQSQQFPSCAGGGEGLQQSGEALDGAM
6749	95	/19	SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFDKAF
			VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQSVSQ
ł	1		INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQLQL
1	1	I	HAKTGOSADSGTIKAKLSGPSVEELERELKAN
		<u> </u>	SCESRPGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRATMGT
6750	3	428	
1	Ī	j .	TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEAERMFTR EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSRRKS
i		Į.	
			RSSQLSSRR PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIV
6751	152	1417	PTKATEMAGASVKVAVKVKPFNSKEBISKUSKCIIQMISGSIIIIV NPKOPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGEEML
1	i		
ì	1	(QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLCEDL
İ	Į	1	FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVRE
1		ı	HPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETS
			SRSHAVFNIIFTQKRHDAETNITTEKVSKISLVDLAGSERADST
]		1.	GAKGTRLKEGANINKSLTTLGKVISALAEMDSGPNKNKKKKKTD
			FIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLR
			YADRAKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQGLGD
	<u> </u>		ITDMTNALVGMSPSSSLSALSSRNV
6752	24	1834	RNCVPPLGCYRSRVKFHSDIKMQYSHHCEHLLERLNKQREAGFL
1		1	CDCTIVIGEFQFKAHRNVLASFSEYFGAIYRSTSENNVFLDQSQ
			VKADGFQKLLEFIYTGTLNLDSWNVKEIHQAADYLKVEEVVTKC
1		1	KIKMEDFAFIANPSSTEISSITGNIELNQQTCLLTLRDYNNREK
1		1	SEVSTDLIQANPKQGALAKKSSQTKKKKKAFNSPKTGQNKTVQY
1	1		PSDILENASVELFLDANKLPTPVVEQVAQINDNSELELTSVVEN
		1	TFPAQDIVHTVTVKRKRGKSQPNCALKEHSMSNIASVKSPYEAE
1			NSGEELDQRYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVKPYV
1		1	CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAQKCQLVF
		1	HSRMHHGEEKPYKCDVCNLQFATSSNLKIHARKHSGEKPYVCDR
1	1	1	CGQRFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLITHSR
1			KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSSAED
Į			HTLSEQDSIQKSPLSETMDVKPSDMTLPLALPLGTEDHHMLLPV
1	Į.	1	TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY
6753	2	1305	VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEEKAS
1	~	1	PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPPAAG
	[SARGEKEMEGVALKHGPSLPQERKQAPSTRRDSAEPSSSRSVPV
Į.		1	AHPGPPPASSQTPAPEHDKAANKMPLAQKPALAPKPTSQTPPAS
1	t	j	THE STATES OF STREET STREET

SEQ	Predicted	Predicted end	l amino poid
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
Ì	location	corresponding	H=H1Stldine, I=Isoleucine K=Lycine
ł	corresponding to first	to first	L=Leucine, M=Methionine N-Asparaging
ļ	amino acid	amino acid	P=Proline, O=Glutamine, R=Arginine
	residue of	residue of	S=Serine, T=Threonine V=Valine
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-Ch
ļ	sequence	sequence	Codon, /=possible nucleotide deletion
			\=possible nucleotide insertion)
1		}	PLSKLSRPYLVELLSRRAGRPDPEPSEPSKEDQESSDRRPPSPP
			GPEERKGQKRDEEEEATERKPASPPLPATQQEKPSQTPEAGRKE KPMLQSRHSLDGSKLTEKVETAQPLWITLALQKQKGFREQQATR
1	ł		EERKQAREAKQAEKLSKENVSVSVQPGSSSVSRAGSLHKSTALP
			EEKRPETAVSRLERREQLKKANTLPTSVTVEISYSSPAAPLVKB
	<u></u>	ŀ	VSKRFSSPDDAPVSSEPAWLALAKRKAKAWSDCPLIIK
6754	2	413	FVRRRRRLGGPEVNTMSSLHKSRIADFQDVLKEPSIALEKLRE
•			LSFSGIPCEGGLRCLCWKILLNYLPLERASWTSILAKOPELVAO
			FLREMIIQPGIAKANMGVSREDVTFEDHPLNPNPDSRWNTYFKD
6755	200		NEVLL
1 0,33	298	1343	PGLQLQVALEADWFLDMPGGRRGPSRQQLSRSALPSLQTLVGGG
1			CGNGTGLRNRNGSAIGLPVPPITALITPGPVRHCOTPDLDVDGG
			LLFEFLFFIYLLVALFIQYINIYKTVWWYPYNHPASCTSLNFHL
ł			IDYHLAAFITVMLARRLVWALISEATKAGAASMIHYMVLISARL
			VLLTLCGWVLCWTLVNLFRSHSVLNLLFLGYPFGVYVPLCCFHQ DSRAHLLLTDYNYVVQHEAVEESASTVGGLAKSKDFLSLLLESL
ļ			KEQFNNATPIPTHSCPLSPDLIRNEVECLKADFNHRIKEVLFNS
			LFSAYYVAFLPLCFVKVSGYLTFMCFLDLCVNYINWVFLV
6756	180	754	IERALGSLPLSIPVSWGSLRTLKYQQQPLRPKVLLCQTRVQCHD
			LRSLQPQPPGLKQSFCLRVLGLOTGATTPGLRDLTCKPLTTLTP
	i		REAQKRKKRKEKESGMALTOGPLTFRDVATEFSOEFWKSLDDVO
			KALYWDVMLENYRNLVFLGKDNFALEVKICPRVFLYFLCCLSWE
6757	2	459	PFHYLTETEALLTHK
	"	459	NSRVEAPEAHSRESQGSDAMRKHLSWWWLATVCMLLFSHLSAVQ
			TRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRKLDID
L			FGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQ AANQGEFQKPDNKLHQQVLW
6758	1	1008	ASGPELPGRRFRDRAPWLPARLLRGVLAVWVSLSALGPGSFCRR
			RVPSLAQLGHSEAAPSPDDVRWSRVPDRCPEERDRAWPPPPPPPS
			LPPSFRRNMANNSPALTGNSOPOHOAAAAAAOOOOOCCCCCA TV
1			PAVSGKQGNVLPLWGNEKTMNLNPMILTNII.SSPVFKVOT.VET.V
	i		TYHEVVDEIYFKVTHVEPWEKGSRKTAGOTGMCGGVRGVGTGGI
1 1			VSTAFCLLYKLFTLKLTRKOVMGLITHTDSPVIRALGEMVIDVT
1 1	1		QPPTDLWDWFESFLDDEEDLDVKAGGGCVMTIGEMLRSFLTKLE
6759	1	513	WFSTLFPRIPVPVQKNIDQQIKTRPRKI
	ł		RKHNFHSLDGTSTRAFHPQTGLPLLSSPVPQRKTQSGCFDLDSS LLHLKSFSSRSPRPCLNIEDDPDIHEKPFLSSSAPPITSLSLLG
1 1		ļ	NFEESVLNYRFDPLGIVDGFTAEVGASGAFCPTHLTLPVEVSFY
<u> </u>	·		SVSDDNAPSPYMGVITLESLGKRGYRVPPSGTIQVVCVL
6760	239	606	VLSKKKGLSAEEKRTRMMEIFSETKDVFOLKDLEKTADVEKGTM
}			AMSVKEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKI.E
6761			VLESQLSEGSQKHASLQKSIEKAKIGRCETEERT
","	29	1733	ERTLRGLREVAAPSDVADAAVSRRGRCCCCLHCTOTOVAODCDS
] [I	SSSSVQRCELSLFQSLHTMTSKKLVNSVAGCADDALAGI.VACND
j	İ		NLQLLQGHRVALRSDLDSLKGRVALLSGGGSGHEPAHAGETGKG
1 1	1	1	MLTGVIAGAVFTSPAVGSILAAIRAVAQAGTVGTLLIVKNYTGD
1 1	İ		RLNFGLAREQARAEGIPVEMVVIGDDSAFTVLKKAGRRGLCGTV
		;	LIHKVAGALAEAGVGLEEIAKQVNVVTKAMGTLGVSLSSCSVPG SKPTEELSADEVELGLGINGBACVDBLYMATADEVELSSCSVPG
	. 1		SKPTFELSADEVELGLGIHGEAGVRRIKMATADEIVKLMLDHMT
1		Ì	NTTNASHVPVQPGSSVVMMVNNLGGLSFLELGIIADATVRSLEG RGVKIARALVGTFMSALEMPGISLTLLLVDEPLLKLIDAETTAA
			AWPNVAAVSITGRKRSRVAPAEPQEAPDSTAAGGSASKRMALVL
			ERVCSTLLGLEEHLNALDRAAGDGDCGTTHSRAARAIQEWLKEG
1	1	4	PPPASPAQLLSKLSVLLLEKMGGSSGALYGIFI.TAAAODI.KAKT
			SLPAWSAAMDAGLEAMQKYGKAAPGDRIMLDSLWAAGQRL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ľ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
- {	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-	amino acid	sequence	Codon, /=possible nucleotide deletion,
į	sequence	Jequence	\=possible nucleotide insertion)
6762	3	613	ASTISWRLCVAGAEARRPVPVAGERAGGGAMWFMYLLSWLSLFI
7,02) 3	623	
i			QVAFITLAVAAGLYYLAELIEEYTVATSRIIKYMIWFSTAVLIG
1	1		LYVFERFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCG
1	l.		LVVVNHYLAFQFFAEEYYPFSEVLAYFTFCLWIIPFAFFVSLSA GENVLPSTMQPGDDVVSNYFTKGKRGK
6763	2	760	SGPDFPGRRFRGCCCVRPPAGAGMELGGHWDMNSAPRLVSETAE
0,03	1 *	/60	
			RKQEQKTGTEAEAADSGAVGARRFLLCLYLGGFLDLFGVSMVVP
			LLSLHVKSLGASPTVAGIVGSSYGILQLFSSTLVGCWSDVVGRR
			SSLLACILLSALGYLLLGAATNVFLFVLARVPAGIFKHTLSISR
1	1		ALLSDVVPEKERPLVIGHFNTASGVGFILGPVVGGYITELEDGF
6764	80	42.0	YLTAFICFLVFILNAGLVWFFPRREAKPGSTE
5/6*	00	438	LKKMDTMMLSVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFR
	I		KKWQRTDHELGKYKDLLMKAETERSALDVKLKHARNQVDVEIKR
6765	3		RQRAEADCEKLERQIQLIREMLMCDTSGSIQ
1 8,63	3	550	ARYSRVDHFCRRCRAVARAPRFLLQFPSGPSRHFLAACVARWL
İ	ĺ		RGSVLVSEALSGSAMDGIVTEVAVGVKRGSDELLSGSVLSSPNS
1	!		NMSSMVVTANGNDSKKFKGEDKMDGAPSRVLHIRKLPGEVTETE
	1		VIALGLPFGKVTNILMLKGKNQAFLELATEEAAITNGNYYSAVT
6766			PHLRNQ
6/86	1	1287	EGGSFKASLTWLWPLGEMKLHCEVEVISRHLPALGLRNRGKGVR
			AVLSLCQQTSRSQPPVRAFLLISTLKDKRGTRYELRENIEQFFT
1	<u> </u>		KFVDEGKATVRLKEPPVDICLSKANSSSLKGFLSAMRLAHRGCN
}	1		VDTPVSTLTPVKTSEFENFKTKMVITSKKDYPLSKNFPYSLEHL
İ			QTSYCGLVRVDMRMLCLKSLRKLDLSHNHIKKLPATIGDLIHLQ
		•	ELNLNDNHLESFSVALCHSTLQKSLWSLDLSKNKIKALPVQFCQ
			LQELKNLKLDDNELIQFPCKIGQLINLRFLSAARNKLPFLPSEF
			RNLSLEYLDLFGNTFEQPKVLPVIKLQAPLTLLESSARTILHNR
			IPYGSHIIPFHLCQDLDTAKICVCGRFCLNSFIQGTTTMNLHSV
6767	336	919	AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI
0,0,	336	313	APMICLCSSDLQFRYKEAFLRDRGLQIGYCSVDDDPRMKHFLNV
į i			GRLQSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY
			RQPLPQPTCDPEQLGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT
· .			PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV
6768	2	363	NPDATEILHVKKKKALLL
"/"	-	303	PGSTISCYLLSEGSLPLCMQVACGEEKHRAPTMKTLRARFKKTE
[LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV
6769	284	306	ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL
6770	1	396	MSTPDFSTAENNQELANEVSCLKAMLTLMLQAMGQAD
"''		397	QRNYQVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK
1 1	l		ITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF
- 			KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS
6771	3	378	APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR
			WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM
1-6			QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG
6772	1	1400	AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA
1 1			CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG
1 1	į		P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL
1 1	1	İ	HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY
1 1	į	ļ	LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT
1 1	1		AVPILGYPRQLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT
] [İ	į	IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES
j l	!		QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK
] [1	ŀ	FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL
] [1	[TAPCNAACSCQPEHYSPVCGSDGLMYFSLCHAGCPAATETNVDG
	I		QKVYRDCSCIPQNLSSGFGHATAGKCTST
			

CEC	Predicted	n 42 - 12 4 - 2 4	
SEQ	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1 100:	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u></u>	sequence		\=possible nucleotide insertion)
6773	ļ	630	PWEAPKEHKYKAEEHTVVLTVTGEPCHFPFQYHRQLYHKCTHKG
1			RPGPQPWCATTPNFDQDQRWGYCLEPKKVKDHCSKHSPCQKGGT
1	1		CVNMPSGPHCLCPQHLTGNHCQKEKCFEPQLLRFFHKNEIWYRT
1		1	EQAAVARCQCKGPDAHCQRLASQACRTNPCLHGGRCLEVEGHRL
			CHCPVGYTGPFCDVGE*GSGASRRPAPRWDGLAR
6774	146	389	LTELSDQQYFLFFILSS/WVPTFLSMDVDGRVIKADSFSKIISS
1	•	1	GLRIGFLTGPKPLIERVILHIQVSTLHPSTFNQLMISQ
6775	104	614	TCPSQLRVLTARGGRRAPSPOLWTLVLALIEEKWRSHRILRMNS
		i	GRPETMENLPALYTIFQGEVAMVTDYGAFIKIPGCRKQGLVHRT
	1		HMSSCRVDKPSEIVDVGDKVWVKLIGREMKNDRIKVSLSMKVVN
	!		QGTGKDLDPNNV\SLSKKRGGGDPSRITLGRRSPLRLS
6776	3	1108	HERHERHEGALSQDALLRISIPLDSNMRPEKCRRFVHPOWOLLH
1	1	1100	LNGTFPNTSDADMEPCVDGWVYDRISFSSTIVTEWDLVCDSOSL
	1		TSVAKFVFMAGMMVGGILGGHLSDRFGRRFVLRWCYLQVAIVGT
1	Ì	ì	CAALAPIFLIYCSLRFLSGIAAMSLITNTIMLIAEWATHRFOAM
į.	1		GITLGMCPSGIAFMTLAGLAFAIRDWHILQLVVSVPYFVIFLTS
1	1	1	SWLLESARWLIINNKPEEGLKELRKAAHRSGMKNARDTLTLEIL
1	1		
		İ	KSTMKKELEAAQKKKPFLGERLHMPNICKRISLLPFTKFANFMA
1		1	YFGLNLHG/LKHLGNNVFLLQTLFGAV/TPPGQLVLHLGHWGSG
6777	550		RVSSRGRVNCLGLFVLQVW
. 6777	779	63	CFFHGPAWRDCEVRATFAKKQGQSGIISCIAFSPAQPLYACGSY
1	i	1	GRSLGLYAWDDGSPLALLGGHQGGITHLCFHPDGNRFFSGARKD
Į.	!	{	AELLCWDLRQSGYPLWSLGREVTTNQRIYFDLDPTGQFLVSGST
1		i .	SGAVSVWDTDGPGNDGKPEPVLSFLPQKDCTNGVSLHPSLPLLG
	1		HCLPVSVCFLSPTESGGRRRGAGPSLGSPRRHVHLECRLQLWWC
			CGGARLQHP++SPRARKGR
6778	311	805	IQSITDESRGSIRRKNPANTRLRLNVP\EBTAGDSE/ERSPEEB
1	ł	ł	VQADPRIRSASPKCPTSSPFPKGRSPEGEGET\DPEKVHFHPGP
		ŀ	KDKSVAEKN\KGP\SPVSSEGIKDFFSMKPEWENLNQSNVRRMH
			T\AVRLNEVIVKKSRDAKLVLLNMPGPPRNRNGDENY
6779	2	535	RALRROPRLLAANGIEPESMAISEPIKGSRKPCVNKEELALKKP
1	İ		MAKCAWKGPREPPQDARAEAESPGGASESDQDGGHESPPKKKAV
	ł	•	AWVSAKNPAPMRKKKKVSLGPVSYVLVDSEDGRKKPVMPKKGPG
1	İ	l	SRREASDQKAPRGQQPAEATASTSRGPKAKPEGSPRRATNESRK
			V
6780	3	403	HEVNDNKPEININLMSPGKEEISYIFEGDPIDTFVALVRVQDKD
1		[SGLNGEIVCKLHGHGHFKLQKTYENNYLILTNATLDREKRSEYS
1	}		LTVIAEDRGTPSLSTVKHFTVQINDINDNPPHFQRSRYEFVISE
		·	K
6781	1	1269	APTRPVFPTLQDLSSSKEPSNSLNLPHSNELCSSLVHPBLSEVS
1	1		SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT
1	l		SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI
}			TPVFINSSSIIQVMKGSQPSTIPAAPLTTNSGLMPPSVAVVGPL
1	i		HIPONIKESSAPVPPNALSSSPAPNIQTGRPLVLSSRATPVOLP
	}		SPPCTSSPVVPSHPPVQQVKELNPDEASPQVNTSADQNTLPSSQ
1 .	ļ		STTMVSPLLTNSPGSSGNRRSPVSSSKGKGKVDKIGOILLTKAC
	ł		KKVTGSLEKGEEQYGADGETEGQGLDTTAPGLMGTEQLSTELDS
1		Ì	KTPTPPAPTLLKMTSSPVGPGTASAGPSLPGGALPTSVRSIVTT
!	!		LVPSELISAVPTTKSNHGGIASESLAG
6782	3	1327	RKPTVIRIPAKPGKCLHEDPQSPPPLPAEKPIGNTFSTVSGKLS
	_		NVERTRNLESNHPGQTGGFVRVPPRLPPRPVNGKTIPTQQPPTK
			VPPERPPPPKLSATRRSNKKLPFNRSSSDMDLQKKQSNLATGLS
			<u> </u>
l l			KAKSQVFKNQDPVLPPRPKPGHPLYSKYMLSVPHGIANEDIVSQ
1	1		NPGELSCKRGDVLVMLKQTENNYLBCQKGEDTGRVHLSQMKLIT
L	L		PLDEHLRSRPNPFSPPKAPSHAQKPVDSGAPHAVVLHDFPAEQV

			, <u>, , , , , , , , , , , , , , , , , , </u>
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
į.	sequence	bequence	\=possible nucleotide insertion)
<u> </u>	sequence		DDLNLTSGEIVYLLEKIDTDWYRGNCRNOIGIFPANYVKVIIDI
}			
	į		PEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
ł		ļ	LKEYVNEEWARGEVRGRTGIFPLNFVEPVEDYPTSGANVLSTKV
į	[1	PLKTKKEDSGSNSQVNSLPAEWCEALHSFTAETSDDLSFKRGDR
İ		1	ļī
6783	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
1	ļ	1	TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLQTSSKV'I
}	ì		GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
ļ	į.	1	LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
1	1		
1	1	l	PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
1	1	1	QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
1	i	1	PQKLAFMVSLGLVTHDHLEEIQSKRQERKRRTTANPVYSGAVFE
}	j	J	PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
!	l	İ	SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC
ĺ		l	RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK
1		1	KEEAIPWPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ
		į	LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH
Į.		Ì	GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSQSCT
		į.	ANCNOGEETK
6784	3	1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
]	1	1	TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLOTSSKVT
1	1	1	GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
1	j.	}	LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
ţ	1	1	PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
İ	1	t .	QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
		į.	POKLAFMVSLGLVTHDHLREIQSKRQERKRRTTANPVYSGAVFE
1	· ·	l	PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
ł	Ĭ		SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC
	1	1	RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK
1		1	KEEAIPWPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ
1	1	1	
1		1	LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH
İ	İ	1	GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSQSCT
L			ANCNQGEETK
6785	1.	528	LGNTVLHYCSMYSKPECLKLLLRSKPTVDIVNQAGETALDIAKR
1		1	LKATQCEDLLSQAKSGKFNPHVHVEYEWNLRQEEIDESDDDLDD
1	ł	l .	KPSPVKKERSPRPQSFCHSSSISPQDKLALPGFSTPRDKQRLSY
1	1		GAFTNOIFVSTSTDSPTSPTTEAPPLPPRNAGKGPTGPPITPHR
6786	1820	1397	RSPKVLVLAPTRELANHVSRDFKDI\TRKLTVARFYGGTSYQSQ
1		1	INHIRNGIDILVGTPGRIKDHLQSGRLDLSKLRHVVLDEVDQML
	Ī		DLGFAEOVEDIIHESYKTDSEDNPOTLLFSATCPQWVYTVA\KK
	1	1	YMKSRYEQVDLDGKMTQKAATTVEHLAIQCHWSQRPAVIGDVLQ
1	1	l .	
1	Į.		VYSGSEGRAIIFCETKKNVTEMAMNPHIKQNAQCLHGDIAQSQR
i	1	}	EITLKGFREGSFKVLVATNVAARGLDIPEVDLVIQSSPPQDVES
1		1	YIHRSGRTGRAGRTGICICFYQPRERGQLRYVEQKAGITFKRVG
1	1		VPSTMDLVKSKSMDAIRSLASVSYAAVDFFRPSAQRLIEEKGAV
1	1	I	DALAAALAHISGASSFEPRSLITSDKGFVTMTLESLEEIQDVSC
1	i		AWKELNRKLSSNAVSQITRMCLLKGNMGVCFDVPTTESERLQAE
1	į.		WHDSDWILSVPAKLPEIEEYYDGNTSSNSRQRSGWSSGRSGRSG
1	1		
I	t		RSGGRSGRSGRQSRQGSRSGSRQDGRRRSGNRNRSRSGGHKRS
1	1		FD+VFYHLVDFLSDFLVDSVYLTGRQIDHLTGLTGLIDHLTSHS
L			SVWN
6787	2646	2270	PSSFPKNVPLEELEEPPK*KRSGLGSLTPKSQIQNGP*PQTFFF
1			FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGIIGTCHHAWLI
1	}	1	LVFLVEMGFHHVGQAGLKLLTL\VIHPPWPPKVLGLQT
6788	16	936	GGTVDLR\DMLAVSVLAAVRGGR/ATVRRVRESNVLHEKSKGKT
1	1) 30	REGAEDKMTSGDVLSNRKMFYLLKTAFPSVQINTEEHVD\ELDQ
1	1	I	WEGNERWITEGO A PONTWEIT TROUTER OA A THITTEN A PERIOD

SEQ	Predicted	Predicted end	I mino acid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ĺ	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Truntonhan V=Truncing V Value
į	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			EVILWGS*DS*GYPKGK*LLPKEVPSR/RVLLSGLTPLDATQE\
			FTEDLSK\YVTTMVCVAVNGKPMLGVIHKPFSEYTAWAMVDGGS
			NVKARSSYNEKTPRIVVSRSHSGMVKQVALQTFGNQTTIIPAGG
1	1	,	AGYKVLALLDVPDKSQEKADLYIHVTYIKKWDICAGNAILKALG
[GHMTTLSGEEISYTGSDGIEGGLLASIRMNHQALVRKLPDLEKT
L	1		GHK
6789	2	678	GNGINVLKIAPESAIKFMAYEQIKRLVW**PGDS*GF/YERLVA
ļ	1	j	GSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMLDCARRILARE
-			GVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSAD
	l i		PGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVT
	i i		MSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLKI
			TLGVOSR
6790	2	4068	APPAGRRRMQAAPRAGCGAALLLWIVSSCLCRAWTAPSTSQKCD
1	[i		EPLVSGLPHVAFSSSSISGSYSPGYAKINKRGGAGGWSPSDSD
	[]		HYQWLQVDFGNRKQISAIATQGRYSSSDWVTQYRMLYSDTGRNW
			KPYHQDGNIWAFPGNINSDGVVRHELQHPIIARYVRIVPLDWNG
			EGRIGLRIEVYGCSYWADVINFDGHVVLPYRFRNKKMKTT.KDVT
i	[ALNFKTSESEGVILHGEGQQGDYITLELKKAKLVLSLNLGSNOL
1	j j		GPIYGHTSVMTGSLLDDHHWHSVVIEROGRSINLTLDRSMOHER
ł			TNGEPDYLDLDYEITFGGIPFSGKPSSSSRKNFKGCMESINYNG
1	İ		VNITDLARRKKLEPSNVGNLSFSCVEPYTVPVFFNATSYLEVDC
1			RLNQDLFSVSFQFRTWNPNGLLVFSHFADNLGNVEIDLTESKVG
1			VHINITQTKMSQIDISSGSGLNDGQWHEVRFLAKENFATT.TTDG
}			DEASAVRTNSPLQVKTGEKYFFGGFLNQMNNSSHSVLQPSFQGC
1			MQLIQVDDQLVNLYEVAQRKPGSFANVSIDMCAIIDRCVPNHCE
1			HGGKCSQTWDSFKCTCDETGYSGATCHNSIYEPSCEAYKHLGQT
1 1	1		SNYYWIDPDGSGPLGPLKVYCNMTEDKVWTIVSHDLQMQTPVVG
1	į		YNPEKYSVTQLVYSASMDQISAITDSAEYCEQYVSYFCKMSRLL
			NTPDGSPYTWWVGKANEKHYYWGGSGPGIQKCACGIERNCTDPK
i i	'		YYCNCDADYKQWRKDAGFLSYKDHLPVSQVVVGDTDRQGSEAKL
	j		SVGPLRCQGDRNYWNAASFPNPSSYLHFSTFQGETSADISFYFK
}			TLTPWGVFLENMGKEDFIKLELKSATEVSFSFDVGNGPVEIVVR SPTPLNDDQWHRVTAERNVKQASLQVDRLPQQIRKAPTEGHTRL
	Į.		ELYSQLFVGGAGGQQGFLGCIRSLRMNGVTLDLEERAKVTSGFI
1	[İ	SGCSGHCTSYGTNCENGGKCLERYHGYSCDCSNTAYDGTFCNKD
1 1			VGAFFEEGMWLRYNFQAPATNARDSSRVDNAPDQQNSHPDLAQ
1 1			EEIRFSFSTTKAPCILLYISSFTTDFLAVLVKPTGSLQIRYNLG
1 ' 1	ł		GTREPYNIDVDHRNMANGQPHSVNITRHEKTIFLKLDHYPSVSY
1			HLPSSSDTLFNSPKSLFLGKVIETGKIDQEIHKYNTPGFTGCLS
1 1		İ	RVQFNQIAPLKAALROTNASAHVHIOGELVESNCGASDI.TLCDM
			SSATDPWHLDHLDSASADFPYNPGOGOATRNGVNPNSATTGGVT
		ĺ	A\VVIFTPSLCTP\VLP*SR*HVSPHKGTLPIPNEAKGAGGPOK
J			KPGRRPSMNNDPPTSQRPIDESKKEWPHLRGGYLAMG
6791	1801	1193	TGHEGAKGEKGDKGDLGPRGERGQHGPKGEKGYPGIPPEL/PGW
1 1		i	SAVV*SWLTAASTKVQAILLPQPLE*LGLOIAFMASLATHESNO
j l	i	Ī	NSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDV
, ,	f		EEVYVYLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVW
- 6300			LRMGNGALHGDHQRFSTFAGFLLFETK
6792	33	1073	VRHTNWGVDMYLFSLGSESPKGAIGHIVSTEKTILAVERNKVLL.
1	}	ł	PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAV
			CPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLROALYGHTOAV
	1	ł	TCLAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISA
		į.	ITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCC
	§	1	CLMEGPAWDTSQIIITGSQDGMVRVWKT/VGCEDVCSWTASRRG
ł		i	APGSASKPKRPQVGEEPGLESRAGR*HCFDREAOONOP\PVTAL
			AVSRNHTKLLVGDERGRIFCWSADG*EERGSRGSGTTVPG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
6793	2340	805	GRKEANY\YGSLTQAGTVSLGLDAEGQEVFVPFSAVLPMVAPND
			LVFDGWDISSLNLAEAMRRAKVLDWGLQEQLWPHMEALRPRPSV
j	}]	YIPEFIAANQSARADNLIPGSRAQQLEQIRRDIRDFRSSAGLDK
1			VIVLWTANTERFCEVIPGLNDTAENLLRTIBLGLEVSPSTLFAV
1]	ASILEGCAFLNGSPQNTLVPGALELAWQHRVFVGGDDFKSGQTK
İ			VKSVLVDFLIGSGLKTMSIVSYNHLGNNDGENLSAPLQFRSKEV
}			SKSNVVDDMVQSNPVLYTPGEEPDHCVVIKYVPYVGDSKRALDE
1		}	YTSELMLGGTNTLVLHNTCEDSLLAAPIMLDLALLTELCQRVSF
1]]	CTDMDPEPQTFHPVLSLLSFLFKAPLVPPGSPVVNALFRQRSCI
1			ENILRACVGLPPQNHMLLEHKMERPGPSLKRVGPVAATYPMLNK
1			KGPVPAATNGCTGDANGHLQEEPPMPTT*GPGHTVSRLFLPAAP
6794	I——3.5.	1349	HDPTLKAPTNKGRCHFSPPSTWGSWGL DDVKRKPEASAH*EKPGPPSRPGVRGGRERAGGRGSHGARSCR\
6/94	169	1349	EPAPPAPAPPEDHPDEEMGFTIDIKSFLKPGEKTYTQRCRLFVG
	Ì		NLPTDITEEDFKRLFERYGEPSEVFINRDRGFGFIRLESRTLAE
ì			IAKAELDGTILKSRPLRIRFATHGAALTVKNLSPVVSNELLEOA
	<u>}</u>		FSQFGPVEKAVVVVDDRGRATGKGFVEFAAKPPARKALERCGDG
1			AFLLTTTPRPVIVEPMEQFDDEDGLPEKLMQKTQQYHKEREQPP
			RFAOPGTFEFEYASRWKALDEMEKOOREOVDRNIREAKEKLEAE
			MEAARHEHOLMLMRODLMRROEELRRLEELRNOELOKRKOIOLR
	}	ļ	HEEEHRRREEEMIRHREQEELRRQQEGFKDNYMENYVCHFLR
6795	1740	1010	GPRRQTQVRDHELDSF*DWAAQETDCAQNSGERL*KGV/LENFS
1			TMSKSAVKISLDLLSNPLCEQDQDLLNMVTALDTAMKRMDAFNQ
			EKVNQIQKTVIEPLKKFGSVFPSLNMAVKRREQALQDYRRLQAK
1	İ	1	VEKYEEKEKTGPVLAKLHQAREELRPVREDFEAKNRQLLEEMPR
1		}	FYGSRLDYFQPSFESLIRAQVVYYSEMHKIFGDLSHQLDQPGHS
L			DEQRERENEAKLSELRALSIVADD
6796	48	683	GKEIQIPTIKLAWLLFGLE*PVGALGKGVVSF**SHVALGQLGW
1		ļ	LTRAVRSSWRWELCVSAQEVVSQRSA*SSPSPVGACPSLNPPET
			SVQEGRDCWQR*LPRLFSALVGQPGCWPQGAPPERCV*PGRCKW
	İ] .	HLQSQVLR*ERRRCCRCLPRFA*GWRRRHQRLGLGIHPAPLGST SPPHPEGNSQQCRR*GWAAELRLPSSVVL*GKLGC*
6797	1620	211	TERMTPSOPTRGSSCTRPSSMLWTSTWRCLTCHWAGMRMSVVGV
0,3,	1020		TLGPMAQGLLSASGTTTEATWTRPTTHLTLIRWWLLTASRVDPP
i	1	i	ERPPPPPSDDLTLLESSSSYKNL/DAOIPO/DWSMSPSTSG*RP
1		1	LTSRASSIMRSRTAIPSAS*SRLTTKHTVGGSPSAWRPRPTSRS
1	1		VSTPVSSSTETTASGSCLTWWSSSPAPCPSSSAPAHSFEASCCK
			TSLWGSCGGSGDGSSACGSGWNLSMAGTSCSSPAMCSPSRAPS*
	1	1	RSASRPRTWRATTSAASSWAPRRCWCGWA+SAT+PSSTTTISSS
1	1		PHCGWPCPASCASAAAWLSSTWATASVAGSCWGPIM*SSAHSPW
			CLSACSRSSMGTTCL*RSPP\SGASRAAAAWCGSSPSSTFTPSS
1		}	ASSSTWCSASSSRSSPAPTTPSSIPAAQAQRRASCRPTSHSART
L			APPPASSAAGAARPAAFSAAAEGTPRRSIRCW
6798	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
	1	1	ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA
1		1	VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
1	1	1	ALPEKAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
1			VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
1			TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
1		l	ENKRRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG
l	1		QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
1	1		PAPTPPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS
i	1	1	PRPGTAACGASDAPLLOPSAPSSSSSQAPLPPPFPAPVVPASVP
1	1	1	APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL
1	1	[DQLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ
L	L	L	1 - E

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ı	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	·		PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
1		1	RILFHPAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLOAAVPKS
)	J]	MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
1	İ		LTFALGEQLSTEVGEVDQFPPVEQWGNL
6799	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
1	305.	1 2050	ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA
Į		Ī	1
1			VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
1			ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
]	VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
1			TKRLHTLEEVNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
	1		ENKRRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG
1		1	QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
1	1		PAPTPPSSGIPILPPPPQASGPPRSRSSQAEATLGPSSTSNAL
1		1	SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS
		1	PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFPAPVVPASVP
l	Į.	1	APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL
	1		DQLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ
1			PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
1		1	RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
ŀ	1	1	MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
6800	404	1646	LTFALGEQLSTEVGEVDQFPPVEQWGNL
1 0000	104	1040	RRSPSTGLSPVPQPSSPSLSDYSIPWSLLLSGTIAWATPGK*AG
		l	*PQAW*LGLAPAIAFI/GLTRGRKQNKEKMAEGGSGDVDDAGDC SGARYNDWSDDDDDSNESKSIVWYPPWARIGTEAGTRARARAR
ı	İ		
ł	ł	1	RATRARRAVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILE
}		,	AALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKAL
İ		i	IVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLL TNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLLNLAE
1	1	i .	
l			NPAMTRELLRAQVPSSLG\SLFNKKENKEVILKLLVIFENINDN
	[· ·	FKWEENEPTQNQFGEGSLFFFLKEFQVCADKVLGIESHHDFLVK VKVGKFMAKLAEHMFPKSQE
6801	2	1755	
""] ~	1755	SAEEFESQQASVTMHDVDAESFEVLVDYCYTGRVSLSEANVERL
	1		YAASDMLQLEYVREACASFLARRLDLTNCTAILKFADAFGHRKL
i	1	l	RSQAQSYIAQNFKQLSHMGSIREETLADLTLAQLLAVLRLDSLD VESEQTVCHVAVOWLEAAPKERGPSAAEVFKCVRWMHFTEEDOD
1		1	
	1	1	YLEGLLTKPIVKKYCLDVIEGALQMRYGDLLYKSLVPVPNSSSS /R*QQQLSCICSRKSTPETGYVCQGDGDLLWTPORSLS\RYDPY
	1		
1	l		SGDIYTMPSPLTSFAHTKTVTSSAVCVSPDHDIYLAAQPRKDLW
1		1	VYKPAQNSWQQLADRLLCREGMDVAYLNGYIYILGGRDPITGVK
1	1		LKEVECYSVQRNQWALVAPVPHSFYSFELIVVQNYLYAVNSKRM LCYDPSHNMWLNCASLKRSDFQEACVFNDEIYCICDIPVMKVYN
1			
1			PARGEWRRISNIPLDSETHNYQIVNHDQKLLLITSTTPQWKKNR
1		ľ	VTVYEYDTREDQWINIGTMLGLLQFDSGFICLCARVYPSCLEPG
ŀ			QSFITEEDDARSESSTEWDLDGFSELDSESGSSSSFSDDEVWVQ
6802	157	1241	VAPQRNAQDQQGSL
1 0002	12,	1341	ETFPLFFFLLSKTPGKTASMAHFVQGTSRMIAAESSTEHKECAE
	i	}	PSTRKNLMNSLEQKIRCLEKQRKELLEVNQQWDQQFRSMKELYE
ļ			RKVAELKTKLDAAERFLSTREKDPHQRQRKDDRQREDDRQRDLT
			RDRLQREEKEKERLNEELHELKEENKLLKGKNTLANKEKEHYEC
l	1		EIKRLNKALQDALNIKCSFSEDCLRKSRVEFCHEEMRTEMEVLK
			QQVQIYEEDFKKERSDRERLNQEKEELQQINETSQSQLNRLNSQ
			IKACQMEKEKLEKQLKQMYCPPCNCGLVFHLQDPWVPTGPGAVQ
		1	KQREHPPDYQWYALDQLPPDVQHKAN/DWCLAPPPVCCQAG/PR
			TPGLK*SSCLWLPKC*NFRFILSKESPSVEVHTNRERQQATRER
C003			G
6803	1	2203	KLSGRPYRHMGVLGTSKLYDIRKTIFTFTPQFIDQQQFYLALDN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i .	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ĺ	sequence	1 -	\=possible nucleotide insertion)
	 		KMIVEMLRTDLSYLCSRWRMTGQPTITFPISHSMLDEDGTSLNS
ł	{	1	SILAALRKMQDGYFGGARVQTGKLSEFLTTSCCTHLSFMDPGPE
1	1	ì	GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDEVARYLDHLL
1	}		AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLVTKAKELHVQ
1	1	1	NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSVRVEIHLPRD
	i		QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKGPDWNTELYN
1	İ		ERSATVRELLTELYGKVGEIRHWGLIRYISGILRKKVEALDEAC
1			TDLLSHQKHLTVGLPPEPREKTISAPLPYEALTQLIDEASEGDM
1		1	SISILTQEIMVYLAMYMRTQPGLFAEMFRLRIGLIIQVMATELA
	1		HSLRCSAEEATEGLMNLSPSAMKNLLHHILSGKEFGVERK/SVR
1 .		1	PTDSNVSPAISIHEIGAVGATKTERTGIMQLKSEIKQVEFRRLS
1			ISAESQSPGTSMTPSSGSFPSAYDQQSSKDSRQGQWQRRRRLDG
1	1		ALNRVPVGFYQKVWKVLQKCHGLSVEGFVLPSSTTREMTPGEIK
1			FSVHVES\VLNVLLRPEYRQLLVEAILVLTMLADIEIHSIGSII
Ì			AVEKIVHIANDLFLQEQKTLGP\DDTMLAKDPASG\ICTLR\YD
1	į.	l	SAPSGREGTMTYLS\RAA\ATYVQEFLP\HSICAMQ
Ĺ	<u> </u>	<u> </u>	GSPGKKEEKAKNKESLCMENSSNSSSDEDEEETKAKMTPTKKYN
6804	1	951	GSPGKKEEKAKNKESLCMENSSNSSSDEDEEETKAKMIFIKKIN
		1	GLEEKRKSLRTTGFYSGFSEVAEKRIKLLNNSDERLQNSRAKDR
1		i	KDVWSSIQGQWPKKTLKELFSDSDTEAAASPPHPAPEGVAEES
Į.	l .	1	LQTVAEEESCSPSVELEKPPPVNVDSKPIEEKTVEVNDRKAEFP
-	i	1	SSGSNFSA*IPLPYLHLNRLHQSL*QKGSRQQSSVTVSEPLAPN
	1	1	QEEVRSIKSETDSTIEVDSVAGELQDLQSERE*LASRF*CQCEL
,	ļ	l l	KQ**SARTRTS*KSLYRSEKSERCSGRRKFIKKAEKKP*SNSGK
1			QQKEGKRHK
6805	1539	206	ROPDLKYFGKSFDVSVSESSSLLSNDLPKFADGIKARNRNQNYL
1	Į.	1	VPSPVLRILDHTAFSTEKSADIVICDEECDSPESVNQQTQEESP
	1		IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLQDQTDEEPPA
	Į		KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS
ļ			DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI
· I		1	CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY
1	1		LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD
ļ		1	KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV
			AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW
1 .	}		EYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP
ł	ı		VHETT
6806	272	3794	VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV
1	1		GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGNPPLSWLVI
1			DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA
1		İ	SLLAQCRALTQACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR
1			MHVVSVPYALMKANPLSWIQKVCFYKARAALVKSRDMHWSLLAQ
1		1	RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV
l			ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD
i		1	TEEKLSVLTVODVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV
ſ		1	SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG
1	1		FIGPDHLVFIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY
		· ·	RGRIAVFSVTVLHDDRIVLVAEQRPDASEEDSFQWMSRVLQAID
	1	1	SIHOVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN
1			VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR
1		1	ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT
i			STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA
1	1	1	FYGCLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVSKSACVLTT
1			QAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVFRPPSP
1		1	DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIKLQCELYPSRQ
1	}		IAICLDPYCGLGFALWCLCSVYSGHQSVLVPPLELESNVSLWLS
1		1	AVSQYKARVTFCCYSVMEMCTKGLGAQTGVLRMKGVNLSCVRTC
-	1	1	MVVAEERP\RIALTQSFSKLFKDLGLPARAVSTTFGCRVNVAIC
1	I		LIA ASTRONE ANTIONIST AND DESCRIPTION OF THE PROPERTY AND DESC

Deginning nucleotide location corresponding to first amino acid amino acid amino acid amino acid sequence sequ	SEQ	Predicted	Predicted end	L Amino and a
No: nuclectide location corresponding to first anino acid residue of amino acid residue of amino acid sequence	. –			Amino acid segment containing signal peptide
Cocresponding to first amino acid Partition Partiti	NO:			Glutamic Acid Papered Latin Carid, E-
Corresponding to first amino acid amino acid amino acid amino acid amino acid sequence sequen	1.			H-Histiding T-I-2 over the state of the stat
to first amino acid residue of samino acid sequence solve the control of the control of samino acid sequence solve the control of the control of sequence solve the control of the control of sequence solve the control of the control	1	corresponding		LeTencine MeMathianine N Assessme,
amino acid residue of amino acid sequence	1			P=Proline O-Glutamine P-Proline,
### ### ### ### ### ### ### ### ### ##	1	amino acid		Seserine Terbragaine W. Waling
Sequence Codon, /-possible nucleotide deletion, /-possible nucleotide desertion) LogTagDPTTVYUMPALRHDRYELVERGSPHSLIMMSSKIL POWKVIIANTEKCPLOSHIGE INVESTMENTYTYVGERGI POWKVIIANTEKCPLOSHIGE INVESTMENTSTYTYVGERGI POWKVIIANTEKCPLOSHIGE INVESTMENTSTYTYVGERGI POWKVIIANTEKCPLOSHIGE INVESTMENTSTYTYVGERGI VUVUSLOETLERGRYHPTDILD VUVUSLOETLERGRYHPTDILGR	1	residue of		W=Truntonhan Y-Timesine V V-Inc.
A-possible nucleotide insertion	ļ	amino acid	i e	Codon (-possible runlantial land)
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GKIGSKTPLMAAATFSUGMNTFACESLEKPLNMLLENYYLLTTC LQSSVMKIRHMFVKQVDMDHVMKAKSIREFDKRFTSVMFGYOTI DDYYTDASPSPRLKSVGIPVLCLMSVDDVFSPSHAIPISTAKON PNVALVLTSYGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVEHGH ELS 6809 939 65 DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKKQDPKRLHVSNIPFRFEDPDLRQMF GQFGKILDVBIIFNERGSKGFGFVTFETSDADRAREKLMGTIV VGGFSYPTTGTAVAYRGAHLRGGGRAVVNTFRAAPPPPPIPTYG AVVYQDGFYGASI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRPLLGP 6810 939 65 DYSGGTFVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ GQFGKILDVBIIFNERGSKGFGFVTFSTSDADRAREKLMGTIV EGRKLEVNNATARVMTNKKTGNPYTNGWKLMPVVGAVYGPEFYA VTGFFYPTTGTAVAYRGAHLRGRGRAVVNTFRAAPPPPPIPTYG GQFGKILDVBIIFNERGSKGFGFVTFSTSDADRAREKLMGTIV EGRKLEVNNATARVMTNKKTGNPYTNGWKLMPVVGAVYGPEFYA VTGFFYPTTGTAVAYRGAHLRGRGRAVVNTFRAPPPPPIPTYG AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP 6811 1522 658 DLVTWSSFVDCRVIASTHGY\KSWVSVVAFDPYTTSVEEGDPME PSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYTRFG SVGQDTQLCLMDLTEDIIFPHQPLSRARTHTNVMNATSPPAGSN GNSVTFDGNSVPPPLDRSNLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLMLVTTKK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRGPGKVVSFNP 6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGEELKSNEPEQQVEPGALRYRIEQ KGLQHRILLHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQRVERSELL VVKNDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGGTVQDPPV HIVDPREHVFHAATTSECVMLACEV\DR\DRATWYKDGQEVE ESDFVVLENEGPHRRVLVLERVLTCELCRPWREYKDGGEVE	1 .			PRTYCCANTEDLETYTURGUEL VDC A DET A A CHOCK CONT. T. AND.
LOSSVNKHRHMFVKQVDMDHVMKAKSIREFDKRFTSVMFGYQTI DDYYTDASPSPRLKSVGIPVLCLINSVDDVFSPSHAIPIETAKQN PNVALVLTSYGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVEHGH ELS DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKQQFKRLHVSNIPFRFRDPDLRQMF GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKINGTIV EGRKIEVNNATARVMTMKKTGMPYTMGWKLNPVVGAVYGPEFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTTRAAPPPPPIPTYG AVVYQDGFYGABI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRPTBALEPCETFHRFLLGP 6810 939 65 DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDBAAQTDSQPLHPSDPTEKQQFKLHVSNIPFRFRDPDLRQMF GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKINGTIV EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGABI\LEATQPDTLSPLQFNCTATAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP 6811 1522 658 DLVTVWSFVDCRVIASTHGH\KSWYSVVAFDPYTTSVEEGDPME FGGSDEDFQDLLHFGRDRADSTQCKLSRRNSTDSRPVSVTYRFG SVGQDTQLCLWBLTEDILFPHQPLGRARTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSOMINLVTKK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP 6812 4001 1682 EDAVFSLDLSTIJQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPSATWYKDGGWVEBSELL VVKNDGRKHRILLPBAKVQDSGEFECRTGGVSAFFGTVTQDPPV HIVDPREHVFHATTSECVMLACEV\DR\EDAPVRWYKDGGEVE ESDFVVLENECHPRRELVVLTCELGRNDFVMSVENGGENSTFTTVTDT TDVSSWIVYPSGKVVVAAVRLERVVLTCELGRNAESVENGERSTFTTVTVDGE				GKIGSKTPI.MAAATESVCWMTEACCECI EVII ATUI I TOVINI TOVI
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TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF GQFGKILDVBIIFMERGSKGFGFVTFETSSDADRAREKLNGTIV EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP DYSGQTPVPTEHGMTLYTPAQTHPBQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFDPDLRQMF GQFGKILDVBIIFNERGSKGFGFVTFETSSDADRAREKLMGTIV EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA VTGFFYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP DLVTWMSFVDCRVIASTHGH\KSWVSVAFDPYTTSVEEGDFME PSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLBPRSNSLPHSAVSNAGSKSSVMDGATASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP 6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTPTTSERVVLTCELSRVDFPATWYRDGQKVERSELL VVKMDGRKRRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYRDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSMIVYPSGKVYVAAVALERVVLTCELCRRWAEVRNYKDGE	6809	939	65	DYSGQTPVPTEHGMTLYTPAOTHPEOPGSEASTOPTAGTOTUPO
GGFGKILUVEII FNERGSKGFGFVTFETSSDADRAREKLNGTIV EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPI PTYG AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRPLLGP DYSGQTFVPTEGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDBAAQTDSQPLHPSDPTEKQQEKRLHVSNII PFRFRDPDIRQMF GQFGKILDVEII FNERGSKGFGFVTFETSSDADRAREKLNGTIV EGRKIEVNNATARVWTNKKTGNPYTNGWKLNPVVGAVYGPEFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPI PTYG AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP BLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVWNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLBLVTKTK TDPAKTLGTFLCPRMEDVPLLEPLICKKIAHERLTVLIFPLEDCI VTACQEGFICTWGRPGKVVSFNP 6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYRNGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKNGQCVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVALERVVLTCELCRPWAEVSWTKNGG	1 1			TDEAAQTDSQPLHPSDPTEKOOPKRLHVSNIPFRFRDPDLROMF
EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPPTTYG AVVYQOGFYGABI \ LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP 6810 939 65 DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNI PREFRDPDLRQMF GQFGKLLDVBLIFNERGSKGFGFVFFETSSDADRAREKLNGTIV EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGFEFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGABI \ LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNISMGHISSKSSDKLMLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIPLEDCI VTACQEGFICTWGRPGKVVSFNP 6812 4001 1682 EDAVFSLDLSTIIQGTWPLNGEELKSNEPEGQVEFGALRYRIEQ KGLQHRLLIHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELGRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWKDGQEVE ESDFVVLENGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE		1		GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGTTV
VTGFPYPTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRPLLGP BYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF GQFGKILDVBIIFNERGSKGFGFVTFETSSDADRAREKIMGTIV EGRKIEVNNATARVMTNKKTGRPYTNGWKLNPVVGAVYGPEFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP BULVTWMSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMGGAIASGV SKFATLSHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP 6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLIHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSECVVLTCELSRVDFPATWYKDGGRVEESELI- VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFHAAITSECVMLACEV\DR\EDAPURWYKDGGQVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVVVAAVRLERVVLTCELCRPWAEVFWTKDGE	1			EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA
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TDEAAQTDSQPLHPSDPTEKQMTKLNSNIPFRFRDPDLRQMF TOBAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGTIV EGRKIEVNNATARVMTNKKTGNPYTNGWKLNFVVGAVYGPEFYA VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP TRTITPSGPRRPTALEPCETFHRFLLGP 658 DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN GNSVTTFGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP 6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEBSELL VVKMDGRKHRLLPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQBVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE				TRTITPSGPRRPTALEPCETFHRFLLGP
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FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSTYRFG SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLALVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP 6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVESELLI VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAPFGVTVTI HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE	6817	1533		TRTITPSGPRRPTALEPCETFHRFLLGP
SVGQDTQLCLMDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPPMEDVPLLEPLICKKIAHERLTVLIPLEDCI VTACQEGFICTWGRPGKVVSFNP 6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRDWAEVRWTKDGE	"""	1042	658	DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME
SVGQDTQLCLMDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPPMEDVPLLEPLICKKIAHERLTVLIPLEDCI VTACQEGFICTWGRPGKVVSFNP 6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRDWAEVRWTKDGE		i	ļ	FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG
GNSVITPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI VTACQEGFICTWGRPGKVVSFNP 6812 4001 1682 EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE		1		SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN
TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIPLEDCI VTACQEGFICTWGRPGKVVSFNP EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE				GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGATASGV
VTACQEGFICTWGRPGKVVSFNP 6812 4001 1682 EDAVFSLDLSTIIQGTWPLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVLTTSERVVLTCELSRVDFPATWYKDGOKVESELL VVKMDGRKHRLILPEAKVQDSGEFBCRTEGVSAPFGVTVQDPPV HIVDPREHVPVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYPTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE	J			SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK
EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGOKVRESELI. VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE				TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI
KGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVESSELL VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE	6812	4001	1602	
SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELI. VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE		3001	1027	EDAVISLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ
VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE		1	ļ	KGLQHKLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHIL
HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE	1	ļ	ļ	SPQDKVSLTFTTSERVVLTCELSRVDFPATWYKDGOKVRESELL.
ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE	i		ĺ	VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV
TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE	1	1	1	HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE
TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE EVVESPALIJOKEDTVRRIVITERGEVLCE INDEGA SEE	- 1	ĺ]	ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI
EVVESPALITOREDIVERDIVERDIVERDIVERDIVERDIVERDIVERDIV	j	j	j	TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE
	1		•	EVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT
VTVTBPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK	ł		!	VTVTEPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK
DGLEVEESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA			ļ	DGLEVEESEALVLERDGPRCRLVLPAAQPEDGGEFVCDAGDDSA
FFTVTVTEPPVQFLALETTPSPLCVAPGEPVVLSCELSRAGAPV				FFTVTVTEPPVQFLALETTPSPLCVAPGEPVVLSCELSRAGAPV

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Asparcic Actu, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		_mossible nucleotide insertion)
	sequence		VWSHNGRPVOEGEGLELHAEGPRRVLCIQAAGPAHAGLYTCQSG
1	1	1	AAPGAPSLSFTVQVAEPPVRVVAPEAAQTRVRSTPGGDLELVVH
		ì	LSGPGGPVRWYKDGERLASQGRVQLEQAGARQVLRVQGARSGDA
}		į.	GEYLCDAPQDSRIFLVSVEEPLLVKLVSDLTPLTVHEGDDATFR
1	ļ		CEVSPPDADVTWLRNGAVVTPGPQRQSCCSYGGCRMCGQRKART
		1	CVSKWRQAEWVQRGPCAGCEVGSPCPTTLACPWPRMGTSTASSS
ļ	1	1	MVSYWPTRAPTAARATTIAPWPGSA
ļ			SSTOORPGVPAGPRPLDGYLGVADHKPLKMHCRDCALVTSSGHL
6813	9	836	LHSRQGSQIDQTECVIRMNDAPTRGYGRDVGNRTSLRVIAHSSI
ļ	i .	1	QRILRNRHDLLNVSQGTVFIFWGPSSYMRRDGKGQVYNNLHLLS
1	· l	1	QRILRNRHDLLNVSQGTVFIFWGPSSIFIKRDGRGQVTHADITADS
	ļ	1	QVLPRLKAFMITRHKMLQFDELFKQETGQ\NRKISNTWLSTGWF
ļ.	1	1	TMTIALELCDRINVYGMGPPDFCRDPNHPSVPYHYYEPFGPDEC
į.	į	1	TMYLSHERGRKGSHHRFITEKRVFKNWARTFNIHFFQPDWKPES
ļ	1		LAINHPENKPVF
6814	3	737	KFRRQEAN/ARERNRMHGLNDALDNLRKVVPCYSKTQKLSKIET
1	1		LRLAKNYIWALSEILRIGKRPDLLTFVQNLCKGLSQPTTNLVAG
1			CLQLNARSFLMGQGGEAAHHTRSPYSTFYPPYHSPELTTPPGHG
1	1	1	TLDNSKSMKPYNYCSAYESFYESTSPECASPQFEGPLSPPPINY
1	1	1	NGIFSLKQEETLDYGKNYNYGMHYCAVPPRGPLGQGAMFRLPTD
		1	SHFPYDLHLRSQSLTMQDELNAVFHN
6815	906	553	QGLDPASQTKVVELLKDGSGRRGDRRSSRDMAGGAGPRSESDLE
6072	1 300	1	DVGPTAEWNGDGSGSLRRSGSFGKLRDALRRSSEMLVKKLQGGT
1			DOEDDNDRMKRASSLNFLNKSVEEPTQPGG
- 2012	1	803	MILKTHEF LLGODEDSLHSVPVAQMGNYQEYLKTLASPLREID
6816	1 -	1	PDOPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN
[SPMSSKRRRSMSLLLRKPQTPPTVTNHVGGKGPPSASWFPSYPN
1	ļ		T.TKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM
1			TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS
1		1	VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF
	1	i	GRSK
		3457	LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS
6817	172	345/	DEYCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL
1			NNLISPOLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA
1		1	IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI
1	Į.	\	LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC
1	1	İ	TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE
1	1	1	ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET
1	1	1	ESIFWRLLTKYNQANTIBITSQUSGVRUGBERRHISSTTMSTT CLNEVRDEIFISLQPQLRCTLGDMESPVFAFPLLLKLETHIEKL
	1	1	CLNEVRDEIFISLOPOLIKCTIGIMESPVFAFFINISKS FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHP
İ			FLYSFSWDFECSQCGHQYQNKHMKSLVIFINVIPEMHPINAAHF GPCNNCNSKSQIRKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHF
1	1		GPCNNCNSKSQIKKNVDERVSPIFIMENT VEGDE QNDDQNIAFAR
1		1	EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH
i	1	1	KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE
1	1		KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD
l	Ţ.		HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV
1	1	Į	AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ
1			VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ
1			LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ
l			SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS
l.			VKGVNNFGGFKTKGINOKASHVSKKARKSASKPPPISKPPAGPP
1			SCHOTA AHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH
1			FDIARGOTHKIRI.KLRKKLKAEKKKLAALMSSPQSRTVRSENLE
l l	J]	OVPODGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS
			OTHERITARIASPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS
1			EFNOVSONTHLRODHNYCSPTKKNPCEVQPDSLTNNACVRTLNL
			FCDMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY
		240	RGFDKVLWT/LSGAVK\CVQFSRISPDGEEGYPGELKVWVTYTL
6818	2		TOT DICATULT AND COLOR OF THE C

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ſ	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	I .	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
6819	1		DGGE/LHS/ATTEHKP/VQATPVNLT\TILTSTWQARLPQI
6619	1 +	961	GIPCTEMGNFDNANVTGEIEFAIHYCFKTHSLEICIKACKNLAY
1	l		GEEKKKKCNPYVKTYLLPDRSSQGKRKTGVQRNTVDPTFQETLK
ŀ			YQVAPAQLVTRQLQVSVWHLGTLARRVFLGEVIIPLATWDFEDS
· l			TTQSFRWHPLRAKADKYEDSVPQSNGELTVRAKLVLPSRPRKLQ
ł	j		EAQEGTDQPSLHGQLCLVVLGAKNLPVRPDGTLNSFVKGCLTLP
J	j		DQQKLRLKSPVLRKQACPQWKHSFVFSGVTPAOLROSSLET.TVW
			DQALFGMNDRLLGGT\RLGSKGDTAVGGDACSQSKLQWQKVLSS
			PNLWTDMTLVLH
6820	1014	340	GDMVYIVGHVPPGFFEKTQNKAWFREGFNEKYLKVVRKHHRVIA
			GQFFGHHHTDSFRMLYDDAGVPISAMFITPGVTPWKTTLPGVVN
ı			GANNPAIRVFEYDRATLSLKDMVTYFMNLSOANAOGTPRWELEY
ľ			QLTEAYGVPDASAHSMHTVLDRIAGDQSTLORYYVYNSVSYSAG
1 .			VCDEACSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLPLLLMAL
		_	LGLCT
6821	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN
	[RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
			FFAFSLIEGYI\SIVMDAETOKKFPSDLLLTSSSGELWRMURIG
ŀ	i		GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
			GSVIEVLQRRQEGLAS
6822	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN
1			RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
			FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG
		•	GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
			GSVIEVLQRRQEGLAS
6823	654	221	PPKLLSRWARMGHGDBIV\LSDLNFPGLLHLPVVGPWRSVQTAC
1 1			GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLOTPVWTE
			YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL
			ILRKGVLALNPLL
6824	858	104	LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG
1 1	1		ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGROFLFHWTV
1 1	1		NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS
			LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYOFYV
, 1	1		WYFHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS
 			AALHICHAVILLQLWLGPQPFPKSTQHSKKAH
6825	3	1173	SSGEFGLOASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL
[PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ
1 1	ļ		NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM
1 1		I	KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI
j		!	GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD
į l		j	IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF
			VILALQFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK
]]			TVTGKIQRA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF
<u> </u>			PFGPLALPMDGYGDSLWEEHEYKFCLALVISTKLYHVRC
6826	2304	954	LKTESFKPW/VNIALAFHLLGERASPNSFWQPYIOTLPREYDTP
	1		LYFEEDEVRYLQSTQAIHDVFSQYKNTARQYAYFYKVIQTHPHA
	}	1	NKLPLKDSFTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPLW
	į	ļ	DMCNHTMGLITTGYNLEDDRCECVALQDFRACEQIYIFYGTRSN
	[İ	AEFVIHSGFFFDNNSHDRVKIKLGVSKSDRLYAMKAEVLARAGI
	}]	PTSSVFALHFTEPPISAQLLAFLRVFCMTEEELKEHLLGDSAID
	i	į	RIFTLGNSEFPVSWDNEVKLWTFLEDRASLLLKTYKTTIEBDKS
	1	į	VLKNHDLSVRAKMAIKLRLGEKEILEKAVKSAAVNREYYRQQME
1	1		EKAPLPKYEESNLGLLESSVGDSRLPLVLRNLEEEAGVQDALNI
-			REAISKAKATENGLVNGENSIPNGTRSENESLNQESKRAVEDAK
_ 1			GSSSDSTAGVKE
		 ,	

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	Glutamic Acid, Farhenylatanine, Gadrycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
-	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion) .
6827	1	779	SSVVEFGLSVLGGLFLLFVLENMLGLLRHRGLRPRCCRRKRRNL
6827	1 -		ETRNLDPENGSGMALQPLQAAPEPGAQGQREKNSQHPPALAPPG
	1	1	HQGHSHGHQGGTDITWMVLLGDGLHNLTDGLAIGAAFSDGFSSG
	1	ļ	LSTTLAVFCHELPHELGDFAMLLQSGLSFRRLLLLSLVSGALGL
		i	GGAVLGVGLSLGPVPLTPWVFGVTAGVFLYVALVDMLPALFPSS
		1	GAPAYA\HVLLQGLGLLLGGCLMLAITLLEERLLPVTTEG
		<u> </u>	KSQHG/WILQLMHSCKEGYVKDLKGNPGLHRAMLDLDNGTRPSE
6828	3	1654	KSQHG/WILQUMHSCKEGIVKDIRGNFGIIHKAMIDDIDNGIKIDD
	!	1	LGHLSQTASLKRGSSFQSGRDDTWRYKTPHRVAFVEKLTKLVLS
	ł.	1	QLPNFWKLWISYVNGSLFSETAEKSGQIERSKNVRQRQNDFKKM
Ì			IQEVMHSLVKLTRGALLPLSIRDGEAKQYGGWEVKCELSGQWLA
	1	1	HAIQTVRLTHESLTALEIPNDLLQTIQDLILDLRVRCVMATLQH
l	}	1	TAEEIKRLAEKEDWIVDNEGLTSLPCQFEQCIVCSLQSLKGVLE
1	1		CKPGEASVFQQPKTQEEVCQLSINIMQVFIYCLEQLSTKPDADI
1	1	i	DTTHLSVDVSSPDLFGSIHEDFSLTSEQRLLIVLSNCCYLERHT
l	1	1	FLNIAEHFEKHNFQGIEKITQVSMASLKELDQRLFENYIELKAD
i	1		PIVGSLEPGIYAGYFDWKDCLPPTGVRNYLKEALVNIIAVHAEV
		•	FTISKELVPRVLSKVIEAVSEBLSRLMQCVSSFSKNGALQARLE
1	· ·		ICALRDTVAVYLTPESKSSFKQALEALPQLSSGADKKLLEELLN
i	\	ł	KFKSSMHLQLTCFQAASSTMMKT
	 	782	MRMEAGEAAPPAGAGGRAAGGWGKWVRLNVGGTVFLTTRQTLCR
6829	1	102 .	BQKSFLSRLCQGEELQSDRDETGAYLIDRDPTYFGPILNFLRHG
ļ		}	KLVLJKDMAEEGVLEEAEFYNIGPLIRIIKDRMEEKDYTVTQVP
1	1		PKHYYRVLQCQEEELTQMVSTMSDGWRFEQLVNIGSSYNYGSED
1	<u>J</u>)	QAEFLCVVSKELHSTPNGLSSESSRKTKSTEEQLEEQQQQEEEV
1		l .	EBVEVEQVQVEADAQEK/CCYKPEAPGCEAPDHLQGLGVPI
			ERAEAEGAGA ENDAGEN CCINERAL CCENERAL DIDECTION OF THE CONTROL OF T
6830	1	939	MEPGSVENLSIVYRSRDFLVVNKHWDVRIDSKAWRETLTLQKQL
		1	RYRFPELADPDTCYGFRFCHQLDFSTSGALCVALNKAAAGSAYR
	1	1	CFKERRVTKAYLALLRGHIQESRVTISHAIGRNSTEGRAHTMCI
ĺ	1	}	EGSQGCENPKPSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHQL
i	1	i	RV\HCSALGHPVVGDLTYGEVSGREDRPFRMMLHAFYLRIPTDT
1	Ï		ECVEVCTPDPFLPSLDACWSPHTLLQSLDQLVQALRATPDPDPE
ì	1		DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT
ì	1		LEPDS
6831	3	1087	SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF
1 5552			NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGQNVKEKSMILSN
1			VEDLOOPKFISEVSREDYGKKEISGDSEEMNINSVVTSADGENL
i			EIOSYSLIGEKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI
1			SIFKEEPRSDOKOKSLLSFDVVDKVPQQPKSASSNFASKNITKE
1	1		SEKPESTTLPVEESKGSLIDFSEDRLKKEMONPTSLKISEEETK
1	1		LRSVSPTEKKDNLENR\SYTL\ABKKVLAEKQNSV\APLELRDS
1	§		NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG
]			
	<u> </u>		SEKEKDEKKKK MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV
6832	1809	412	MGSGLISGPPQUNSGEALALPERAQERSUPRIFAGGQUIFFEILLV
1			VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF
1		1	CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG
1		1	PRLPKVYCIISCIGCFGLFSKILDEVEKRHQISMAVIYPFMQGL
[}	1	REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL
		1	LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY
1		1	PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME
		1	EVILLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT
	į .		AEOINEHVSGPFVOFFVKIVGHYASYIKREANGQGHFQERSFCK
i	1	1	ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE
ì	İ	}	VEEOKKO/TETKGKNCEIRAVVNKND
6033		1120	PLMTLSOCGGIPGHGHSHGGHGHGHGLPKGPRVKSTRPGSSDIN
6833	1	1129	VAPGEQGPDQEETNTLVANTSNSNGLKLDPADPENPRSGDTVEV
l			QVNGNLVREPDHMELEEDRAGQLNMRGVFLHVLGDALGSVIVVV
1	1	i i	ΔΛΙΑΡΙΑΤΑ ΚΕΕΡΙΠΙΕΠΕΠΡΙΦΙΟ-ΙΟΣΙΜΙΙΙΟ 1. THE THE TOTAL

SEQ	Predicted	Predicted end	I Amino and I
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tvrosine, X=Unknown *-Stop
1	amino acid	sequence	(Codon, /=possible nucleotide deletion
ļ	sequence		\=possible nucleotide insertion)
			NALVFYFSWKGCSEGDFCVNPCFPDPCKAFVEI INSTHA SVVFA
		i	GPCWVLYLDPTLCVVMVCILLYTTYPLLKESALIILOTVPKOID
			IRNLIKELRNVEGVEEVHELHVWOLAGSRIIATAHIKCEDDTSV
1	1	1	MEVAKTIKDVFHNHGIHATTIOPEFASVGSKSSVVPCELACPTO
1]		CALKQCCGTLPOAPSGKDAEKTPAVSISCIELSNNIEVYDDDTV
6834	78	1151	AENIPA\VVIEIKN\IPNK\QPESSL
'	1	1131	AGQERPAPIWRLLWLPTPSVSRKAEPAHIPINR*GA*E*RGGLP
			LCGSSASAYGWH*RLTPWSPGGS*HM*SSKAPVTQAREVLVAGP
ļ	j		CSKLVLSGARGIVGTTVQVLVEAQQPLLLLFTGVWGLNLRAGEE
1			SRAL+LIBEVTQVRDAHLGNAVVGCAQCLSQGQVGSALAKALLE
1	<u> </u>	!	AAAAVRDCKEVLTVSGDKQQAEVSVRL+VRDVCVEEAGCVEFGQ
1			AHGRPGLALAKGRGGTNEVEEQVQVDGVQKLVLSAHECHELVAG QQDGEDQAARTRLLQAGAHSVAHGRRQGQAPCRPHQEAGVSCHE
	, ,		LQQVVGDAL*ARE*APQIIVLLLLEDVAQLRTGKKA*DLVVDVE
			QLLRQL
6835	1	834	GIPAADR\EASLELIKLDISRTFPNLCIFQQGGPYHDMLHSILG
1			AYTCYRPDVGYVQGMSFIAAVLILNLDTADAFIAFSNIINKDCO
1			MAFFRVDHGLMLTYFAAFEVFFEENLPKLFAHFKKNNI.TPDTVI.
1	1		1DW1FTLYSKSLPLDLACRIWDVFCRDGERFLFRTALGILKI.FE
			DILTKMDFIHMAQFLTRLPEDLPAEELFASIATIOMOSPNEKWA
			QVLTALQKDSREMREGKSVPPTLRLOREFALGTNOSPMPRPL.CC
6836	1	050	FRLTPGQPRRTDAL
	•	850	MSCGRPPPDVDGMITLKV\DNLTYRTSPDSLRRVFEKYGRVGDV
1 1			YIPREPHTKAPRGFAFVRFHDRRDAQDAEAAMDGAELDGRELRV
1 1	ļ ļ		QVARYGRRDLPRSRQGRRHAAGPEAA/RYGRRSRSYGRRSRSPR
! !			RRHRSRSRGPSCSRSRSRSRSRYRGSRYSRSPYSRSPYSRSRYSRS
1 1			PYSRSRYRESRYGGSHYSSSGYSNSRYSRYHSSRSHSKSGSSTS SRSASTSKSSSARRSKSSSVSRSRSRSRSSSMTRSPPRVSKRKS
			KSRSRSKRPPKSPEEEGQMSS
6837	1	1369	TDGAAVAGNPGSDYFPGGTAP/GGPRTRRP\SGTSSSGSKASGP
1 1			PNPPAQGDGTSLSPNYTLESTSGNDGKPVSGGGGRGRGRKRDS
) }	[GHVSPGTFFDKYSAAPDSGGAPGVSPGQQQASGAAVGGSSAGET
ļ f			RGAPTPHEKALTSPSWGKGAELLLGDOPDLIGSLDGGAKEDESS
1 1			PNVGEFASDEVSTSYANEDEVSSSSDNPOALVKASRSDLATGED
! [1		KLPPRGVGAGEHGPKAPPPALGLGIMSNSTSTPDSYGGGGGPGH
			PGTPGLEQVRTPTSSSGAPPPDEIHPLEILOAOIOLOROOFSIS
1 1			EDQPLGLKGGKKGECAVGASGAONGDSELGSCCSFAVKSAMSTT
]		i	DLDSLMAEHSAAWYMPADKALVDSADDDKTLAPWEKAKDONDNS
	1		KEAHDLPANKASASQPGSHLQCLSVHCTDDVGDAKARASVPTWR
6838	16	499	SLHSDISNRFGTFVAALT
			LTDTPPPKTHMIHHSISDYKATLRCWALGFYPMEITLTWQQDEE
l l	1		DQTRDMELVETRPAGDGTFQKWAAVVVPSGEB/Q/RYMCHVQHE
		Ì	GLPEPLTLRWEQSSQPTIPIVGIVAGLVLLGAVVTGAVVSAVMC RKKNSDRVSYSEAASSDHAQGSDVSLTACKV
6839	1	1195	AAPAGGGDDEAT CARRENT COLGODOWN DOLLARS
	l		AAPAGGGPDPEALSAFPGRHLSGLSWPQVKRLDALLSEPIPIHG RGNFPTLSVQPRQIRAGGPQHPGGAG\IHVHRVRLHGSAASHVL
1		ľ	HPESGLGYKDLDLVFRMDLRSEASFQLTKAVVLACLLDFLPAGV
!	1	ļ	SRAKITPLTLKEAYVQKLVKVCTDSDKWSLISLSNKSGKNVELK
ĺ	Ī		FVDSVRRQFEFSIDSFQIILDSLLLFGQCSSTPMSEAFHPTVTG
			ESLYGDFTEALEHLRHRVIATRSPEEIRGGGLLKYCHLLVRGFR
j			PRPSTDVRALQRYMCSRFFIDFPDLVEQRRTLERYLEAHFGGAD
j		İ	AARRYACLVTLHRVVNESTVCLMNHERROTLDLIAALALODI.AE
	[1	QGPAATAALAWRPPGTDGVVPATVNYYVTPVQPLLAHAYPTWLP
6840	4354		CN
0040	4254	2061	ELQGDFSVPDVPKSMAWCENSICVGFKRDYYLIRVDGKGSIKEL
			FPTGKQLEPLVAPLADGKVAVGQDDLTVVLNEEGICTQKCALNW

			[32:22 2:23 20mm]
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide		
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
ł	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
•	to first	amino acid	· · · · · · · · · · · · · · · · · · ·
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	residue of	amino acid	
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			TDIPVAMEHQPPYIIAVLPRYVEIRTFEPRLLVQSIELQRPRFI
1		i	TSGGSNIIYVASNHFVWRLIPVPMATQIQQLLQDKQFELALQLA
1	į	,	EMKDDSDSEKQQQIHHIKNLYAFNLFCQKRFDESMQVFAKLGTD
			PTHVMGLYPDLLPTDYRKQLQYPNPLPVLSGAELEKAHLALIDY
}]	}	LTQKRSQLVKKLNDSDHQSSTSPLMEGTPTIKSKKKLLQIIDTT
!			LLKCYLHTNVALVAPLLRLENNHCHIEESEHVLKKAHKYSELII
	1	1	LYEKKGLHEKALQVLVDQSKKANSPLKGHERTVQYLQHLGTENL
1	1	!	HLIFSYSVWVLRDFPEDGLKIFTEDLPEVESLPRDRVLGFLIEN
į .	1	1	FKGLAIPYLEHIIHVWEETGSRFHNCLIQLYCEKVQGLMKEYLL
1			SFPAGKTPVPAGEEEGELGEYRQKLLMFLEISSYYDPGRLICDF
	l	1	PFDGLLEERALLLGRMGKHEQALFIYVHILKDTRMABEYCHKHY
,	1		DRNKDGNKDVYLSLLRMYLSPPSIHCLGPIKLELLEPKANLQAA
1	1	1	LQVLELHHSKLDTTKALNLLPANTQINDIRIFLEKVLEENAQKK
Į	1		RFNQVLKNLLHAEFLRV\QEERILHQQVKCIITEEKVCMVCKKK
1			IGNSAFARYPNGVVVHYFCS\KEVNPADT
6841	1	3206	TPSTTGTKSNTPTSSVPSAAVTPLNESLQPLGDYGVGSKNSKRA
1	1		REKRDSRNMEVQVTQEMRNVSIGMGSSDEWSDVQDIIDSTPELD
1	ļi.		MCPETRLDRTGSSPTQGIVNKAFGINTDSLYHELSTAGSEVIGD
1	İ		VDEGADLLGEFSGMGKEVGNLLLENSQLLETKNALNVVKNDLIA
j	Į.	ì	KVDQLSGEQEVLRGELEAAKQAKVKLENRIKELEEELKRVKSEA
1	l .		IIARREPKEEAEDVSSYLCTESDKIPMAQRRRFTRVEMARVLME
	į.		RNQYKERLMELQEAVRWTEMIRASREHPSVQEKKKSTIWQFFSR
1			LFSSSSSPPPAKRPYPSGNIHYKSPTTAGFSQRRNHAMCPISAG
		1	SRPLEFFPDDDCTSSARREQKREQYRQVREHVRNDDGRLQACGW
1	l .	1	SLPAKYKQLSPNGGQEDTRMKNVPVPVYCRPLVEKDPTMKLWCA
\ ·			AGVNLSGWRPNEDDAGNGVKPAPGRDPLTCDREGDGEPKSAHTS
	[1	PEKKKAKELPEMDATSSRVWILTSTLTTSKVVIIDANQPGTVVD
1	İ	1	QFTVCNAHVLCISSIPAASDSDYPPGEMFLDSDVNPEDPGADGV
İ		1	LAGITLVGCATRCNVPRSNCSSRGDTPVLDKGQGEVATIANGKV
İ	ł	1	NPSQSTEEATEATEVPDPGPSEPETATLRPGPLTEHVFTDPAPT
l			PSSGPQPGSENGPEPDSSSTRPEPEPSGDPTGAGSSAAPTMWLG
Ī		1	AQNGWLYVHSAVANWKKCLHSIKLKDSVLSLVHVKGRVLVALAD
1			GTLAIFHRGEDGQWDLSNYHLMDLGHPHHSIRCMAVVYDRVWCG
1			YKNKVHVIQPKTMQIEKSFDAHPRRESQVRQLAWIGDGVWVSIR
1		1	LDSTLRLYHAHTHQHLQDVDIEPYVSKMLGTGKLGFSFVRITAL
1	J	1	LVAGSRLWVGTGNGVVISIPLTETVVLHRGQ\LLG\LRANKTSP
1	1		TSGEG\ARPGG\IIHVYG\DDSSDRAARSFIPYCSMAQAQLCFH
1	1		GHRDAVKFFVSVPGNVLATLNGSVLDSPAEGPGPAAPASEVEGQ
1	1		KLRNVLVLSGGEGYIDFRIGDGEDDETEEGAGDMSQVKPVLSKA
J		1	ERSHIIVWQVSYTPE
6842	3	926	RCQQLSATILTDHQYLERTPLCAILKQKAPQQYRIRAKLRSYKP
1	1		RRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDGATKTPDVKLQN
1		1	TSLYDSKIWTTKNQKGRKVAVHFVKNNGILPLSNECLLLIEGGT
1			LSEICKLSNKFNSVIPVRSGHEDLELLDLSAPFLIQGTVHHYGC
1		1	KQWST*RSIQNLNSLVDKTSWIPSSVAEALGIVPLQYVFVMTFT
1	1	1	LDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMIMDMFC
ł	1		PPGIKIDAYPWLECFIKSYNVTNGTDNQICYQIFDTTVAEDVI
6843	2	851	NHRKVLSGAKRYECNECGKSFAYTSSLIKHRRIHTGERPYECSE
1		1	CGRSFAENSSLIKHLRVHTGERPYECVECGKSFRRSSSLLQHQR
			VHTRERPYECSECGKSFSLRSNLIHHQRVHTGERHECGQCGKSF
1			SRKSSLIIHLRVHTGERPYECSDCGKSFAENSSLIKHLRVHTGE
1		1	RPYECIDCGKSFRHSSSFRRHQRVHTGMRPYK*SKFWKFSCPGF
1	j	1	LLLOGORVHTGSRCYECDKWGIFFS*NASFFT*KSAPTEEVPFE
		1	CNECEKAFSPLSLVTTIFT
6844	244	642	EHQLAGFELRKTQTSMSLGTTREKTDRVKSTAYLSPQELEDVFY
0844		044	QYDVKSEIYSFGIVLWEIATGDIPFQGCNSEKIRKLVAVKRQQE
L	1		ATD A POST TOTAL A THIND THE LANGE OF COMMENTAL STATES AND ASSESSMENT OF THE PARTY

SEQ	Predicted	Predicted end	Dring
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=PIOLINE, O=Glutamine P-Arginine
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, Y=Unknown * Star
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion\
	1	}	PLGEDCPSELREIIDECRAHDPSVRPSVDEILKKLSTFSK*CIK
6845	3	1519	L
		1519	VAVRDECYWRHVFWDQDLWMLLFILMCHPETARARLEYRIRTLD
ŀ			GALENAQNLGYQGAKFAWESADSGLEVCPEDIYGVQEVHVNGAV
1		}	GLAFELYYHTTQDLQLFREAGGWDVVRAVAEFWCSRVEWSPREE
ł			KYHLRGVMSPDEYHSGVNNSVYTNVLVQNSLRFAAALAQDLGLP
			IPSQWLAVADKIKVPFDVEQNFHPEFDGYEPGEVVKQADVVLLG
•			YPVPFSLSPDVRRKNLEIYEAVTSPQGPAMTWSMFAVGWMELKD AVRARGLLDRSFANMAEPFKVWTENADGSGAVNFLTGMGGFLQA
ł	,		VVFGCTGFRVTRAGVTFDPVCLSGISRVSVSGIFYQGNKLNFSF
	[SEDSVTVEVTARAGPWAPHLEAELWPSQSRLSLLPGHKVSFPRS
			AGRIQMSPPKLPGSSSSEFPGRTFSDVRDPLQSPLWVTLGSSSP
			TESTTVDPASE*SGTGASETSLGPSI.WPRI.HPPI.TGTT.TACUDE
6846	0.00		PAARLSGKVHAAWPEFKAFCL
0040	213	1258	LYFLKTIK*LNRLAEHP*YENEKLTKLRNTIMEQYTRTEESARG
1			IIFTKTRQSAYALSQWITENEKFAEVGVKAHHI.TGAGUGGEPPVD
			MTQNEQKEVISKFRTGKINLLIATTVAEEGLDTKFCNTVTBVCT
ľ			VINEIAMVQARGRARADESTYVLVAHSGSGVIEHETUNDEDEVM
			MYKAIHCVQNMKPEEYAHKILELQMQSIMEKKMKTKRNIAKHYK
		•	NNPSLITFLCKNCSVLACSGEDIHVIEKMHHVNMTPEFKELYIV
			RENKTLOKKCADYQINGEIICKCGQAWGTMMVHKGLDLPCLKIR
6847	1450	348	NFVVVFKNNSTKKQYKKWVELPITFPNLDYSECCLFSDED SMCWNSDRLEMPLIDLALILYPPSYVPYTGHLSDDSLSRKYCLT
			WFEDALNGVL*RAEAIQPHCVNAGDRMEKFRQKYWNKLQTLRQQ
i .			PFAYGTLTVRSLLDTREHCLNEFNFPDPYSKVKQRENGVALRCF
			PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP
]			YFGFEEAKRKLQERPWLVDSYSEWLORLKGPPHKCALTEADNEC
1 1			IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTHSESLIVAE
1]	ľ		KIAGMDPVVHSALREERLLLVOTGSSSPCIDI.SPIDKGIAALUD
1 1	†		ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERI.G
6848	19		GRLFSVIFKYEVPAE
	19	16	AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND
1 1			LKVIIISAEGPVFSSGHDLKELTEEOGRDVHAEVFOTCERIMMI
1 1			IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN
1 1]		VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK
<u> </u>			VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH
6849	70	821	SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC
1 1			VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK
]	ľ		PRESGVEKIKTIGSTYMAATGI.NATSGODAOODAEDGGGVEGGVEGG
1	1		VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ
			YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG
6850			VIKVKGKGQLCTYFLNTDLTRTGPPSATLG
6630	2	1235	ARGLNHEWTFEKLROHISRNAODKOELHLFMISGVPDAVEDLTD
1			LDVLKLELIPEAKIPAKISQMTNLOELHLCHCPAKVEOTAFGET
1		ļ	RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNINSENNKMT
1	1	İ	GLESLRELRHLKILHVKSNLTKVPSNITDVAPHITKI.VTVNDCT
\$	1	}	KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLOELDLKS
į.		į	NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNI.FSI.
1	İ	ŀ	YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGIJONIO
Í			HLHITGNKVDILPKQLFKCIKLRTLNLGONCITSLPEKVGOLSO
}			LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK
6851	1765	660	EALNQDINIPFANGI
		980	VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD
		į	LRDLFNQVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA
			CYCVYKLTIGRDDSEKLEEEGEEEWDDDQELDEEEPDIWFDFET

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid		Codon, /=possible nucleotide deletion.
		sequence	\=possible nucleotide insertion)
ļ	sequence .	<u> </u>	MARPWTEDGDWTEPGAPGGTEDRPSGGGKANRAHPIKORPFPYE
1	1		·-
1	ļ	1	HKNTWSAQNCKNGSCVLDLSKCLFIQGKLLFAEPKDAGFPFSQD
1	1	1	INSHLASLSMARNTSPTPDPTVREALCAPDNLNASIESQGQIKM
I		ł	YINEVCRETVSRCCNSFLQQAGLNLLISMTVINNMLAKSASDLK FPLISEGSGCAKVQVLKPLMGLSEKPVLAGELVGAOMLFSFMSL
1	ļ	1	
			FIRNGNREILLETPAP
6852	1	407	RTRGEETYANFIKHNDGKNIFYAARTPATLFAVMFAMYIISGLT
1			GFIGLNSIAVLCNLVMGLALIFLCTWAYVKYSGEFREIGTVIDQ
1			IAETLWEQVLKPLGDNLMEENIRQSVTNSIKAGLTDQVSHHARL
			KTD
6853	3	469	GDSCAVCIELYKPNDLVRILTCNHIFHKTCVDPWLLEHRTCPMC
		1	KCDILKALGIEVDVEDGSVSLQVPVSNEIFNSASSHEEDNRSET
1			ASSGYASVQGTYEPPLEEHVQSTNESLQLVNHEANSVAVDVIPH
		<u> </u>	VDNPTFEEDETPNQETAVREIKS
6854	1148	585	HESYIGTFDPGELCVCAAIQWLQDNSASYFLNRKLVYEPSTQAK
	1	ł	PVKNTFLRMWIYSHHIYQQDLRKKILDVGKRLDVTGFCMTGKPG
1		ļ	IICVEGFKEHCEEFWHTIRYPNWKHISCKHAESVETEGNGEDLR
j]	}	LFHSFEELLLEAHGDYGLRNDYHMNLGQFLEFLKKHKSEHVFQI
L			LFGIESKSSDS
6855	1913	1148	GRVGGRVGRICSPLSGANEYIASTDTLKTEEVLLFTDQTDDLAK
1		1	EEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALASRF
1	1		YIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHI
j	ļ	ļ	QLTYFSRWSEVEDSCDSDAIERMYCAPEVGAITEETEACDWWSL
i		j	GAVLFELLTGKTLVECHPAGINTHTTLNMPEWVSEEARSLIQQL
	İ		LQFNPLERLGAGVAGVEDIKSHPFFTPVDWAELMR
6856	1617	997	VTQLYVSVDASTKDSLKKIDRPLFKDFWQQFLDSLKALAVKQQR
1	1	1	TVYRLTLVKAWNVDELQAYAQLVSLGNPDFIEVKGVTYCGESSA
1	1	1	SSLTMAHVPWHEEVVQFVRELVDLIPEYEIACEHEHSNCLLIAH
1	1		RKFKIGGEWWTWINYNRFQELIQEYEDSGSKTFSAKDYMARTP
	1	<u>i</u>	HWALFGASERGFDPKDTRHQRKNKSKAISGC
6857	1	617	KGPEATAMVCVCSHPNCRQNHIKPSHSAAQTWCGSPTPASAPNH
ł			KLMAMEQGKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF
1	1	1	DLQQRLSDEDGTNMHLQLVRQEMAVCPEQLSEFLDSLRQYLRGT
1		1	TGVRNCFHITAVRLSDGFTFVIYEFWETEEAWKRHLQSPLCKAF
L	<u> </u>	<u> </u>	RHVKVDTLSQPEALSRILVPAAWCTVGRD
6858	.2	669	RSRGIKDFENDPPLSSCGIFQSRIAGDALLDSGIRISSVFASPA
	1		LRCVQTAKLILEELKLEKKIKIRVEPGIFEWTKWEAGKTTPTLM
1			SLEELKEANFNIDTDYRPAFPLSALMPAESYQEYMDRCTASMVQ
		1	IVNTCPQDTGVILIVSHGSTLDSCTRPLLGLPPRECGDFAQLVR
1		1	KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS
			GN
6859	1	1150	GETMFKKAKTKAKKKPRKRSDSSGGYNLSDI1QSPSSTGLLKSG
1			KTNSVESLPELLTSDSEGSYAGVGSPRDLQSPDFTTGFHSDKIE
			AKVKPYVNGTSPVYSREDLKPWEKSPILKISAPQPIPSNRIDTT
1		1	SSASWVAGSFSPVSPPVVDLRTIMEIEESROKCGATPKSHLGKT
	1		VSHGVKLSQKQRKMIALTTKENNSGMNSMETVLFTPSKAPKPVN
	,		AWASSLHSVSSKSFRDFLLEEKKSVTSHSSGDHVKKVSFKGIEN
1			SQAPKIVRCSTHGTPGPEGNHISDLPLLDSPNPWLSSSVTAPSM
			VAPVTFASIVEEELOQEAALIRSREKPLALIQIEEHAIQDLLVF
			YEAFGNPEEFVIVERTPOGPLAVPMWNKHGC
6860	1889	1515	DKDKKROKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ
1			DTGLT1LQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP
			MGSPVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
6861	1889	1515	DKDKKRQKKRGIFPKVATNIMRAWLFQHLTHPYPSEEQKKQLAQ
		1 2323	DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQP
<u> </u>	<u> </u>	<u> </u>	PYON'T TO KAMME THE WORLT A KENITO KONIGATO KON THE PORT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1 1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
] }	sequence	0040000	\=possible nucleotide insertion)
		***************************************	MGSFVLDGQQHMGIRPAGPMSGMGMNMGMDGQWHYM
6862		471	EEIDREFHNKLKLKEDKLEKQEKPVNGEDKGDSGVDTQNSEGNA
1 1	_		DEEDPLGPNCYYDKTKSFFDNISCDDNRERRPTWAEERRLNAET
1			FGIPLRPNRGRGGYRGRGGLGFRGGRGGGRGGTFTAPRGFRG
1			GFRGGRGGREFADFEYRKTTAFGP
6863	2216	487	PQEPALKSEFSQVASNTIPLPLPQPNTCKDNGPCKQVCSTVGGS
1			AICSCFPGYAIMADGVSCEDQDECLMGAHDCSRRQFCVNTLGSF
1 1			YCVNHTVLCADGYILNAHRKCVDINECVTDLHTCSRGEHCVNTL
1	·		GSFHCYKALTCEPGYALKDGECEDVDECAMGTHTCOPGFLCONT
1			KGSFYCQARQRCMDGFLQDPEGNCVDINECTSLSEPCRPGFSCI
}			NTVGSYTCQRNPLICARGYHASDDGTKCVDVNECETGVHRCGEG
			QVCHNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCOHT
			CENTLGSYRCSCASGFLLAADGKRCEDVNECEAQRCSQECANIY
]			GSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILCTFRCLNVPGS
į l			YQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIOGS
1 1			FRCLRFECPPNYVQVSKTKCERTTCHDFLECQNSPARITHYQLN
			FQTGLLVPAHIFRIGPAPAFTGDTIALNIIKGNEEGYFGTRRLN
1			AYTGVVYLQRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHIFFT
<u> </u>			TFAL
6864	2	2933	LADSSPSNLQIIIKELLSMHHQPDPALTKEFDYLPPVDSRSSSG
1			FVGLRNGGATCYMNAVFQQLYMQPGLPESLLSVDDDTDNPDDSV
1			FYQVQSLFGHLMESKLQYYVPENFWKIFKMWNKELYVREQQDAY
1			EFFTSLIDQMDEYLKKMGRDQIFKNTFQGIYSDQKICKDCPHRY
1			EREEAFMALNLGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK
1			EKRITVKRTCIKSLPSVLVIHLMRFGFDWESGRSIKYDEQIRFP
			WMLNMEPYTVSGMARQDSSSEVGENGRSVDQGGGGSPRKKVALT
1			ENYELVGVIVHSGQAHAGHYYSFIKDRRGCGKGKWYKFNDTVIE
1			EFDLNDETLEYECFGGEYRPKVYDQTNPYTDVRRRYWNAYMLFY
1 1			QRVSDQNSPVLPKKSRVSVVRQEAEDLSLSAPSSPEISPQSSPR
1		l	PHRPNNDRLSILTKLVKKGEKKGLFVEKMPARIYQMVRDENLKF
		l	MKNRDVYSSDYFSFVLSLASLNATKLKHPYYPCMAKVSLQLAIQ
1	3		
			FLFQTYLRTKKKLRVDTEEWIATIEALLSKSFDACQWLVEYFIS
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVYYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL
6865	1820	1242	SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP
6865	1820	1242	SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQSMMPSCNRS
6865	1820	1242	SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV
6865	1820	1242	SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVYYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPFKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ
6865	1820	1242	SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVYYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVQTIQPKRDS
6865	1820	1242	SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVQTIQPKRDS DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVQTIQPKRDS DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF IIEGMBEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVQTIQPKRDS DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVQTIQPKRDS DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF IIEGMBEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLBEYRNSSR
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVYYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGTAVPFKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVQTIQPKRDS DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP ALTYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFILIGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVYYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVQTIQPKRDS DCPRPYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKATHLDLEEYRNSSR VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTL
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFLIGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIPRNASGQSWFSPPAS PFGQSSVQTIQPKRDS DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV IGKFSIRLVPHMNVSAVEKQVTRHLEDVPSKRNSSNKMVVSMTL GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL LRHSALRHMISFILIGASRQNNQIRRWSSAQAREFGNLHNTVALL VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM SEGKPYLLEVMFALRELTGSLLALIEMVYYCCFCNEHFSFTMLH FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFETEN GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL RSDLDDVDP DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS PFGQSSVQTIQPKRDS DCPRPYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG SLVDSSGHILVPGIYDEVVPLTEEEINTYKATHLDLEEYRNSSR VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ		sequence	\=possible nucleotide insertion)
	sequence	1704	GTRIMSQPKQKELAGFVRQKMLLDYSVYMGRCVPQESRSPQRSP
6867	2833	1704	LOSAESSPTAGKKLPEVPPSEEEEQEAWVNALLGRIFWDFLGEK
1	1		YWSDLVSKKIQMKLSKIKLPYFMNELTLTELDMGVAVPKILQAF
1	ļ	ł	IMSDBVSKTQMALSKIKIPIPINEBIBIBIBIDIOVAVPKISQMI
1	1	}	KPYVDHQGLWIDLEMSYNGSFLMTLETKMNLTKLGKEPLVEALK
ì	Ļ		VGEIGKEGCRPRAFCLADSDEESSSAGSSEEDDAPEPSGGDKQL
		Į.	LPGAEGYVGGHRTSKIMRFVDKITKSKYFQKATETEFIKKKIEE
1		(VSNTPLLLTVEVQECRGTLAVNIPPPPTDRVWYGFRKPPHVELK
			ARPKLGEREVTLVHVTDWIEKKLEQEFQKVFVMPNMDDVYITIM
1	1	Ţ	HSAMDPRSTSCLLKDPPVEAADQP
6868	1	346	RPTRPPTRPEEIKNLILPYISDMNFVQDLCEDFYELFKTDKGFD
1	<u> </u>		KATFESQMSVMRGQILNLTQALRDGKSPFQLVQIPCVIVERSQG
Ì	1		GSQGRIVHLSNSFTQTVNCRKPFFSSW
6869	3	1619	MYMERMDKRALISFWESVEHLKNANKNEIPQLVGEIYQNFFVES
6009	1 3	1017	KEISVEKSLYKEIQQCLVGNKGIEVFYKIQEDVYETLKDRYYPS
1	1		FIVSDLYEKLLIKEEEKHASQMISNKDEMGPRDEAGEEAVDDGT
1	i	1	NQINEQASFAVNKLRELNEKLEYKRQALNSIQNAPKPDKKIVSK
1	}	1	LKDEIILIEKERTDIQLHMARTDWWCENLGMWKASITSGEVTEE
Į.	,	1	NGEQLPCYFVMVSLQEVGGVETKNWTVPKRLSEFHNLHRKLSEC
1	1	ì	VPSLKKDQLPSLSKLPFKSIDHTFMEKFENQLNKFLQNLLSDER
		ſ	VPSLKKDQLPSLSKLPFKSIDHIFMEKFENQDIKKFDQKDDSDBK
	1	ł	LCQSEALYAPLSPSPDYLKVIDVQGKKNSFSLSSFLERLPRDFF
	1	1	SHQEEETEEDSDLSDYGDDVDGRKDALAEPCFMLIGEIFELRGM
Ì			FKWVRRTLIALVQVTFGRTINKQIRDTVSWIFSEQMLVYYINIF
1	1	Ì	RDAFWPNGKLAPPTTIRSKEQSQETKQRAQQKLLENIPDMLQSL
ì	· ·	1	VGQQNARHGIIKIFNALQETRANKHLLYALMELLLIELCPELRV
Ì		1	HLDQLKAGQV
6870	1	1566	MAAVVAATRWWQLLLVLSAAGMGASGAPQPPNILLLLMDDMGWG
1		ł	DLGVYGEPSRETPNLDRMAAEGLLFPNFYSANPLCSPSRAALLT
1		4	GRLPIRNGFYTTNAHARNAYTPQEIVGGIPDSEQLLPELLKKAG
		ţ	YVSKIVGKWHLGHRPQFHPLKHGFDEWFGSPNCHFGPYDNKARP
		1	NIPVYRDWEMVGRYYEEFPINLKTGEANLTQIYLQEALDFIKRQ
ļ		ļ	ARHHPFFLYWAVDATHAPVYASKPFLGTSQRGRYGDAVREIDDS
]	ļ	1	IGKILELLQDLHVADNTFVFFTSDNGAALISAPEQGGSNGPFLC
	Į	1	GKQTTFEGGMREPALAWWPGHVTAGQVSHQLGSIMDLFTTSLAL
-			AGLTPPSDRAIDGLNLLPTLLQGRLMDRPIFYYRGDTLMAATLG
	1		QHKAHFWTWTNSWENFRQGIDFCPGQNVSGVTTHNLEDHTKLPL
1	1		IFHLGRDPGERFPLSFASAEYQEALSRITSVVQQHQEALVPAQP
1			QLNVCNWAVMNWAPPGCEKLGKCLTPPESIPKKCLWSH
	 	1126	RMSLNPP1FLKRSEENSSKFVETKQSQTTS1ASEDPLQNLCLAS
6871	209	1126	QEVLQKAQQSGRSKCLKCGGSRMFYCYTCYVPVENVPIEQIPLV
1			QEVLQKAQQSGRSKCbkccgSkmfiCifCivFvEnvFiEQIFDV KLPLKIDIIKHPNETDGKSTAIHAKLLAPEFVNIYTYPCIPEYE
1	ļ		VPBPVIDITYWENPIDOVOTOTADIOMA OAD TONIMOOANDODDA DO
1	l l	İ	EKDHEVALIFPGPQSISIKDISFHLQKRIQNNVRGKNDDPDKPS
1	1	1	FKRKRTEEQEFCDLNDSKCKGTTLKKIIFIDSTWNQTNKIFTDE
ł			RLQGLLQVELKTRKTCFWRHQKGKPDTFLSTIEAIYYFLVDYHT
1	1		DILKEKYRGQYDNLLFFYSFMYQLIKNAKCSGDKETGKLTH
6872	880	459	FGLLMVVLSLIFMKGNCVREDLIFNFLFKLGLDVRETNGLFGNT
1	1		KKLITEVFVRQKYLEYRRIPYTEPAEYEFLWGPRAFLETSKMLV
1			LRFLAKLHKKDPQSWPFHYLEALAECEWEDTDEDEPDTGDSAHG
1		1	PTSRPPPR
6873	1929	955	DEQAVLCSKDKTYDLKIADTSNMLLFIPGCKTPDQLKKEDSHCN
1 30,3	1929	1	IIHTEIFGFSNNYWELRRRRPKLKKLKKLLMENPYEGPDSQKEK
1		1	DSNSSKYTTEDLLDQIQASEEEIMTQLQVLNACKIGGYWRILEF
		1	DYEMKILNHVTQLVDSESWSFGKVPLNTCLQELGPLEPEEMIEH
1			CLKCYGKKYVDEGEVYFELDADKICRAAARMLLQNAVKFNLAEF
1			QEVWQQSVPEGMVTSLDQLKGLALVDRHSRPEIJFLLKVDDLPE
1			QEVWQQSVPEGMVTSLDQLKGLALVDRHSKPEIIFDBKVDDFF DNQERFNSLFSLREKWTEEDIAPYIQDLCGEKQTIGALLTKYSH
		1	TOWNED PROTERO DECEMBER OF A DY LODD COMMUNICATION
	1		SSMONGVKVYNSRRPIS

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
6874	1	207	\=possible nucleotide insertion)
-0.1	1 -	307	DSIADHVNSAAVNVEEGTKNLGKAAKYKLAALPVAGALIGGMVG
1		ł	GPIGLLAGFKVAGIAAALGGGVLGFTGGKLIQRKKQKMMEKLTS
6875	1688		SCPDLPSQTDKKCS
***	1000	349	VIGTGERGNSASEKWEIMFNEELGDPFIIIHSISLLNAEEHSIA
}			TLLLRIEKEELDMKGSGFYVSLEWVTISKKNQDNKKYEIIKRDI
			LRGKSVPHYAAIEPDGNGLMIVSYKSLTFVQAGQDLEENMDEDI
1			SEKIKEPLYYWQQTEDDLTVTIRLPEDNTKEDIQIQFLPDHINI
l l	ł.		VLKDHQFLEGKLYSSIDHESSTWIIKESNSLEISLIKKNEGLTW
	}		PELVIGDKQGELIRDSAQCAAIAERLMHLTSEELNPNPDKEKPP
į.			CNAQELEECDIFFEESSSLCRFDGNTLKTTHVVNLGSNQYLFSV
	į		IVDPKEMPCFCLRHDVDALLWQPHSSKQDDMWEHIATFNALGYV
İ	1		QASKRDKKFFACAPNYSYAALCECLRRVFIYRQPAPMSTVLYNR
1	}		KEGRQVGQVAKQQVASLETNDPILGFQATNBRLFVLTTKNLFLI
6876	41	1205	KVNTEN
1	7.4	1285	VGEMTLIWRHLLRPLCLVTSAPRILEMHPFLSLGTSRTSVTKLS
Į.			LHTKPRMPPCDFMPERYQVIFLVNSGSEANELAMLMARAHSNNI
1			DIISFRGAYHGCSPYTLGLTNVGIYKMELPGGTGCQPTMCPDVF
1			RGPWGGSHCRDSPVQTIRKCSCAPDCCQAKDQYIEQFKDTLSTS
1			VAKSIAGFFAEPIQGVNGVVQYPKGFLKEAFELVRARGGVCIAN
			EVQTGFGRLGSHFWGFQTHDVLPDIVTMAKGIGNGFPMAAVITT
1			PEIAKSLAKCLQHFNTFGGNPMACAIGSAVLEVIKEENLQENSQ
			EVGTYMLLKFAKLRDEFEIVGDVRGKGLMIGIEMVQDKISCRPL
	1		PREEVNQIHEDCKHMGLLVGRGSIFSQTFRIAPSMCITKPEVDF
6877	1	778	AVEVFRSALTQHMERRAK
			GTSPSPARAYAPPTERKRFYQNVSITQGEGGFEINLDHRKLKTP
			QAKLFTVPSEALAIAVATEWDSQQDTIKYYTMHLTTLCNTSLDN
1 .			PTQRNKDQLIRAAVKFLDTDTICYRVEEPETLVELQRNEWDPII
1			EWAEKRYGVEISSSTSIMGPSIPAKTREVLVSHLASYNTWALQG
1 1			IEFVAAQLKSMVLTLGLIDLRLTVEQAVLLSRLEEEYQIQKWGN IEWAHDYELQELRARTAAGTLFIHLCSESTTVKHKLLKE
6878	931	263	QTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
1 1			LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAP
	1		EYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLD
	1		TGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVIS
			VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSF
<u> </u>	}	ĺ	II
6879	3	845	IRVIGESDIMQEFLSESDENYNGVSDVELRVALPDGTTVTVRVK
1			KNSTTDQVYQAIAAKVGMDSTTVNYFALFEVISHSFVRKLAPNE
1			FPHKLYIQNYTSAVPGTCLTIRKWLFTTEEEILLNDNDLAVTYF
i 1	.		FHQAVDDVKKGYIKAEEKSYQLQKLYEQRKMVMYLNMLRTCEGY
	j		NEIIFPHCACDSRRKGHVITAISITHFKLHACTEEGQLENQVIA
] [i	FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWVKIFTPYPNYMHE
		1	CFERVFCELKWRKEEY
6880	2110	1437	RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISS
1		1	MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRS
		l	NRDQIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMFH
1	1	ĺ	VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNAS
!!	!	ļ	KPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESD
		. (EDTP
6881	2638	2244	NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEPR
			QRVAAVKDLIRQLPKPNQDTMQILFRHLRRVIENGEKNRMTYQS
<u> </u>			IAIVFGPTLLKPEKETGNIAVHTVYQNQIVELILLELSSIFGR
6882	1	850	GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVIN
1	i	i	QEGNMVTARQEPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTPT
1			TNAVHKCRVHGLEIEGRDCGEATAQWITSFLKSQPYRLVHFEPH
<u> </u>			MRPRRPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLEK
		<u> </u>	THE TOTAL TOTAL STATE OF THE ST

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	1		Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		KVKATNFRPNIVISGCDVYAEDSWDELLIGDVELKRVMACSRCI
			KVKATNYRPNIVISGCDVIAEDSWDEIDIGDVEDKKVIACSKCI
		i	LTTVDPDTGVMSRKEPLETLKSYRQCDPSERKLYGKSPLFGQYF
	1	Į	VLENPGTIKVGDPVYLLGQ
6883	2794	2256	NSKLKLNQNLKLFITLTYQVLSLHGWGPGIHLQKEGAFPVTQNR
0003	1		ALQLLYDLRYLNIVLTAKGDEVKSGRSKPDSRIEKVTDHLEALI
	i	}	DPFDLDVFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPRSSTF
	Į.		NSQEPHNILPLASSQIRFGLLPLSMTSTRKAKSTRNIETKAQYD
	1	1	
			ANC
6884	2	99	EFERVTAEAVKPRETSEPRAAAQRFCEKFPFL
6885	297	1554	STGQFWHVTDLHLDPTYHITDDHTKVCASSKGANASNPGPFGDV
		I	LCDSPYQLILSAFDFIKNSGQEASFMIWTGDSPPHVPVPELSTD
			TVINVITNMTTTIOSLFPNLQVFPALGNHDYWPQDQLSVVTSKV
1		}	YNAVANLWKPWLDEEAISTLRKGGFYSQKVTTNPNLRIISLNTN
	1	1	LYYGPNIMTLNKTDPANQFEWLESTLNNSQQNKEKVYIIAHVPV
ļ			GYLPSSQNITAMREYYNEKLIDIFQKYSDVIAGQFYGHTHRDSI
]	1	1	MVLSDKKGSPVNSLFVAPAVTPVKSVLEKQTNNPGIRLFQYDPR
			DYKLLDMLQYYLNLTEANLKGESIWKLEYILTQTYDIEDLQPES
ļ		ì	DYKPPDWFGAAFURGESIMMTETTHATATATATATATATATATATATATATATATATATA
ļ.		i	LYGLAKQFTILDSKQFIKYYNYFFVSYDSSVTCDKTCKAFQICA
1		1	IMNLDNISYADCLKQLYIKHNY
6886	2	1341	QCGGIPGREGGSSRPLEEGTGSSPACVRGAAPGSEDAFYPTRAK
1 0000	-	l	QARVSQELKKAAKRTVSISEGPDTLGDGMRERRETLALAPEPEP
	1	1	LEKEACEKWKRPFRSASATSLTLSHCVDVVKGLLDFKKRRGHSI
i	1	1	GGAPEQRYQIIPVCVAARLPTRAQDVLDAHLSEVNAVRFGPNSS
ì	1	1	LLATGGADRLIHLWNVVGSRLEANQTLEGAGGSITSVDFDPSGY
1	1	· I	QVLAATYNQAAQLWKVGEAQSKETLSGHKDKVTAAKFKLTRHQA
I	1	1	VTGSRDRTVKEWDLGRAYCSRTINVLSYCNDVVCGDHIIISGHN
1	l .	ì	DQKIRFWDSRGPHCTQVIPVQGRVTSLSLSHDQLHLLSCSRDNT
			DOKIRFWDSRGPHCTQVIPVQGRVISISISISIDQUINDISCSRDNI
l .	1	1	LKVIDLRVSNIRQVFRADGFKCGSDWTKAVFSPDRSYALAGSCD
1 .	l l	1	GALYIWDVDTGKLESRLQGPHCAAVNAVAWCYSGSHMVSVDQGR
1	1		KVVLWQ
6887	1047	116	WTARPSQKPFWEAGAVPGDPLSTGCSQAQLGGCCPRGPWGPQHG
""	104,		GOORAAGPTLPRGERGGPQQSGPGLAAQTPPTSKQVAWRAFLTG
1	Į.	ŀ	TYRSQSPRSPAGPFRGGTGWWPEPAVCLCVAVGPQRLSSPGLVY
1			NASGSEHCYDIYRLYHSCADPTGCGTGPDARAWDYQACTEINLT
1	1	l l	FASNNVTDMFPDLPFTDELRQRYCLDTWGVWPRPDWLLTSFWGG
1			PASNNVTDMFPDLPFTDEEKQRICLDIWGVWFRFDWHDHISPWGG DLRAASNIIFSNGNLDPWAGGGIRRNLSASVIAVTIQGGAHHLD
1			DLRAASNIIFSNGNLDPWAGGGIKKNLSASVIAVIIVGGARRUD
1		1	LRASHPEDPASVVEARKLEATIIGEWVKAARREQQPALRGGPRL
1			SL
6888	1	992	FVAYVKKEIPHIVVTHCLLNPHALVIKTLPTKLRDALFTVVRVI
	_		NETKCRAPNHRLFOAFFEEIGIEYSVLLFHTEMRWLSRGQILTH
ŀ	1	1	IFEMYEEINQFLHHKSSNLVDGFENKEFKIHLAYLADLFKHLNE
1	1		LSASMORTGMNTVSAREKLSAFVRKFPFWQKRIEKRNFTNFPFL
1	{		EEIIVSDNEGIFIAAEITLHLQQLSNFFHGYFSIGDLNEASKWI
1		1	LDPFLFNIDFVDDSYLMKNDLAELRASGQILMEFETMKLEDFWC
1	1	ł	POLLPRATOLAND I PRIMANTATIVA CEL CECTEBEBONAMENT
1		1	AQFTAFPNLAKTALEILMPFATTYLCELGFSITFTFQNKVPEAA
1	1	1	LILSDDIRVAISKKVPSFLGHH
6889	1	1534	LTLENQIKEEREQDNSESPNGRTSPLVSQNNEQGSTLRDLLTTT
	1 -		AGKLRVGSTDAGIAFAPVYSMGAPSSKSGRTMPNILDDIIASVV
1		1	ENKIPPSKTSKINVKPELKEEPEESIISAVDENNKLYSDIPHSW
1	1	I	ICEKHILWLKDYKNSSNWKLFKECWKQGQPAVVSGVHKKMNISL
i		1	WKAESISLDFGDHQADLLNCKDSIISNANVKEFWDGFEEVSKRQ
1			WKAESIShDFGDMQADDBWCKDSIISMAKVKBFWDGFBBVSKQ
			KNKSGETVVLKLKDWPSGEDFKTMMPARYEDLLKSLPLPEYCNP
1	1	1	EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI
1	l .	1	EVSDVVNILVYVGIAKGNGILSKAGILKKFEEEDLDDILRKRLK
1	1	i	DSSEIPGALWHIYAGKDVDKIREFLQKISKEQGLEVLPEHDPIR
1	Į.		DOSWYVNKKLRQRLLEEYGVRTWTLIQFLGDAIVLPAGALHQVQ
1	1	i	

SEO	Predicted	I Buoglana	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-ct
1	amino acid	sequence	Codon, /=possible nucleotide deletion
-	sequence		\=possible nucleotide insertion)
j			NFHSCIQVTEDFVSPEHLVESFHLTQELRLLKEEINYDDKLQVK
6890	3		NILYHAVKEMVRALKIHEDEVDDMEEN
1 3333	,	667	THACGMWIPLYLHRALVVHKTAETCNSPPCGAKDSLIFGAITCF
1			TGFLGVDTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFV
			AAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAV
1	1		ALQSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYA LMLCPFVVVLGGMFFLATALFFVSDRARAEQQVNQLAMPPASVK
Ī			V V VIGGER FILATADE F VSDRARAE QQVNQLAMPPASVK
6891	1980	1262	LRIHQELLSKELKLLRGITIESIIHIGLAAGKEQFMQDASNVMQ
1			LLLKTQSHLYNMEDNNPEVROAAAYGLGVMAOFGGDDVPCLCCE
			AVPLLVKVIKRAHSKTKKNVIATENCISAIGKILKEKPNCVARD
1			EVLPHWLSWLPLHEDKEEAIQTLSFLCDLIESNHPUVIGPNNSN
			LPKIISIIAEGKINETINYEDPCAKRLANVVROVOTSEDI.WI.EC
6892	3	076	VSQLDDEQQEALQELLNFA
	}	876	RSVAAASGPGAWGTDHYCLELLRKRDYEGYLCSLLLPAESRSSV
			FALRAFNVELAQVKDSVSEKTIGLMRMQFWKKTVEDIYCDNPPH
			QPVAIELWKAVKRHNLTKRWLMKIVDEREKNLDDKAYRNIKELE NYAENTQSSLLYLTLEILGIKDLHADHAASHIGKAQGIVTCLRA
			TPYHGSRRKVFLPMDICMLHGVSQEDFLRRNQDKNVRDVIYDIA
} .			SQAHLHLKHARSFHKTVPVKAFPAFLQTVSLEDFLKKIQRVDFD
			IFHPSLQQKNTLLPLYLYIQSWRKTY
6893	1	842	DGERKSMSVERTFSEINKAEEQYSLCOELCSELAODLOKERLKG
			RTVTIKLKNVNFEVKTRASTVSSVVSTAEEIFAIAKELLKTEID
]			ADFPHPLRLRLMGVRISSFPNEEDRKHOORSIIGFLOAGNOALS
1			ATECTLEKTOKOKFVKPLEMSHKKSFFDKKRSERKWSHQDTFKC
1 1			EAVNKQSFQTSQPFQVLKKKMNENLEISENSDDCQILTCPVCFR
			AQGCISLEALNKHVDECLDGPSISENFKMFSCSHVSATKVNKKE NVPASSLCEKQDYEAH
6894	1742	1463	TTLCKPLVPREHQFYETLPAEMRKFTPQYKGKSQLLEGLPHWRG
1 1	ľ		DVRDRGHGRPWQPSLEPSLPPTLCFPSLSSFSSSWPSAQHLTPS
- 5005			VFNPW
6895	2379	478	VTYVELCOLASPTALLIMRTVLDLIVEDLQSTSEDKEQQYTSQT
1 1	{		TRLLALLYALASHKACKLAILHLINGTIKGDERVAETFODLLAI.
1 1	1		VRSPGDSVIRQQCVEYVTSILQSLCDQDIALILPSSSEGSISEL
} }	ļ		EQLSNSLPNKELMTSICDCLLATLANSESSYNCLLTCVRTMMFL
			AEHDYGLFHLKSSLRKNSSALHSLLKRVVSTFSKDTGELASSFL EFMRQILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAAELKQLL
1			OSKEESPENLFLELEKLVLEHSKDDDNLDSLLDSVVGLKQMLES
1 1			SGDPLPLSDQDVEPVLSAPESLQNLFNNRTAYVLADVMDDQLKS
		ĺ	MWFTPFQAEEIDTDLDLVKVDLIELSEKCCSDFDLHSELERSFI.
			SEPSSPGRTKTTKGFKLGKHKHETFITSSGKSEYIEPAKRAHVV
] [I	PPPRGRGGGGGGGIRPHDIFRQRKQNTSRPPSMHVDDFVAARS
1		İ	KEVVPQDGIPPPKRPLKVSQKISSRGGFSGNRGGRGAFHSONRF
1 1		ł	FTPPASKGNYSRREGTRGSSWSAQNTPRGNYNESRGGQSNFNRG
[[i i	İ	PLPPLRPLSSTGYRPSPRDRASRGRGGLGPSWASANSGSGGSRG
6896	1	. 555	KFVSGGSGRGRHVRSFTR GNIVIQKKKYNKQHIIPLENVTIDSIKDEGDLRNGWLIKTPTKS
]]	1		FAVYAATATEKSEWMMHINKCVTDLLSKSGKTPSNEHAAVWVPD
	1		SEATVCMRCQKAKFTPVNRRHHCRKCGFVVCGPCSEKRFLLPSQ
			SSKPVRICDFCYDLLSAGDMATCQPARSDSYSQSLKSPLNDMSD
6965			DDDDDDSSD
6897	3	920	GDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY
		į.	AGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVT.
		į.	SLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLA
1			YLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDR
			DFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid		Codon, /=possible nucleotide deletion,
	į .	sequence	\=possible nucleotide insertion)
<u> </u>	sequence		LRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGE
1	Ì		LMVSEAVOGQVHPNYFWMVSGCVEPPPSWKPQQMPPPEEPL
1000			
6898	919	346	QKTVTAVASLLKGRQGIYTENERRMGAVIKIRFFKIMLVLIICW
]	1		LSNIINESLLFYLEMQTDINGGSLKPVRTAAKTTWFIMGILNPA
1	ļ		QGFLLSLAFYGWTGCSLGFQSPRKEIQWESLTTSAAEGAHPSPL
			MPHENPASGKVSQVGGQTSDEALSMLSEGSDASTIEIHTASESC
1			NKNEGDPALPTHGDL
6899	120	827	MKVRKNNDAYLLDKNKINMDCFISCFFKKMLTTLMFSHSGILSL
			LEHGEEYTFSLPCAYARSILTVPWVELGGKVSVNCAKTGYSASI
1	1		TFHTKPFYGGKLHRVTAEVKHNITNTVVCRVQGEWNSVLEFTYS
!	İ	1	NGETKYVDLTKLAVTKKRVRPLEKQDPFESRRLWKNVTDSLRES
			EIDKATEHKHTLEERQRTEERHRTETGTPWKTKYFIKEGDGWVY
	<u> </u>		HKPLWKIIPTTQPAE
6900	3	451	TEVLGSKGIHELRSSTSALHHALBESASLLTMFWRAALPSTHIP
	!		VLPGKVGESTERELLELRTKVSQQEQLLQSTTEHLKNANQQKES
1			MEQFIVSQLTRTHDVLKKARTNLEVRKLLHQSEAPSLSPTHHHP
L			LADLVGDSWPALRFQEK
6901	1	201	DDNMVQRLETDFKMTLQQQSTLEQWAAWLDNVMMQALKPYEGRP
			SFPKAARQFLLKWSFYRYHLGFS
6902	2	267	GAPPPPPSQPPRQPPQAAPSSHPHSDLTFNPSSALEGQAGAQGA
			SDMPEPSLDLLPELTNPDELLSYLDPPDLPSNSNDDLLSLFENN
6903	1	149	RINQVYRQGPTGIHILVIDQMVQNFQDESCFLFSTVKAESSDGI
			HIILK
6904	464	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC
]	1		VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA
1	!		DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF
1	i		SPKDVSSLRMMLCTTSQPKGVDILLTSPWPKCVGNFGNSSGEVD
1	1		TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN
ł			AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD
1			VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS
	1		TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH
1			CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL
1	İ		RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR
1			IKKNFPLOFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR
1	1		FRKDPEPYDFTLDD
6905	1	226	VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI
1 3,03	1.	220	VAGLVOTVLYCDFFYLYITKVLKGKKLSLPA
6906	3	611	SYDDHNGHIDFITAASNLRAKMYSIEPADRFKTKRIAGKIIPAI
5500]		ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET
	1		TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGIE
	1		PTMVVOGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV
1	1		SFAPDIDGDEDLPGPPVRYYFSHDTD
6907	2	2228	LRGVPVWAAGAFRFSSGEESTSHLIMSRRSORLTRYSOGDDDGS
1	_	2260	SSSGGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPSS
			DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRGT
1	}		GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDOOSS
			SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTAA
1	1		SLLDVFVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGLQ
			TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHSL
1			ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGGLSHED
İ			TLALLEGLVSRREAALKEDFRRETAARIOEELSALRAEHOODSE
1			DLFKKIVRASQESEARIOOLKSEWQSMTQESFQESSVKELRRLE
			DQLAGLQQELAALALKQSSVAEEVGLLPQQIQAVRDDVESQFPA
		i	WISQFLARGGGGRVGLLQREEMQAQLRELESKILTHVAEMQGKS
L	L	<u></u>	X- THOOGOVI CONNECTION OF THE PROPERTY AND ACTION

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			AREAAASLSLTLOKEGVIGVTEEOVHHIVKQALORYSEDRIGLA
1	i	1	DYALESGASVISTRCSETYETKTALLSLFGIPLWYHSQSPRVI
1			LQPDVHPGNCWAFQGPQGFAVVRLSARIRPTAVTLEHVPKALSP
	1		NSTISSAPKDFAIFGFDEDLQQEGTLLGKFTYDQDGEPIQTFHF
.	1		QAPTMATYQVVELRILTNWGHPEYTCIYRFRVHGEPAH
6908	3	780	QVPSAAWLMAVCGLGSRLGLGSRLGLOGCFGAARLLYPRFQSRG
1 0500	!	/80	POGVEDGDRPOPSSKTPRIPKIYTKTGDKGFSSTFTGERRPKDD
	i	ł	QVFEAVGTTDELSSAIGFALELVTEKGHTFAEELOKIQCTLQDV
1		ł	GSALATPCSSAREAHLKYTTFKAGPILELEQWIDKYTSQLPPLT
1	į.	Ì	AFILPSGGKISSALHFCRAVCRRAERRVVPLVQMGETDANVAKF
}	ì		
6909	 	400	LNRLSDYLFTLARYAAMKEGNQEKIYKKNDPSAESEGL
6909	3	409	GRLLAVGTDLYGQRSSAPEQELLVQDATPVSNSLLPEKAFSDIP
1	1		SPYLRGTIKMMQAVRQAFQDQDDRRTWDGRPLTMAATFDDCLYA
1	i		LCVVDTIKRSSQTGEWQNIAIMTEEPELSPAYLISEAMRRSRMS
6910			LYC
6910	1	1068	LVPVVVIDSYYYGKLVIAPLNIVLYNIFTPHGPDLYGTEPWYFY
	Į.		LINGFLNFNVAFALALLVLPLTSLMEYLLQRFHVQNLGHPYWLT
1		ł	LAPMYIWFIIFFIQPHKEERFLFPVYPLICLCGAVALSALQHSF
		[LYFQKCYHFVFQRYRLEHYTVTSNWLALGTVFLFGLLSFSRSVA
1			LFRGYHGPLDLYPEFYRIATDPTIHTVPEGRPVNVCVGKEWYRF
			PSSFLLPDNWQLQFIPSEFRGQLPKPFAEGPLATRIVPTDMNDQ
l l			NLEEPSRYIDISKCHYLVDLDTMRETPREPKYSSNKEEWISLAY
1	ł	ì	RPFLDASRSSKLLRAFYVPFLSDQYTVYVNYTILKPRKAKQIRK
6911	1104		KSGG
6311	1184	966	GEDAEEMETGNVANLISIFGSSFSGLLRKSPGGGREEEEGEESG
6912	ļ		PEAAEPGQICCDKPVLRDMNPWSTAIVAF
0912	1	844	AMKPVETHSFQMLFTILSTGSALKAQSYEDAYRCIKSSILLGSI
1	1	l	SGGTDIISCFMGHNFSLPVYKGEIQARNLGMAVEAWNEEGKAVW
}	1		GESGELVCTKPIPCQPTHFWNDENGNKYRKAYFSKFPGIWAHGD
	1		YCRINPKTGGIVMLGRSDGTLNPNGVRFGSSEIYNIVESFEEVE
	1		DSLCVPQYNKYREERVILFLKMASGHAFQPDLVKRIRDAIRMGL
1	1	ł	SARHVPSLILETKGIPYTLNGKKVEVAVKQIIAGKAVEQGGAFS
6913	1643	155	NPETLDLYRDIPELQGF
	1643	. 1558	KKSHEESHKEELSYGAQASLPLPCSDFR
6914	1251	615	ELAAECKSAGYPGTLIPYRCDLSNEEDILSMFSATRSQHSGVDI
1	1	l	CINNAGLARPDTLLSGSTSGWKDMFNVNVLALSICTREAYQSMK
1	1		ERNVDDGHIININSMSGHRVLPLSVTHFYSATKYAVTALTEGLR
1	1	l	QELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMK
L-	ļ		CLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT
6915	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
	l		ALILTELLMVALTVRTWHWLMVVABFLSLGCYVSSLAFLNEYFD
			VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6916	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
1			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
	L	<u>[</u>	VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6917	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISFT
i			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYFD
	<u>L</u>	i	VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLAS
6918	28	921	PEAGTRSWREPDPEDLRRFLLSAACRSFPQWLPGGGGGQVSSCS
1		i	DTDVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLGSP
1			VGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLAW
			LGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLGE
			VFTQAMPLRKPGGPFYVPESFFEGGYPAYASGGGYVIAGRLAPW
1			LLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADRT
1			ADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC
		L	_ = = = = = = = = = = = = = = = = = = =

		n - 3/ 3 3	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Tsoleucine, K=Lysine,
	location	corresponding	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first		P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	, · · · · · · · · · · · · · · · · · · ·
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sedneuce	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6919	850	41	QGRRELSGSVFCPFIQQEPKEMLTLSEYHERVRSQGQQLQQLQA
1	[ELDKLHKEVSTVRAANSERVAKLVFQRLNEDFVRKPDYALSSVG
	1	}	ASIDLQKTSHDYADRNTAYFWNRFSFWNYARPPTVILEPHVFPG
	1	ļ	NCWAFEGDQGQVVIQLPGRVQLSDITLQHPPPSVEHTGGANSAP
1	1		RDFAVFFLLSFFTHQGLQVYDETEVSLGKFTFDVEKSEIQTFHL
1	1		QNDPPAAFPKVKIQILSNWGHPRFTCLYRVRAHGVRTSEGAEGS
			AQGPH
6920	1418	591	EAQGPSKVHLTLKKKK
6921	2	1711	MNATRSEEQFHVINHAEQTLRKMENYLKEKQLCDVLLIAGHLRI
1			PAHRLVLSAVSDYFAAMFTNDVLEAKQEEVRMEGVDPNALNSLV
1		1	QYAYTGVLQLKEDTIESLLAAACLLQLTQVIDVCSNFLIKQLHP
1	1]	SNCLGIRSFGDAQGCTELLNVAHKYTMEHFIEVIKNQEFLLLPA
1	1		NEISKLLCSDDINVPDEETIFHALMQWVGHDVQNRQGELGMLLS
1	1	1	YIRLPLLPPQLLADLETSSMFTGDLECQKLLMEAMKYHLLPERR
		1	SMMQSPRTKPRKSTVGALYAVGGMDAMKGTTTIEKYDLRTNSWL
1	1		HIGTMNGRRLQFGVAVIDNKLYVVGGRDGLKTLNTVECFNPVGK
i	•	1	IWTVMPPMSTHRHGLGVATLEGPMYAVGGHDGWSYLNTVERWDP
1			EGRQWNYVASMSTPRSTVGVVALNNKLYAIGGRDGSSCLKSMEY
		İ	FDPHTNKWSLCAPMSKRRGGVGVATYNGFLYVVGGHDAPASNHC
	1	<u> </u>	SRLSDCVERYDPKGDSWSTVAPLSVPRDAVAVCPLGDKLYVVGG
}	}		YDGHTYLNTVESYDAQRNEWKEEVPVNIGRAGACVVVVKLP
6922	1075	369	LTPPAGIRHEVRDREREREREREREKFPLDSTGSELKQNIHSIT
1		ľ	GLPPAMQKVMYKGLAPEDKTLREIKVTSGAKIMGGGSTINDVLA
)		1	VNTPKDAAQQDAKAEENKKEPLCRQKQHRKVLDKGKPEDVMPSV
1	1	1	KGAQERLPTVPLSGMYNKSGGKVRLTFKLEQDQLWIGTKERTEK
			LPMGSIKNVVSEPIEGHEDYHMMAFQLGPTEASYYWVYWVPTQY
			VDAIKDTVLGKWQYF
6923	2469	1660	LGLFCILPIDTLCAVLERDTLSIRESRLFGAVVRWAEAECQRQQ
		İ	LPVTFGNKQKVLGKALSLIRFPLMTIEEFAAGPAQSGILSDREV
1	ł		VNLFLHFTVNPKPRVEYIDRPRCCLRGKECCINRFQQVESRWGY
1			SGTSDRIRFTVNRRISIVGFGLYGSIHGPTDYQVNIQIIEYEKK
	1		QTLGQNDTGFSCDGTANTFRVMFKEPIEILPNVCYTACATLKGP
1			DSHYGTKGLKKVVHETPAASKTVFFFFSSPGNNNGTSIEDGQIP
L			EIIFYT
6924	2210	1235	PEERVICEVEYYLTAFHEGRKGALAKKPYNPI IGETFHCSWEVP
1			KDRVKPKRTASRSPASCHEHPMADDPSKSYKLRFVAEQVSHHPP
1			ISCFYCECEEKRLCVNTHVWTKSKFMGMSVGVSMIGEGVLRLLE
1	1		HGEEYVFTLPSAYARSILTIPWVELGGKVSINCAKTGYSATVIF
ì		1	HTKPFYGGKVHRVTAEVKHNPTNTIVCKAHGEWNGTLEFTYNNG
1	1		ETKVIDTTTLPVYPKKIRPLEKQGPMESRNLWREVTRYLRLGDI
1			DAATEQKRHLEEKQRVEERKRENLRTPWKPKYFIQEGDGSGILQ
		L	SPLESTLMGLEVQSFPV
6925	2	1653	RGGAAGAAMEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCAL
Į.			SCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYF
1			DQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALP
1			EQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI
			ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKI
l		1	IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISG
1			LRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS
Ī			TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAV
1		,	WDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW
1	}	j	STSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIEC
1			GACLRVLEGHERLVRCIRFDNKRIVSGAYDGKIKVWDLQAALDP
Į.			RAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFL
1		1	NVPPSAQNETRSPSRTYTYISR
6926	1	733	SGRVAMDGLGLQFPEQGFPAGPPLLPPHMGGHYRDCQSLGAPPL
			

SEQ	Predicted	Predicted end	Lamino
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, O=Glutamine, R=Arginine
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine
· ·	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown +-et
1	amino acid	sequence	Codon, /=possible nucleotide deletion
	sequence		\=possible nucleotide insertion)
			DGYPLPTPDTSPLDGVDPDPAFFAAPMPGDCPAAGTYSYAQVSD
ł			YAGPPEPPAGPMHPRLGPEPAGPSIPGLLAPPSALHVVVGAMGS
]		PGAGGGRGFQMQPQHQHQHQHQHHPPGPGQPTPPPEALPCRDGT
1	•	İ	DPSQPAELLGEVDRTEFEQYLHFVCKPEMGLPYQGHDSGVNLPD SHGAISSVVSDASSAVYYCNYPDV
6927	2	1484	I.T.I.CGDTOT.M. A ONANIMO PARIS PROPERTY OF THE PROPERTY OF TH
			LTLCGDIQLMLAQNANNRAAHLEEFHYQTKEDQETLHSLHRESS CQGFAWATDLSTDLESQLSVSCKCYEAANEILQFRDLKSQNPEH
			YVQVLKRMGNIRNEIGVFYMNQAAALQSERLVSKSVSAAEQQLW
			KKSFSCFEKGIHNFESIEDATNAALLLCNTGRLMRICAQAHCGA
			GDELKREFSPEEGLYYNKAIDYYLKALRSLGTRDIHPAVWDSVN
1 1			WELSTTYFTMATLQQDYAPLSRKAOEOIEKEVSEAMMKSLKVCD
			VDSVSARQPLCQYRAATIHHRLASMYHSCLRNOVGDEHLRKOUP
			VLADLHYSKAAKLFOLLKDAPCELLRVOLERVAFAFFOMTSONG
		"	NVGKLKTLSGALDIMVRTEHAFOLIOKELIEEFGOPKSCDAAAA
			ADASPSENREEVMKLLSIFESRLSFLLLOSIKLLSSTKKKTSNN
1 1			IEDDTILKTNKHIYSQLLRATANKTATLLERINVIVHLLGOLAA
6928	1086	777	GSAASSNAVQ
		,,,	EAIDLINNLLQVKMRKRYSVDKTLSHPWLQDYQTWLDLRELECK
			IGERYITHESDDLRWEKYAGEQGLQYPTHLINPSASHSDTPETE ETEMKALGERVSIL
6929	1749	607	RDORGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG
1			NLHQHDPQDLRHNGNVVVAGRPSCSRGPRRAIQKPQPAGGRRSG
1 . 1			RGPAAGGLCLQPPDGGTCVPEEPPVPPMDWEALEKHLAGLQFRE
			QEVRNQGQARTNSTSAQKNERESIROKLALGSFFDDGDGTVTCC
1 1			SKSGKPSLSSRLQSGMNLOICFVNDSGSDKDSDADDSKTETELD
! -			TPLSPMSKQSSSYSDRDTTEEESESLDDMDFI.TROKKI.OAFAKM
1 1			ALAMAKPMAKMQVEVEKONRKKSPVADLLPHMPHTSECT.MKPct
1 1	1	1	KPTDLRDMTIGQLQVIVNDLHSQIESLNEELVQLLLIRDELHTE
6930	131	545	QDAMLVDIEDLTRHAESQQKHMAEKMPAK
1		3.3	FKDTANVFVSLFQMRNNFRHYFIEPSQLKLFYDVITWIVTQVAI
1 1	ĺ		SYTVVPFVLLSIKPSLTFYSSWYYCLHILGILVLLLLPVKKTOR RKNTHENIQLSQSKKFDEGENSLGQNSFSTTNNVCNQNQEIASR
			HSSLKO
6931	2	659	FVERLPNRPACLLVASGAAEGVSAQSFLHCFTMASTAFNLQVAT
1	ļ	1	PGGKAMEFVDVTESNARWVODFRLKAYASPAKTESTDGADVUAT
1	ŀ	İ	LIPSCPGALTDLASSGSLARILOHFHSESKPTCAVGUGVAALCC
1 1	į	İ	ATNEDRSWVFDSYSLTGPSVCELVRAPGFARLPLVVEDFVKDCC
6932	2		ACPSASEPDAVHVVLDRHLVTGONASSTVPAVONIJ.FLOGSPK
	2	1131	FVDSPGQGEQAEEEEGGIOMNSRMRAHSPAEGASVFSSSBGBVV
1		i	SDMCEGCRSLAAGHPGYISHDKETSIKYVSHQHPSHPQLFSIVR
1		ľ	QACVRSLSCEVCPGREGPIFFGDEQHGFVFSHTFFIKDSLARGF
1	[1	QKWISIITIMMUKIYLINSWPFLLGKVRGIIDELOGKALKUFFA
			EQFGCPQRAQRMNTAFTPFLHQRNGNAARSLTSLTSDDNLWACL HTSFAWLLKACGSRLTEKLLEGAPTEDTLVQMEKLADLEEESES
1 1	i		WDNSEAEEEEKAPVLPESTEGRELTQGPAESSSLSGCGSWQPRK
1 1	1		LPVFKSLRHMRQVGGRGTAHHELRRRANHGLCLPTRLASGPSTL
 			KTLQEVTDSLLGGWLMAOGVGGII
6933	1431	890	SLNLHCTLPPPPPHQYPNGYPSDKEGKKPKGOSKKOPSGTPKPPT
1 1	1	1	SDDDCPSASKVYKASDSAEAIEAFOLTPOOOHI.TREDCONOKIN
	1	1	DEVLSHLVEGPNFLKKLEOSFMCVCCOELVYOPVTTFCFUNICV
1 1	1	1	DCLQRSFKAQVFSCPACRHDLGQNYIMIPNEILQTLLDLFFPGY
6934	3030		SKGR
5534	3030	2588	DRDHSQCGGIRRVALARVSSVKLISKAKIRTVKMTFIIVLAFIV
		[1	CWTPFFFVQMWSVWDANAPKRASAFIIVMIJASINSCCNDWTVM
1	ļ	1	LFTGHLFHELVQRFLCCSASYLKGRRLGETSASKKSNSSSFVLS
<u> </u>		1 1	HRSSSQRSCSQPSTA

			Company of the Compan
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	-	\=possible nucleotide insertion)
6935	886	543	NSALYVAGGNDGTSCLNSVERYSPKAGAWESVAPMNIRRSTHDL
0,55	1	Ī	VAMDGWLYAVGGNDGSSSLNSIEKYNPRTNKWVAASCMFTRRSS
1	l .	1	VGVAVLELLNFPPPSSPTLSVSSTSL
6936	1347	567	RSHRRQFLSRALLEFFGKSHPPPHRLFRKSLNVGLHYSHIPFLT
0936	1337	1 33.	TCLHFLRKRLQKGEVGLSVETSKPQVPVGGLSRKKVPQEPWATV
1	1	1	MEKRLQEAQLYKEEGNQRYREGKYRDAVSRYHRALLQLRGLDPS
	İ		LPSPLPNLGPQGPALTPEQENILHTTQTDCYNNLAACLLQMEPV
1	1	1	NYERVREYSQKVLERQPDNAKALYRAGVAFFHLQDYDQARHYLL
[·	AAVNROPKDANVRRYLOLTQSELSSYHRKEKQLYLGMFG
		<u> </u>	AVVNROPADANVARILODIQUEDESTIMATERQUITOTIC
6937	1	727	AVEFRCCPGRIPACFARGWRDDRVIGTCFCDQACRFTGDCCFD1
1		1	DRACPARPCFVGEWSPWSGCADQCKPTTRVRRRSVQQEPQNGGA
1			PCPPLEERAGCLEYSTPQGQDCGHTYVPAFITTSAFNKERTRQA
	1	<u> </u>	TSPHWSTHTEDAGYCMEFKTESLTPHCALENRPLTRWMQYLREG
]	}	YTVCVDCQPPAMNSVSLRCSGDGLDSDGNQTLHWQAIGNPRCQG
	l	<u> </u>	TWKKVRRVDQCSCPAVHSFIFI
6938	3	719	NSRKLELAERVDTDFMQLKKRRQSSEKENDSGTLDTVGAVVVDH
· i	ļ	1	EGNVAAAVSSGGLALKHPGRVGQAALYGCGCWAENTGAHNPYST
1		•	AVSTSGCGEHLVRTILARECSHALQAEDAHQALLETMQNKFISS
1			PFLASEDGVLGGVIVLRSCRCSAEPDSSQNKQTLLVEFLWSHTT
}		1	ESMCVGYMSAQDGKAKTHISRLPPGAVAGQSVAIEGGVCRLGEP
1			SELTLQAECEASQRHFRT
6939	3	810	KVTAPRRPORYSSGHGSDNSSVLSGELPPAMGRTALFHHSGGSS
l l		J	GYESLRRDSEATGSASSAPDSMSESGAASPGARTRSLKSPKKRA
ĺ	[ł	TGLQRRRLIPAPLPDTTALGRKPSLPGQWVDLPPPLAGSLKEPF
1	1	1	EIKVYEIDDVERLQRPRPTPREAPTQGLACVSTRLRLAERRQQR
1		l .	LREVQAKHKHLCEELAETQGRLMLEPGRWLEQFEVDPELEPESA
ì		1	EYLAALERATAALEQCVNLCKAHVMMVTCFDISVAASAAIPGPQ
1		ļ	EVDV
6940	1188	496	GKMAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQ
	1		VVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAV
1	•	1	LADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKGS
1	1	1	TYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLL
ĺ		(KTKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILS
1			EVTPDQSKPEN
6941	 	713	SLSRADSDPHGPHTCGHVLNVIIGSNVLALAEAQRQAEALGYQA
	-		VVLSAAMQGDVKSMAQFYGLLAHVARTRLTPSMAGASVEEDAQL
ı		İ	HELAAELQIPDLQLEEALETMAWGRGPVCLLAGGEPTVQLQGSG
1		İ	RGGRNQELALRVGAELRRWPLGPIDVLFLSGGTDGQDGPTEAAG
1		1	AWVTPELASQAAAEGLDIATFLAHNDSHTFFCCLQGGAHLLHTG
		1	MTGTNVMDTHLLFLRPR
6942	1	246	GDYVERYDPKTDTWTMGAPLSMPTNAVGGCLLGDRLYADGGYDG
1 0942	1	1	QTYLNTMESYDPQTNEWTQMASLNIGRAGACVVVIKQP
6043	+ - 1	739	PMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLG
6943	1	/39	HSPAGGSITETLVQGDKTEYLLTALEPKPTYIICMVTMETTNAY
1		1	VADETPVCAKAETADSYGPTTTLNQEQNAGPMASLPLAGIIGGA
1		1	VALVFLFLVLGAICWYVHQAGELLTRERAYNRGSRKKDDYMESG
1			TKKDNSILEIRGPGLQMLPINPYRAKEEYVVHTIFPSNGSSLCK
1	}	1	
<u> </u>			ATHTIGYGTTRGYRDGGIPDIDYSYT
6944	960	156	VANILLINGVKYESELTGSSERAEQPLSVGRLCSTICNMPKALRT
1	1	1	LCVNHFLGWLSFEGMLLFYTDFMGEVVFQGDPKAPHTSEAYQKY
1			NSGVTMGCWGMCIYAFSAAFYSAILEKLEEFLSVRTLYFIAYLA
Ī			FGLGTGLATLSRNLYVVLSLCITYGILFSTLCTLPYSLLCDYYQ
4	1	I .	SKKFAGSSADGTRRGMGVDISLLSCQYFLAQILVSLVLGPLTSA
1	ĺ	I .	The state of the s
		Ĭ	VGSANGVMYFSSLVSFLGCLYSSLFVIYETPPSDAADEEHRPLL LNV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
]	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	amino acid	sequence	Codon, /=possible nucleotide deletion
6945	sequence 2067		\=possible nucleotide insertion)
0,43	2067	179	EGEDRGLPRTMGAALGTGTRLAPWPGRACGALPRWTPTAPAQGC
			HSKPGPARPVPLKKRGYDVTRNPHLNKGMAFTLEERIOLGTHGL
		}	IPPCFLSQDVQLLRIMRYYERQQSDLDKYIILMTLQDRNEKLFY
		[RVLTSDVEKFMPIVYTPTVGLACQHYGLTFRRPRGLFITIHDKG
1]	•	HLATMLNSWPEDNIKAVVVTDGERILGLGDLGCYGMGIPVGKLA
1	J		LYTACGGVNPQQCLPVLLDVGTNNEELLRDPLYIGLKHQRVHGK
1		[AYDDLLDEFMQAVTDKFGINCLIQFEDFANANAFRLLNKYRNKY
I	1	ļ	CMFNDDIQGTASVAVAGILAALRITKNKLSNHVFGFQGAGEAAM
			G\IAHLLVMALE\KEGVPKA\EATRKIW\MVDF\KGLIVQGRDH
			LNHEKEMFAQD\HPEVNSLEEVVRLVKPTAIIGVAAIAEA\FTE
			QILRDMASFHERP\IIFALSNPTSKAECTA\EKCYRVTEGPRGF
			FAS\GSPF*GVLIWEMGKTFIPGGRGNNA*RVPRGWQLGVHSPG
}			GDPGHIP\DEIFLPDSRAKLPQEVSEQHLSQGRLYP\PLST\IR
L	1		NVFLRIAIKVFD*GYKHNLV\SYYPEPKD\KEAFCKIPGSYTPD YDSFYT/VDSYIWAQGKAMNVQTV
6946	133	2551	SCEYSGITVAPGDPCPGVAHLLAPSMASDTPESLMALCTDFCLR
1	1 !		NLDGTLGYLLDKETLRLHPDIFLPSEI\CDRLVNEYVELVNAAC
1	1		NP\EPHE\SPFNPLFRDPRKQPASRRIHL\RED\LVQD\QD\LE
1			AIRKQDL\VEL\YLTN\CEKLSAKSLQTLRSFSHTLGVP*AFFG
	1		C\TNILLLRKENPGGL/CEDEYLFNPTCQVLVKDFTFEGFSRLR
ļ]		F\LKLGRMIDWVPVES\LLRPLNSLAALDLSGIQTSDAA\FLTQ
			WKDSL\VSLVL\YNMDLSDDHIR\VIVOLHKLRHLDISRDRISS
}	} !		YYKFKLTREVLSLFVQKLGNLMSLDISG\HMILENCSISKIGKR
i	i i		EAGQTSI\EPSK\SSIIPFRGFEGGPLOF\LGVF*GIFCGRLTH
1	l		IPAYKVSGDKNEEQVLNAIEAYTEHRPEITSRAINLLEDIARIE
	ļ i		RCNQLLRALKLVITALKCHKYDRNIOVTGSAALFYLTNSEVRSE
i i			QSVKLRRQVIQVVLNGMESYQEVTVORNCCLTLCNFSIPERLEF
			QYRRVNELLLSILNPTRQDESIQRIAVHLCNALVCQVDNDHKEA
	1		VGKMGFVVTMLKLTQKKLLDKTCDQVMEFSW\SALWNITDETPD
ļ	ŀ		NCEMFLNFNGMKLFLDCLNEFPEKQELHRNMLGLLGNVAEVKEL
			RPÓLMTSQFISVFSNLLESKADGIEVSYNACGVLSHIMFDGPEA
1 1	ì		WGVCEPQREEVEERMWAAIQSWDINSRRNINYRSFEPILRLLPQ
1 1			GISPVSQHWATWALYNLVSVYPDKYCPLLIKEGGMPLLRDIIKM
6947	2	1682	ATARQETKEMARKVIEHCSNFKEENMDTSR
1 1	ł		TSVSTIPRGLASARPOSRSWRCCPVWRRSPGRARGRGLKMLNVP
1	1		SQSFPAPRSQQRVASGGRSKVPLKQGRSLMDWIRLTKSGKDLTG LKGRLIEVTEBELKKHNKKDDCWICIRGFVYNVSPYMEYHPGGE
] [DELMRAAGSDGTELFDQVHRWVNYESMLKECLVGRMAIKPAVLK
1			DYREEEKKVLNGMLPKSQVTDTLAKEGPSYPSYDWFQTDSLVTI
1			/EHIY*TEGYQFRLNNS*SSE*FLYSRNNY*GLLISYTYW/R*A
			MRFRKIFLCGL/CESVGKIEIVLQKKENTSWDFLGHPLKNHNSL
1			IPRKDTGLYYRKCQLISKEDVTHDTRLFCLMLPPSTHLQVPIGQ
, 1			HVYLKLPITGTEIVKPYTPVSGSLLSEFKEPVLPNNKYIYFLIK
			IYPTGLFTPELDRLQIGDFVSVSSPEGNFKISKFOELEDLFLLA
1 1		ļ	AGTGFTPMVKILNYALTDIPSLRKVKLMFFNKTEDDIIWRSOLE
1 1	j		KLAPKDKRLDVEFVLSAPISEWNGKQGHISPALLSEFLKRNLDK
6948			SKVLVCICGPVPFTEQGVRLLHDLNFSKNEIHSFTA
0348	104	58	PDGAHSFFPDEYFTCSSLCLSCGVGCKKSMNHGKRGVPHRAKSD
1	1		CRYSHQYDNRVYTCKACYERGEEVSVVPKTSASTDSPWMGLAKY
j	İ		AWSGYVIECPNCGVVYRSRQYWFGNQDPVDTVVRTEIVHVWPGT
1 !	į		DGFLKDNNNAAQRLLDGMNFMAQSVSELSLGPTKAVTSWLTDOI
	ļ	ļ	APAYWRPNSQILSCNKCATSFKDNDTKHHCRACGEGFCDSCSSK
]	}	ļ	TRPVPERGWGPAPVRVCDNCYEAR/TRPVSCYRGTSGR*RRRT
6949	152		QETVE
0049	134	4656	GLRLCLSRPLTRPGDDSVGGSAMASGAGGVGGGGGGKIRTRRCH
			QGPIKPYQQGRQQHQGILSRVTESVKNIVPGWLQRYFNKNEDVC

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	1	Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
!	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į	amino acid	sequence	Codon, /=possible nucleotide deletion,
ŀ	sequence		\=possible nucleotide insertion)
			SCSTDTSEVPRWPENKEDHLVYADEESSNITDGRITPEPAVSNT
1	ì	ł	EEPSTTSTAST\YPDVLTRVSLYRSHLNFSMLESPALHCQPSTS
1	1	Ì	SAFPIGSSGFSLVKEIKDSTSQHDDDNISTTSGFSSRASDKDIT
		ļ	
1	ì	[VSKNTSLPPLWSPEAERSHSLSQHTATSSKKPAFNLSAFGTLSP
1		ţ	SLGNSSILKTSQLGDSPFYPGKTTYGGAAAAVRQSKLRNTPYQA
1	i	i	PVRRQMKAKQLSAQSYGVTSSTARRILQSLEKMSSPLADAKRIP
1	1		SIVSSPLNSPLDRSGIDITDFQAKREKVDSQYPPVQRLMTPKPV
	i		SIATNRSVYFKPSLTPSGEFRKTNQRIDKKCSTGYEKNMTPGQN
1	1	ĺ	REQRESGFSYPNFSLPAANGLSSGVGGGGGKMRRERHAFVASKP
	ļ	1	LEEEEMEGPVLPKISLPITSSSLPTFNFSSPEITTSSPSPINSS
1	i	<u> </u>	QALTNKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF
İ	1	,	SVPVAKTAELSGSSSTLEPIISSSAHHVTTVNSTNCKKTPPEDC
1	1	}	EGPFRPAEILKEGSVLDILKSPGFASPKIDSVAAOPTATSPVVY
	}	į	TRPAISSFSSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC
	1	}	QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT
1		Į	WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET
1			MTASSSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC
		ļ	
}	}	ļ	VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC
	1	į	ELCLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASS
	1		SFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP
ı	1	İ	MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL
j	1	ĺ	SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR
	Ì		VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA
1	4		TKGGFSFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGEG
1			KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE
1	1	İ	SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS
1		ł	AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST
			SQSLLFSQDSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG
			ATTTSSSAGSSFVFGTGPSAPSASPAFGANQTPTFGQSQGASQP
1	1		NPPGFGSISSTALFPTGSQPAPPTFGTVSSSSQPPVFGOOPSO
]		
j	1		SAFGSGTTPNSSSAFQFGSSTTNFNFTNNSPSGVFTFGANSSTP
,			AASAQPSGSGGFPFNQSPAAFTVGSNGKNVFSSSGTSFSGRKIK
1			TAVRRK
6950	2585	411	PRPGSRSGLCRRAGERGAVRAGGLSRRTRAE*IMDELHYQDTDS
l			DVPEQRDSKCKVKWTHEEDEQLRALVRQFGQQDWKFLASHFPNR
1	1		TDQQCQYRWLRVLNPDLVKGPWTKEEDQKVIELVKKYGTKQWTL
1	Į l		IAKHLKGRLGKQCRERWHNHLNPEVKKSCWTEEEDRIICEAHKV
i	1		LGNRWAEIAKMLPGRTDNAVKNHWNSTIKRKVDTGGFLSESKDC
i			KPPVYLLLELEDKDGLQSAQPTEGQGSLLTNWPSVPPTIKEEEN
į	. I		SEEELAAATTSKEQEPIGTDLDAVRTPEPLEEFPKREDQEGSPP
}	{		ETSLPYKWVVEAANLLIPAVGSSLSEALDLIESDPDAWCDLSKF
1			DLPEEPSAEDSINNSLVQLQASHQQQVLPPRQPSA\LVPSVTEY
1			RLDGHTISDLSRSSRGELIPISPSTEVGGSGIGTPPSVLKRORK
1			RRVALSPVTENSTSLSFLDSCNSLTPKSTPVKTLPFSPSOFLNF
	[
	 		WNKQDTLELESPSLTSTPVCSQKVVVTTPLHRDKTPLHQKHAAF
1	· •		VTPDQKYSMDNTPHTPTPFKNALEKYGPLKPLPQTPHLEEDLKE
]			VLRSEAGIELIIEDDIRPEKQKRKPGLRRSPIKKVRKSLALDIV
1			DEDMKLMMSTLPKSLSLPTTAPSNSSSLTLSGIKEDNSLLNQGF
1			LQAKPEKAAVAQKPRSHFTTPAPMSSAWKTVACGGTRDQLFMQE
L			KARQLLGRLKPSHTSRTLILS
6951	1940	239	AGPDDTMKRSLQALYCQLLSFLLILALTEALAFAIQEPSPRESL
}			QVLPSGTPPGTMVTAPHSSTRHTSVVMLTPNPDGPPSQAAAPMA
1			TPTPRAEGHPPT\TPSPPSLRO*PPPILKAP/SSTGPAPAAMAT
1			TSSKPEGRPRGQAAPTILLTKPPGATSRPTTAPPRTTTRRPPRP
			PGSSRKGAGNSSRPVPPAPGGHSRSKEGQRGRNPSSTPLGQKRP
1			·- ·- ·
L			LGKIFQIYKGNFTGSVEPEPSTLTPRTPLWGYSSSPQPQTVAAT

SEO	Predicted	Dun Ad ab a 3	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	Managanine, CaCvateine, Dalamartic loid p
i	location	corresponding	Glutamic Acid, F=Phenylalanine C-Clusina
	corresponding	to first	H=H1Stldine, I=Iso]eucine K-Lycine
į	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R≈Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	bequence	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
i		}	TVPSNTSWAPTTTSLGPAKDKPGLRRAAQGGGSTFTSQGGTPDA
	•	1	TAASGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYCYP\CT
			SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTTPQAP
	1		THPSRVSESTISGAKEETVA\PSP*PTGCPVLSPQWYPQPQAIS
ļ	1	İ	STAWSPPGPGSLGQQGTSPMWPRGTNRSTEPPSA*ARWISPG*S
1	1	ļ	WPSACPSPP\LCPADGVLHEEEEEDRQPGEQPEAYGNNTHHPGT
	1		TFQQAC\RGAAPGEIPVPLKPLRTQLSEPRSPANGDYRDTGMVP
6952	658	304	1 =
		1	PESEGESGEMTDRYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE PTPRLVLLLHGPLRPSQLLRHCGE*EQSASPLQLDGKDASALWT
L	<u> </u>	1	ASRQARGELRLCLTTAVRGTSPSVSPVCQSS
6953	1512	349	NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES
1	1]	FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD
1			PLLELCQCPLCQLDCGSREQLIAHVYQHTAAVVSAKSYM\CPVC
1			GRALSSPGSLGRHLLIHSEDQRSNCAVCGARFTSHATFNSEKLP
			EVLNMESLPTVHNEGPSSAEGKDIAFSPPVYPAGILLVCNNCAA
ł			YRKLLEAQTPSVRKWALRRQNEPLEVRLQRLERERTAKKSRRDN
1			ETPEEREVRRMRDREAKRLQRMQETDEQRARRLQRDREAMRLKR
	}		ALETPEKRQARLIREREAKRLKRRLEKMDMMLRAOFGODBGAMA
6054			ALAAEMNFFQLPVSGVELDSOLLGKMAFEEONSSSLH
6954	819	1	PPPPFIIPSHPREAGT*AG*KRSGDSECSPPVEO*A*TPAAAON
4	}		*PQR*RWTEGNSPQASAVATPGOGASPAAPRC"P*DSDDUBDID
	ì		PGARPPAG*AAPAPTKPWLAGPASAPOPGAAPI.SDDADDI.TDTD
j	j l		*CAGAAARGRPRRDRSPRPRTPGGCSWSEPPTPDAVGAGAOTTC
	į		DAG*AGGR*GQRQRPSTGR*PPGVGGAGRSHPPRGTT DCMBUDD
ļ			AS*RAGWQR*PGP/REWGL*EPQGEEMSGPGGPGGAPPNOVGSS
6955	1968		VMQAMSTGI
	1 1500	782	PPGRRQVRAQVAGAPVGHWGTRARQVKTGGRRRARRTMPFLGQD
1	l		WRSPGWSWIKTEDGWKRCESCSQKLERENNHCNISHSIILNSED
	1		GEIFNNEEHEYASKKRKKDHFRNDTNTQSFYREKWIYVHKESTK
			ERHGYCTLGEAFNRLDFSSAIQDIRRFNYVVKLLQLIAKSQLTS
]	1		LSGVAQKNYFNILDKIVQKVLDDHHNPRLIKDLLQDLSSTLCIL
			/N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\NG
]			LTLSDLPLHMLNNILYRPSDGWDIITLGQVTPTLYMLSEDRQLW
1 1	•		KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPAKEQY
			GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLFK
6956	8605	3839	QTSTS1FASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQSS
]]	!		DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAAS
1 1	i i		PEISPEVCPAASTVVSPAVFSVVSPASSAVLPAVSLEVPLTASV
]]	j		TSPKASPVTSPAAAFPTASPANKDVSSFLETTADVEEITGEGLT
]	j	l	ASGSGDVMRRRIATPEEVRLPLQHGWRREVRIKKGSHRWQGETW
) l]	Í	YYGPCGKRMKQFPEVIKYLSRNVVHSVRREHFSFSPRMPVGDFF
	ļ	i	EERDTPEGLQWVQLSAEEIPSRIQAITGKRGRPRNTEKARTKEV
			PKVKRGRGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAKI
		i	AKSKKKMRQKVQRGECQTTIOGOARNKRKOETKSI.KOVFAVVVC
1		1	KAEKEKGKTKQEKLKEKVKREKKEKVKMKEKEEVTKAKDACVAD
		1	KTLATQRRLEERQRQQMILEEMKKPTEDMCLTDHOPI.PDFSPVp
İ	j	i i	GLTLPSGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLORGI
}	1		LCQGDSLGEVQDLLVRLLKAALHDPGFPSYCQSLKILGEKVSEI
1	Į	1	PLTRDNVSEILRCFLMAYGVEPALCDRIRTOPFOAODDOOVANU
- 1	Ì	i	LAFLVHELNGSTLIINEIDKTLESMSSYRKNKWIVEGPI.PPI PT
- 1	İ	j	VLAKRIGRSEVEMEGPEECLGRRRSSRIMEVTSGMERERFERET
ŀ	[1.	AAVPGRRGRRDGEVDATASSIPELERQIEKLSKRQLFFRKKLLH
1	İ		SSQMLRAVSLGQDRYRRRYWVLPYLAGIFVEGTEGNT.VDEEVTV
			KETDSLKVAAHASLNPALFSMKMELAGSNTTASSPARARGRPRK
			THE TOTAL TRANSPORT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	<u> </u>	\=possible nucleotide insertion)
			TKPGSMQPRHLKSPVRGODSEQPQAQLQPEAQLHAPAQPQPQLQ
ļ			LQLQSHKGFLEQEGSPLSLGQSQHDLSQSAFLSWLSQTQSHSSL
l	· ·		LSSSVLTPDSSPGKLDPAPSQPPEEPEPDEAESSPDPQALWFNI
1	Į		SAQMPCNAAPTPPPAVSEDQPTPSPQQLASSKPMNRPSAANPCS
1			PVQFSSTPLAGLAPKRRAGDPGEMPQSPTGLGQPKRRGRPPSKF
Ì	1	1	FKOMEORYLTOLTAOPVPPEMCSGWWWIRDPEMLDAMLKALHPR
l	Ì	}	GIREKALHKHLNKHRDFLQEVCLRPSADPIFEPRQLPAFQEGIM
			SWSPKEKTYETDLAVLOWVEELEQRVIMSDLQIRGWTCPSPDST
	<u> </u>	{	REDLAYCEHLSDSQEDITWRGRGREGLAPQRKTTNPLDLAVMRL
}	1		AALEQNVERRYLREPLWPTHEVVLEKALLSTPNGAPEGTTTEIS
	1	!	YEITPRIRVWRQTLERCRSAAQVCLCLGQLERSIAWEKSVNKVT
	1	1	CLVCRKGDNDEFLLLCDGCDRGCHIYCHRPKMEAVPEGDWFCTV
1	1	}	CLAQQVEGEFTQKPGFPKRGQKRKSGYSLNFSEGDGRRRRVLLR
1	1		GRESPAAGPRYSEEGLSPSKRRRLSMRNHHSDLTFCEIILMEME
t	i	1	SHDAANPFLEPVNPRLVSGYRRIIKNPMDFSTMRERLLRGGYTS
		1	SEEFAADALLVFDNCQTFNEDDSEVGKAGHIMRRFFE\SRWEEF
	1		YQGKQGQSVRQGRWGVTLWHLPPTFQTKTCHFHLLMLPWVQTQV
1		1	RYNPDF
6957	82	3514	HLIVAMPEPTKKEENEVPAPAPPPEEPSKEKEAGTTPAKDWTLV
(Ì	j	etppgeeqakqnansqlsilfiekpqggtvkvgeditfiakvka
[1	1	EDLSEKPTINGSRKWMDLASKAGKHLQLKETFERHSRVYTFEMQ
J	ì	į.	IIKAKDNFAGNYRCEVTYKDKFDSCSFDLEVHESTGTTPNIDIR
	}		SAFKRSGEGQEDAGELDFSGLLKRREVKQQEEEPQVDVWELLKN
			TKPSEYEKIAFQYESPTCSGMLKRLKRSIREEKKSAAFAKILDP
			VYQVDKGGRVRFVVELADPKLEVKWNKNGQELRPSTKYIFEDTR
1)	CQSILNIDNCQMTDDSEYYVTAGDEKCSTELLVREPPIMVTKQL
			EDTTDYCGERVELECEVSEDDAQVKWFKNGEEIILVQTRYRIRV
		ļ	EGKKHILIIEGATKADAADYSVMTTGGQSSAKLSVDLKPLKILT
	/	Į	PLTDQTVNLGKEICLKCEISENIPGKWTKNGLPVQESDRLKVVH
1			KGRIHKLVIDHALTEDEGDYVFAPDAYNVTLPAKVHVIDPPKII
1		ľ	LDGLDADNTVTVIAGNKLRLEIPISGEPPPKAMWSRGDKAIMEG
1	Į.	1	SGRIRTESYPDSSTLVIDIAERDDSGVYHINLKNEAGEAHASIK
ł			VKVVDFPDPPVAPTVTEVGDDWCIMNWEPPAYDGGSPILGYFIE
ł			RKKKQSSRWMRLNFDLCKETTFEPKKMIEGVAYEVRIFAVNA\I GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI
1	1	}	GAAGLDGYVLEYCFEGSTSAKOSDENGEAAYDLPAEDWIVANKD
į			LIDKTKFTITGLPTDAKIFVRVKAVNAAGASEPKYYSQPILVKE
	İ		IIEPPKIHSPKHLKOTYIRRVGDRVILVIPFQGKPRPELTWKKD
1		1	GAEIDKNQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDKFVE
	1		TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT
			GYTIQKADKKSMEWLRVIEHIIEPVPHTELVIGNEYYFRVFSEN
}	İ	1.	MCGLSEDATMTKESAVIARDGKIYKNPVYEDFDFSEAPMFTQPL
1			VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPRYRMFS
			NOGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ
6958	274	1663	PRTSRVKTEGSQGSSAMDFSVKVDIEKEVTCPICLELLTEPLSL
1 3338	2/3	7003	DCGHSFCQACITAKIKESVIISRGESSCPVCQTRFQPGNLRPNR
	1		HLANIVERVKEVKMSPQEGQKRDVCEHHGKKLQIFCKEDGKVIC
l			WVCELSQEHQGHQTFRINEVVKECQEKLQVALQRLIKENQEAEK
1			LEDDIRQERTAWKNYIQIERQKILKGFNEMRVILDNEEQRELQK
1			LEEGEVNVLDNLAAATDOLVQQRQDASTLISDLQRRLRGSSVEM
1			LQDVIDVMKRSESWTLKKPKSVSKKLKSVFRVPDLSGMLQVLKE
			LTDVQYYWVDVMLNPGSATSNVAISVDQRQVKTVRTCTFKNSNP
1			CDFSAFGVFGCQYFSSGKYYWEVDVSGKIAWILGVHSKISSLNK
1			RKSSGFAFDPSVNYSKVYSRYRPQYGYWVIGLQNTCEYNAFEDS
			SSSDPKVLTLFMAV\LPVVLGFS
6959	1	1469	SLVHVVEFGRGIEDFPYLFFQLTHCQQRICSVTQAGVQWCDHSS
	, -	1 7402	CONTRACT THE CONCERN TO THE PARTITION AND THE PARTITION OF THE PARTITION O

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corresponding to first anino acid residue of anino acid residue of anino acid sequence of acid sequence of	NO:		I '	Glutamic Acid Emphanical and Colori
to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence solvence amino acid sequence solvence amino acid sequence solvence amino acid sequence solvence amino acid sequence solvence amino acid sequence solvence amino acid sequence solvence amino acid sequence solvence amino acid sequence solvence amino acid sequence solvence amino acid sequence solvence amino acid sequence solvence amino acid sequence solvence amino acid sequence solvence amino acid sequence solvence amino acid sequence solvence acid sequence solvence amino acid sequence solvence amino acid sequence solvence acid sequence solvence acid sequence solvence acid sequence solvence acid sequence solvence acid sequence solvence acid sequence solvence acid sequence solvence acid sequence solvence acid sequence solvence acid sequence solvence acid sequence solvence acid sequence solvence solvence acid sequence solvence so		location		H=Histidine T-Teologoine V Lugine
amino acid residue of amino acid	1	corresponding		Labeleine, Manual Manua
### seidue of amino acid sequence S=Serine, T=Threonine, V=Valine, maino acid sequence S=Geography V=Vprosible nucleotide deletion, V=possible nucleotide insertion)	1			P=Proline, O=Glutamine, N=Arginine
residue of amino acid sequence WHITYPLOSIAN, X-DURKOWN, *-Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion /-		amino acid	residue of	S=Serine, T=Threonine, W=Waline
amino acid sequence Codon, /-possible nucleotide deletion, /-possible nucleotide inertion) LOPOTPOLINGSSHISILISEDYRHUSSEPRUMMODEFELSPUM YEELEDRORGY/PHODLALAL/PLAWHLAWHLAWHLAWFETTEIDED, RELEGRORGY/PHODLALAL/PLAWHLAWHLAWFETTEIDED, RELEGRORGY/PHODLALAL/PLAWHLAWFETTEIDED, RELEGRORGY/PHODLALAL/PLAWHLAWFETTEIDED, RELEGRORGY/PHODLALAL/PLAWHLAWFETTEIDED, PROJECT TO TOTORW/RERERERORGE/PLAWHLAWFETTEIDED, PROJECT TO TOTORW/RERERERORGE/PLAWHLAWFETTEIDED, PROJECT TO TOTORW/RERERERORGE/PLAWHLAWFETTEIDED, PROJECT TO TOTORW/RERERORGE/PLAWHLAWFETTEIDED, PROJECT TO TOTORW/RERERORGE/PLAWHLAWFETTEIDED, PROJECT TO TOTORW/RERERORGE/PLAWHLAWFETTEIDED, PROJECT TO TOTORW/RERERORGE/PLAWHLAWFETTEIDED, PROJECT TO TOTORW/RERERORGE/PLAWHLAWFETTION/PTO/INTITYSA/PHOKEOCHE/PLAWHL	1	residue of		W=Truntonhan V=Truncing V=U=l==== + c
Apossible nucleotide insertion		amino acid	1	Codon /-nossible muslostide deletide
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WTELEDROGRYPHPODLIAALPILAULIMRILARERPILIPLICS RRIGORDOTROGUPATILERHITISTIRPREPOLISILAAQCOL THQOTGRWFRRRRNORPQLITKFCCASAWRFLFYLSSFVUGLSV LYHESMUAR/PWCOREYPROLITSCRAADSELYHWILLELG FYLSLLIRLPPOVERRGGSPSIKPRPHYPPSTADPERGVIH HPVAVILIMTSYSANLLRIGSLVLLIRHISSTVLRGKOMENDIRSDV QQVCDALFLIFSFVSFTRRLVIFFPOLITTYYSSISINGGFF GYYFPROLIMILOLLHVWSFULLIRHISSTVLRGREDIRSDVL RESDSSERAAAQEFLOLKNOTAGGRPAPTDGPRSRVAGRITN RHTTAT AKWAREKEWGFYTRSFF\RGFDLSTLITHSTVRRFTLASGES HLEPERGALKRUEEFLEKWOYDEAARSHGALDITKKGREPF PCSDPERRFFFRNSSSSGSEASSPDYSGPPARNOVASRSHHP KESPHRRA\SKAVESSDSERGRORDLPAGRGESEEEKKYKKK KOKTSKKSSSGSSESEASSPDYSGPPARNOVASRSHHP KESPHRRA\SKAVESSDSERGRORDLPAGRGESEEEKKYKKK KOKTSKKSSSGSSESELSEESERSKERGEBEKKYKKK KOSKRAARLGSTSGESSEELLGKGKKGKGSGRESEEBERGKYKKK KOSKRAARLGSTSGESSEELLGKGKKGKGSGRESEEBERGKYKKK KOSKRAARLGSTSGESSEELLGKGKKGKGKESEEBEEGKKYKK KOSKRAARLGSTSGESSEELLGKGKGKGKGSGGRGGGGGGRANSG GROWARDAVRILLGSCCSKKERGSEEVEBEEGKKYKKE ALKKORERBARAVSLOVANILISGSGCPRRTRANGEGAPGGE LYRRTLDSDEERPRAPPDMSHMRGITSSGGERNINGSKKS GRKGRTSSSSSSDSSPBAGGAGGAGGAGGGGGGGGGGG LYRRTLDSDEERPRAPPDMSHMRGITSSGGERNINGSKKS GRKAARAVSTULLABEVERGUDFYVANAVERGPTISKKKC ALKKORERBARAVSLOVANILISGSGGPRRTRENGEGFF, NQSSPOLALLEEWBSGDFYYRROKLSFTYPAAHHFRSGITISG LCVPSKHPIGELTQHITYLIKAFWGOTYLYKAVGGFTISKGKSFT TTGFDHRGTFISDHEALMATFYNGKDTYLAHRVAQAWELAQFIHRTSK ADVVLLCOBLINMIPEDLOCCLKERFOTGHATAVGFTISKGKSFT TTGFDHRGTFISDHEALMATFYNGKDTYLAHRVAQAWELAQFIHRTSK ADVVLLCOBLINMIPEDLOCCLKERFOTGHATAVGRAFTLEHVGSWG SGWILAAVTHLHASYNGKDTYLAHRVAQAWELAQFIHRTSK ADVVLLCOBLINMIPEDLOCCLKERKTGHADAVGRRILGIALL LALLCULAAGGGGBAATLLWFWSGVTYNH HIGHDFRARRILGGFL NQSSFDLALLEEWBSGDPFYTRACHTFYNGLOFT TTGFDHRGFTFISDHEALMATTLYFNGKOTTYLAKANGGFTISKGKSFT TTGFPHRGTFFISDHEALMATTLYFNGKTYDTYNH HIGHDFRAKGGILALL LALLCULAAGGGGGAATLLTHTYSUGLUMAAGAFTLHFYNGSVA ADVVLLCOBLINMIPEDLOCCLKERKTGHHATAVGAPTLFHYOSVAN SGWILAAVTHLHASYNGKODTYLAHRAVAAWELAQFIHRTSKI LALLCULAAGGGGGAATLLTHTYSUGLUMAAGAFTLHFYNGSVAN ADVVLLCOBLANGFFIGDHEALMATTLYFNGKOTTYALLACGROMGSCE TSFSGTAVSHRIFTHEALGRANGHTYNGKOTTALLACGROMGSCE TSFSGTAVSHRIFTHALLACHTYNGKOTTALLACGROMGSCE TFSGTTS			 	LOPOTRICI NOCCUL CLI CORPURAL CORPURA CORPURAL CORPURAL CORPURAL CORPURAL CORPURAL CORPURAL CORPURA CORPURAL CORPURA CORPU
RMLGVEROTTRQVEPNATLECHFLTEGREPKEPOLSLIAAQCGL TLQCTGRWFRERRNORPGLIKFYCEASWRFATSPSTVGLSV LYHESWWAPPWCNDEYPNQLTLSCCPAADSEA\SLYWWILELG FYLSLILIRJPGVARTGGEPSIKRPRHYDFATADPKROVIH HPVAVILMTFSYSANLBIGSLVLLLHDSSDYLLEACCMWYNG VQVCDALFITSSYFFTTHLVFPTOLLTYSISNRGFF GYYFPNGLIMILGLHYWSCLLIRWIJSFPKKGGMEKDISDV EESSSSEBAAAGEPLGLKNGTAGGGPRAPTIGPFSYAGRITN RHITTAT 6960 387 2068 AKWARKERGEPYTRSFF\RGRPDLSTTTTSIVRRYLAISGGR HLEPERKOALKRIVBEEPLKMOVDEAAARGEPLLTKRGKRPT PCSDPERKRFFPNSSESGSGEASSPDYNGPTAKEVGGN HLEPERKOALKRIVBEEPLKMOVDEAAARGENLDLTKKGRPPT PCSDPERKRFFPNSSESGSGEASSPDYNGPARAGESSESEEKKYKK KREMPFRA\SKAVEESSDERRODILPAGGEESSEEEKKYKK KREMPFRA\SKAVEESSDERRODILPAGGEESSEEEKKYKK KRYEVKKOAPKGAVSVERKOAREESSEESEEKKYKK KRYEVKKOAPKGAVSVERKOAREESSEESEEKKYKK KRYEVKKOAPKGAVSVERKOAREESSEESEEGKRAASG DDSGRRBPVQRKSEDETOLKGGRLSGSEDEEDGKORDST KOSKMARLIGSTGSEEDLEGKSAASGE DDSGRRBPVQRKSEDETOLKGGRLSGSEDEEDGKORDST KOSKMARLIGSTGSEEDLEGKSAASGERGEEDHPAVRIKKYN IR ACGAIRNYKKLIGSCCSKIKERSIESILAREAFTSAMPELGEAAPPGE LYRRTLDSDEERFRPAPPDDSKRIGSILSSGEDERIKRSSKKS SRKGRTRSSSSSDSPBAKGGKAGSGRRGEDHPAVRIKKYN IR ACGAIRNYKKLIGSCCSKIKERSIESILAREAFTSAMPELGEAAPPGE LYRRTLDSDEERFRPAPPDDSKRIGSILSSGEDERIKRTSELSK SRKGRTRSSSSDOSPBAKGGKAGSGRRGEDHPAVRIKKYN IR ACGAIRNYKKLIGSCCSKIKERSIESILAREAFTSAMPELGEAAPPGE LYRRTLDSDEERRPAPPDOSKRIGSILSGEREKKATASGE SRKGRTRSSSSSOLSPBAKGGKAGSGRRGEDHPAVRIKKYN IR ACGAIRNYKKLIGSCCSKIKERSIESILAREAFTSAMPELGEAAPPGE LYRRTLDSCHERRAPPGENERSIESILAREAFTSAMPELGEAAPPGE LYRRTLDSCHERRAPPGENERSIESILAREAFTSAMPELGEAAPPGE LYRRTLDSCHERRAPPGENERSIESILAREAFTSAMPELGEAAPPGE LYRRTLDSCHERRAPPGENERSIESILAREAFTSAMPELGEAAPPGE LYRRTLDSCHERRAPPGENERSIESILAREAFTSAMPELGEAAPPGE LYRRTLDSCHERRAPPGENERSIESILAREAFTSAMPELGEAAPPGE LYRRTLDSCHERRAPPGENERSIESILAREAFTSAMPELGEAAPPGE LYRRTLDSCHERRAPPGENERSIESILAREAFTSAMPELGEAAPPGE LYRRTLDSCHERRAPPGENERSIESILAREAFTSAMPELGEAAPPGE LYRRTLDSCHERRAPPGENERSIESILAREAFTSAMPELGEAAPPGE LYRRTLTGCHERRAPPGENERSIESILAREAFTSAMPELGEAAPPGE LYRRTLTGCHERRAPPGENERSIESINGTBOOM LALLCULAAGGGGGRAALLANTENDERDSNITGIALAGRCULAABP				WTELEODDCDVVDUDODLE AND RINKS FINEW FWQDRFWLDPNVT
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RGTKSLKESEGESSEETLAGKKEGREEVEEREKEEDEKGDMK PRTRSNGRKASARBERSCKOKGOAKRILIGDSDSEEGKEAASG DDSGRDREPPVQRKSEDTOLKGGKRIJGSSEEDEDSGKGEPTA KGSRKMARLGSTSGEESDLEREVSDSEEAGGGPQGERKNRSSKKS SRKGRTRSSSSSDGSPEAKGGKAGSGRGEDHPAVMRLKRYIR ACGAIRNYKKLLGSCCHKERLSILRAELEALGMKGTPSIGKCR ALKEQREEAAFVASLDVANI ISGGGPRRRTTAMPLGEAAPFOB LYRRTLDSDEERRPAPPDMSHMRGIISGDESN 6961 340 1646 RPWSSPTMKNPFSLREIF IFJACKGFTYLSKHRADRMRRLGDFL NQESFDLALLEEVWSEQDFQYLRGKLSPTTYPAAHHFRSGIIGSG LCVPSKHPIGELTQHIYTILMGYPYMIHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEVNRGKIDTDYLYKAVSGFYISCKSFFT TTGFDPRRGTPLSDHERALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMAA\GARWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTBSVGLVALMGAFYLFHVQEVNG LYRAQBELGRUFGRAFAQOLGPEPQLYALL\LGOQGEGRTKEQ NGESFDLALLEEVWSEQDFQYLRGKLSPTYPAAHHFRSGIIGSG LCVPSKHPIGELTQHIYTILNGYPYMIHGDWFSGKAVGLLVUHL SGMVLNAYVTHLHAEVNRGKDIYLARAGAFYLFHVQEVNG LYRAQBELGRUFGRAFAQOLGPEPQLYALL\LGOQGEGRTKEQ NGESFDLALLEEVWSEQDFQYLRGKLSPTYPAAHHFRSGIIGSG LCVPSKHPIGELTQHIYTILNGYPYMIHGDWFSGKAVGLLVUHL SGMVLNAYVTHLHAEVNRGKDIYLARARAGPTLFHVGENG LCVPSKHPIGELTQHIYTILNGYPYMIHGDWFSGKAVGLLVUHL SGMVLNAYVTHLHAEVNRGKDIYLARARAGPTLFHVGENG LCVPSKHPIGELTQHIYTLNGYPYMIHGDWFSGKAVGLLVUHL SGMVLNAYVTHLHAEVNRGKDIYLARARAFPTLFHVGSEEG NITMYPKNCYVSQCLKPFFPGUDTVYLKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\ARRS PL/MCVLKEALDGSLGLGMA\QARWA\TPA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVALWAGAFYLFHVQENG LYRAQAELDHVLGRAREAQDLGPEPQLYALL\LGQGEGRTKEQ TTFSGFGGSSTHEGPLAARGS EAVLISPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETHLEQRNRGHENDLTOVTVR HIGSMRADAGGCUAAGS PFFOOKLLLGYSDIETSVVSVQSVQKLTDFMVSQVFRQVAAGS PFFOOKLLLGYSDIETSPSVVSVQSVQKLTDFMVSQVFRQSEA LQILTAASILQIKTVIDECTRIVOGNVGDVFPGIQDSGDTFRG TFSSGTSGGSSTESGYLQGSPROHDSFNITTRHERSQMRRYL STTPFETHCKROPRPVHICTULVININIKOMEGGE RSFYSGAVVSHHETALGLPRDHHMEDDFNITTRHERSQMRRYL STTPFETTHCRORPRYHICTHUNININIKOMEDDDTDYYXGORPQ ILERNESEECTEDTDQAAEAPAGGGPGTNOLETGASSPE EQGFGFGAARDSQAEPTGDEQAAEAPAGGGPGTNOLETGASSPE	1			TRKKPINIKKOADCKA SUSDKOADEESPESPA EDWODDA WARDON
PRTRENGERKSAREERSCKGKGOAKRLIGUEDSEEGKERAASSG DDSGRDREPPVQRXSEDTOLKGGKRLIGUEDSEEGKERPTA KGSRKMARLGSTSGESDLEREVSDSEAGGGPQGERKNRSSKKS SRKGRTRSSSSSSBGSPEAKGGKAGSGRGEDHPAWRILKRYIR ACGAIRMYKKLIGSCCSHKERLSIIRAELEALGMKGTPSIGKCR ALKEQREEAAEVASLDVANIISGSGRRETHAWRPLGEAAPPGB LYRRILDSGEBRPRPAPPDRINKINGIISJOESSN 6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRIGGEL CVPSKHPIGELTCHITTINGYPYMIHHGWFSGKAVGLUMIL SGMYLNAYVTHLHAEVARQKDIYLAHHVAQAWELAQPIHHTSKK ADVVLLGGBLINMHPEDLGCLLKEWTGLHDAYLETRPRKSEBG NTMYPKNCYVSQQELKPPPFGVRIDYVLYKAVSGFYISCKSFFI TTGFDPHRGTPLSDHEALMATLEVRHSPPQQNESSTRGP\ACES NTMYPKNCYVSQQELKPPPFGVRIDYVLYKAVSGFYISCKSFFI TTGFDPHRGTPLSDHEALMATLEVRHSPPQQNESSTRGP\ACES PL/MCVLLKAALGGGAGEAAILLMTPSVGLTUMAGAFYLHVQEVNG LYRAQASLGHUKGRAREAQDLGPPQLYALL/LGQGEGDRTKQQ 1478AQASLGHUKGRAREAQDLGPPQLYALL/LGQGEGDRTKQQ CVPSKHPIGELTQHITTINGYPYMIHHGWFSGKAVGLIVHL SGMYLNAYVTHLHAEVNROKDIYLARHVAQAWELAQPIHHTSKK ADVVLLCGBLINMHPEDLGCLLKEWTGLHDAYLETRDPKGSEG UTWSKHPIGLTQHITTINGYPYMIHHGWFSGKAVGLIVHL SGMYLNAYVTHLHAEVNROKDIYLARHVAQAWELAQPIHTTSKK ADVVLLCGBLINMHPEDLGCLLKEWTGLHDAYLETRDPKGSEG NTMYPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRISPPQQNPSSTHGP\ACES NTMYPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRISPPQQNPSSTHGP\ACES PL/MCVLKEALDGSLGLGMA\QARWMA\TPA\SYVIGLG\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELGHUVGRAREAQDLEPPQLYALL/IGQOGGDRTKKQ CYALLGSLINMHPEDLGCLLKEWTGLHDAYLETRDPKGSEG PL/MCVLKEALDGSLGLGMA\QARWMA\TPA\SYVIGLG\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELGHUVGRAREAQDCHOPPQLYALL/IGQOGGDRTKKQ PL/MCVLKEALDGSLGLGMA\QARWMA\TPA\SYVIGLG\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELGHUVGRAREAQDCHOPPQLYALL/IGQOGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	}	1		KGTKSI-KRSEOFSEFFII. AOVVEODEDEDUEEDEDVEDDEDVED
DDSGRDRPPVQRKSEDRTQLKGGKRLSGSEDEEDGSKGEPTA KGSRMARLGSTSGEESDLEEVSDSRAGGGPQGERKNRSSKK SRKGRTRSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKYIR ACGAIRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSIGKCR ALKEQREEABAVASLDVANI ISGGRPRRTTAMPLGEAPPGB LYRRTLDSDEERRPAPPDRSHMRGI ISSDGESN FPWSSPTMKPNFSLRLRIFNILNGGIPYLSKHRADRMRRLGDFL NQESPDLALLEEWSEQDFQYLRGKLSPTTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTIKNGYPYHIHHGDWFSGKAVGLLVLHI SGMVLNAYVFILHAEYNRGNOIYLAHBVAQAMELAQPIHTISKK ADVVLLGGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDVYLYKAVSGFYISCKSFFT TTGFDPHRGTPLSDHEALMATLFVRHSPPQONDFSSTTIGF)AERS PL/MCVCLKEALDGSLGLGMA\QARWAA\TFA\SYVIGLGL\LL LLLCVLAAGGGAGEAAILMFSVGLYLMAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQGEGRTKEQ AQSSPDLALLEEWSEQDPGYLRKKLSPTTYPAAHFFSGI IGSG LCVFSKHPIQELTQHIYTLMGYPYHHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRGKDIYLAHRVQAWELAAGFIHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDVYLYKAVSGFYISCKSFET TTGFDPHRGTPLEBUMSDDMFYLRKLSPTTYPAAHFFSGI IGSG LCVFSKHPIQELTQHIYTLMGYPYHLHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRGKDIYLAHRVQAWELAAGFIHTTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDVYLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHRALMATLEVRISPPQDMPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWMAGAFYLFHVQENNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\JGQQGGGFTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\JGQQGGGFTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\JGQQGGGFTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\JGQQGGGFTKEQ TPSGTGGSSDTESGYLQSHPGPSVTGTYRYGQGEA LYRASALGHVLGRAFFEAGHTFOYTYR HIGSMLRAQRCULAGS PFFQDKLLLGYSDI ETPSVVSVQSVQKL TDFMYSGVLRYGQEA LYRASSLETHENGNRGHFFCVVTVR HIGSMLRAQRCULAGS PFFQDKLLLGYSDI ETPSVVSVQSVQKL TDFMYSGVLRYGQEA LYRASSLETHENGNRGHFFCVVTVR HIGSMLRAQRCULAGGS FSFYSGAVVSHHETALGLPROHHMEDPSWITTR THERSQMERYL STTPETHCKRQCRPRVNICHTVONNICH KOEMBEDDDYDYYGQDRQ LLERNESEECTEDDTQAECTESEPRGESPDSCYSSSIGTEPDDSV LGQGFGGAARDSQAEPTUTGGRAARDABGGGFOTNOLDTGAASSPE EQQFGGGGGARDSQAEPTUTGRAARDABGGGFOTNOLDTGAASSPE EQQFGGGGGARDSQAEPTUTGRAARDABGGGFOTNOLDTGAASSPE	1			PRTRSNGRPKSAPEEPSCKOKSOAKDLI CDSDSSESOVER ROSS
KGSRMARLGSTSGESDLERBYSDEAGGGPQGERNNRSSKKS SRKGRTRSSSSSSDSDSPBAKGGKAGSGRRGEDHPAVMRLKRYIR ACGAHRNYKKLLGSCCSHKERLS ILRAELEALGMKGTPSLGKCR ALKEQREBABVASLDVANI ISGSGRPRRRTAMPLGEAAPPGE LYRRTLGSDEERPRPAPPGSMRGGI ISSGESDEN FWSSPTMKPBFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL NQESPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGI IGSG LCVPSKHBIGDLTQHIYTINGYPYMIHHGDWFSGKAVGLUVHL SGMYLNAVYTHLHABYNRQKDIYLAHRVAQAMBLAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETTDFKGSEEG NTMYPKNCYVSQOELKPPFFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTFLSDHEALMATLFVHSPPQORPSSTHGP\ARRS PL/MCVCLKEALDGSSLGLGMA\QARWMA\TPA\SYVIGIGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQABLQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQABLQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ NOSSPDLALLEEVWSEQDPQYLRQKLSPTYPAAHHFRSGI IGSG LCVPSKHPIQELTQHIYTLNGYFYHIHGDWFSGKAVGLLVHLL SGMYLNAYVTHLHAEYNRQKDIYLAHRVAQAWBLAQFIHTISKK ADVVLLCGDLNMHPEDLGCCLLKBWTGLHDAYLETTDPKGSEG NTMYPKNCYVSQQELKPFPFBVRIDYLYLAHRVAQABFLAGFIHTISK ADVVLLCGDLNMHPEDLGCCLLKBWTGLHDAYLETTDPKGSEG NTMYPKNCYVSQQELKPFPFBVRIDYLYLAHRVAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQCEGDRTKEQ LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQCEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQCEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQCEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQCEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQCEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQCEGDRTKEQ LYRAQAELGHVLGRAREAQDLGPEPQLYALL\LGQCEGDRTKEQ LYRAQAELGHVLGRAREAQDLGPEPQLYALL\LGQCEGDRTKEQ LYRAQAELGHVLGRAREAQDLGPEPQLYALL\LGQCEGDRTKEQ LYRAQAELGHVLGRAREAQDLGPEPQLYALL\LGQCEGDRTKEQ LYRAQAELGHVLGRAREAQDLGPEPQLYALL\LGQCEGDRTKEQ LYRAQAELGHVLGRAREAQDLGPPPQLYALLXLGGCAGAGA PFFGDKLLLGYSDLETPSVUSVQSVQKI.TDFMYSQVLRVSQEEA LQTLTAASTLQTKTYTDECTRIVSQNVSDVPFGIQDSGQTFRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHETTALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQRPRPURICTUVGNIHLKQRMEDDDSVYTYGQQRVQ LLERNSSEECTRDTDQAEGTSEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPOTNQLETGASSPE EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPTTNQLETGASSPE	1			DDSGRDREPPVORKSEDPTOLKGGKDLGGSSSSEEGKEAASSG
SRKGRTRSSSSIGSPEAKGGKAGGRAGEDHPAWRIKRYIR ACGARIRNYKKLIGSCCSHKELTS ILRAELEALGMKGTPSLGKCR ALKEQREEAAEVASLDVANI ISGGRPRRTAWNPIGEAAPPGB LYRRILDSDEERPRPAPPDWSHRMGIISSDGESN 6961 340 1646 RPWSSPTMKPMFSILRIF IRINGVGIPYLSKHRADRMRRLGPEL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLINGYPYMIHHGDWFSGKAVGLUVHL SGMYLNAYVTHLHAEYNRQKDIYJAHRVAQAWELAQFIHHTSKK ADVVLLCGDLMMHPEDLGCCLLKEWTGLHDAYLETRDFKSSEG NTMPKNCYVSQQELKPFGVRIDYVLYKAVSGFYISCKSPET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGIGMA\QARMWA\TFA\SYVIGLGL\LL LALLCVLAAGGAGAEAAILLWTPSVGLVLWAGGFYLFHVQEVMG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ APSSFTMKPNFSLRIRIFNLCWGIFYLFAKHRADRMRRLGDFL NQESFDLALLEEVWSEQDFQYLRQKLSFTYPFAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTILNGYPYMIHHGDWFSGKAVGLLVHL SGMVLNAYVTHLHAEYNRGVIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTWYPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQOMPSSTHGP\AERS PL/MCVCLKEALDGSLCLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAGFYLFHVQEVMG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGGRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQCGGGTTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQCGGGTTKEG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQCGGGTTKEG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQCGGGTTKEG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQCGGGTTKEG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQCGGTTKEG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQCGGTTKEG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQCGGTTKEG LYRAQAELGHVLGRAREAQDLGPEPQLYALL\LGQCGGTTKEG LQLILTAASILQLKTVIDECTRIVSGNVGDVPFGIQDSCGDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSGYLRVSQSEA LQLILTAASILQLKTVIDECTRIVSGNVGDVPFGIQDSCGDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSGYLRVSQSEA LQLILTAASILQLKTVIDECTRIVSGNVGBVFFGIDSCGDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSWQMSGE RSFYSGAVVSHHETALGLPRDHHMDEDSWITRIHRSQQMRRYL STTPETTHCKRQFPPVBICQTLVGMIHKGWEEDDDVBYGQGRV LLGRINSSEECTRDTDQAEGTSEPKGESFDSCVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPTUNQLETGASSPE EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPTUNQLETGASSPE EQQFGPGAARDSRVSVLQQPSVNTSIGQPLSTGLYFT	1			KGSRKMARIGSTSGEESDIEDEVSDSPAGGGDOGEDVNDSOVVO
ACGAHRNYKKLLIGSCCSHKERLS ILRABLEALGMKGTPSLGKCR ALKEGREBAEVASLDVANI ISGSGRPRRRTAMNPLGEAAPPGB LYRRTLDSDEERPRPAPPDWSHMKGI ISSDGESN 6961 340 1646 RPWSSPTMKPMPSLRLR I PMILNCGI PYLKKRADDMRRLGGPL NQESFDLALLEEVWSEDDFQYLRCKLSFTYPAAHHFRSGI IGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMYLNAVVTHLHAEYNRCKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGIDLMMHPEDLGCCLLKEWTGLHDAYLETTDPFKGSEG NTMYPKNCYVSQOELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWMA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTFSVGLUVLMAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPPQLYALL\LGQOEGDRTKEQ NQESFDLALLEEVWSEQDFQYLRCKLSFTYPAAHHFRSGI IGSG LCVPSKHPIQELTQHIYTINGYPYMIHHGDWFSGKAVGLLVHL SGMVLNAYVTHLHAEYNRCKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLMMHPBDLGCCLLKEWTGLHDAYLETTDPKGSEG NTMYPKNCYVSQGELKPFPGWRITYLAWASGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS ADVVLLCGDLMMHPBDLGCCLLKEWTGLHDAYLETTDPKGSEG NTMYPKNCYVSQGELKPFPGWRITYLMAGAFYLFHVQSVMG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ NTMYPKNCYVSQGELKPFFGWRITYLMFAGFYLFHVQSVMG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSDPDALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHAFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFOKLLLGYSDIEIPSVVSVQSVGKLTDFMSGGVLRAVSGEA LOILTAASILQIKTVIDECTRIVSQNVGVFQTDFGGGDGDTPRG TPESGTSGOSSDTESGYLQSHPOHSVDRIVSALYACSMQNGGE RSFYSGAVSHHETALGLPRDHHMEDPSWITRHERSQQMRYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYGGQQPVQ LLERNBSEECTEDTDQAAETSSEPKGESPDSGVSSSIGTEDDSV EQQFGPGAARDSQAAEPTQPEQAAEAPAEGGPQTNQLETGASSPE EQQFGPGAARDSQAAEPTQPEQAAEAPAEGGPQTNQLETGASSPE	1	}		SRKGRTRSSSSSSDGSPEAKGGKAGSGPRGEDUDAUMDLYDYTD
ALKEGRERAEVASLDVANIISGGRPRRTTAMNPLGEAAPPGB LYRRTLDSDEERPRPAPPWSHMRGI ISDGESN 6961 340 1646 RPWSSPTMKPMFSLRLRIFMLMCMGI PYLSKHRADRMRRLGDFL NQESFDLALLEEVWSEODFGYLRGKLSFTYPAAHHERSGI IGSG LCVFSKHPIQELTQHIYTLMGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAVYTHLHAEVNRGKDIYLAHRVAQAWELAGFIHHTSKK ADVVLLCGDLMMHPEDLGCCLLKEWTGLHDAYLETRDFRGSEEG NTMPKNCYSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLEVRHSPPQONPSSTHGF\ASRS PL/MCVCLKEALDGSLGLGMA\QARWA\TFA\SYVIGIGL\LL LALLCVLAAGGGAGRAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGGRTKEQ ADVLLCGDLLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGI IGSG LCVFSKHPIQELTQHIYTLNGWFYMIHHGDWFSGKAVGLLVHL SGMVLNAYVTHLHAEYNRGKDIYLARRVAQAWELAGFIHHTSKK ADVVLLCGDLMMHPBLGCCLLKEWTGLHDAYLETRDPKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTFLSDHEALMATLFVRHSPPQQNPSSTHGP\ASRS PL/MCVCLKEALDGSLGCLLKAWTGLDAYLETRDPKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTFLSDHEALMATLFVRHSPPQQNPSSTHGP\ASRS PFL/MCVCLKEALDGSLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFFHVQSVNG LYRAQAELQHVLGRARRAQDLGPEPQLYALL\LGQQEGGRTKEQ PL/MCVCLKEALDGSLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQSVNG LYRAQAELQHVLGRARRAQDLGPEPQLYALL\LGQQEGGRTKEQ PL/MCVCLKEALDGSLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQSVNG LYRAQAELQHVLGRARRAQDLGPEPQLYALL\LGGQEGGRTKEQ PL/MCVCLKEALDGSLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQSVNG LYRAQAELQHVLGRARRAQDLGPEPQLYALL\LGGQEGGPTTEQ PL/MCVCLKEALDGSLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQSVNG PFFODKLLLGYSDIEIPGVVSVQSVQKLIDFMYGCVLRAGSGE PFFFODKLLLGYSDIEIPGVVSVQSVQKLIDFMYGCVLRAGSGE PFFFODKLLLGYSDIEIPGVVSVQSVQKLIDFMYGCVLRAGSGE PFFFODKLLLGYSDIEIPGVVSVQSVQNGLIDFMYGCVLRAGSGE TTESGTSGGSSDTESGYLQGSHPOHSDFTGLDSGQDTPRG TTESGTSGGSGSDTSGYVGGSHPOHSDFTGLDSGVSSIGTEPDSV STTPETTHCKKQRPPVRLQTLVGNIHKQCBEEDPSVGRQPU TLERNRSEECTBDTDQAAETBAEGFPQTNQLETGASSPE EQQGFPGAARDSQAAPTQEPQAAEAPAEGGPQTNQLETGASSPE RSNEVENDSTVITVSNSSDKSVLQQPSVNTSIGQPLBSTQLYLG				ACGAHRNYKKLLGSCCSHKERISTIRAFI.FALCMYGTDELCYCD
6961 340 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL NQSSPDLALLEEVWSRQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVPSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMYLLNAVYHLHJARVRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMYDKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHRALMATLFVKHSPPQONPSSTHGP\ARRS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREQOLGPPPQLYALL\LGQQEGGPTKEQ AQUELQHVLGRAREQOLGPPPQLYALL\LGQQEGGPTKEQ NQESFDLALLEEVWSEQDFQVLRQKLSFTYPAAHHFRSGIIGSG LCVPSKHPIQELTOHIYTLNGYPYMIHHGDWFSGKAVGLLVHL SGMYLNAVYTHLHAEYNRQKDIYLKAVAGFYISCKSFET TTGFDPHRGTPLSDHRALMATLFVKHSPQONPSSTHGP\ARRS ADVVLLCGDLINMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMYPKNCYVSQQELKFFPFGVRIDYVLKAVSGFYISCKSFET TTGFDPHRGTPLSDHRALMATLFVKHSPQONPSSTHGP\ARRS PL/MCVCLKEALDGSLGLMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQENG LYRAQAELQHVLGRAREAQDLGPPQLYALL\LGQQEGDRTKEQ ARVENCEVSQELKFFFTSDHRALMATLFVRHSPVGLVLWAGAFYLFHVQENG LYRAQAELQHVLGRAREAQDLGPPQLYLLALLAGQGEDRTKEQ LYRAQAELGHVLGRAREAQDLGPPQLYALL\LGQQEGDRTKEQ LYRAQAELGHVLGRAREAQDLGPPQLYALLALGQQEGDRTKEQ LYRAQAELGHVLGRAREAQDLGPPQLYLLALLAGQGEDRTKEQ LYRAQAELGHVLGRAREAGDLGPPQLYLLALLAGGGGAGEARILLWTPSVGLVLWAGAFYLFHVQENG LYRAQAELGHVLGRAREAGDLGPPQLYLLALLAGGGAGCAAILLWTPSVGLVLWAGAFYLFHVQENG LYRAQAELGHVLGRAREAGDLGPPQLYALLALAGGGAGCAAILLWTPSVGLVLWAGAFYLFHVQENG LYRAQAELGHVLGRAREAGDLGPPQLYALLALAGGAGGAGCAAILLWTPSVGLVLWAGAFYLFHVQENG LYRAQAELGHVLGRAREAGDLGPPQLYALLALAGGAGGAGCAAILLWTPSVGLVLWAGAFYLFHVGENG LYRAQAELGHVLGRAREAGDLGPPQLYLLALAGGAGGAGCAAILLWTPSVGLVLWAGAFYLFHVGENG LYRAQAELGHVLGRAREAGDLGPPQLYLLALAGAGGAGCAAILLWTPSVGLUWAGAFYLFHVGENG LYRAQAELGHVLGRAREAGDLGPPQLYLLALAGAGGAGGAGAAILLWTPSVGLUWAGAFYLFHVGHAGAGAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAA	1			ALKEOREEAAEVASLDVANITSGSGRPRRRTAWNDIGRAADDGR
6961 340 1646 RPWSSPTMKPNPSLRLRIFNINCWGIPYLSKHRADRMRRLGDFL NQESPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVPSKHPIQELTQHIYTHLNGYPYMIHHGBWFSGKAVGLUVHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMYPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TGFDPHRGTPLSDHERLMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLUVLWGARFYLFHVQEVNG LYRAQAELQHVUGRARFAQDLGPEPQLYALL\LGQQEGDRTKEQ RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVPSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLMNHPBEDLGCCLLKEWTGLHDAYLETNDFKGSEEG NTWYPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQNNSSTHGP\AERS PL/MCVCLKEALDGSIGLGMA\QARWWA\TFA\SYVIGLG\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVUGRAREAQDLGPEPQLVALL\LGQQEGDRTKEQ LYRAQAELQHVUGRAREAQDLGPEPQLVALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERHSIN LHNFSNSVLETILNEQRNGHFFCDVTVRIHGSMLRAQRCVLAAGS PFFGOKLLLGYSDIEIPSVVSVQSVQKILDFWYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TEESGTSGQSSDTESGYLQSHPOHSVDRIYSALVACSMQNGSGE RSPYSGAVVSHHETLGLPRDHHMEDPSWITRIHERSQMERYL STTPETTHCRKQPRPVRIQTLVCNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESFPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSDKSVLQQPSVNTSIGQPLYSLYK				LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN
NQESPDLALLEEWSEQDFOYLRQKLSFTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLUVHLL SGMVLNAVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKEPFPFGVRIDYVLYKAVSGFYLSCKSFET TTGFDPHRCTPLSDHEALMATLFVRHSPPGONPSSTHOP\ARSS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAALLWTPSVGLVUWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGCQEGDTKEQ AQAGELQHVLGRAREAQDLGPPQLYALL\LGCQEGDTKEQ NQESFDLALLEEWSEQDFQYLRQKLSFTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVHL SGMVLNAVYTHLHAEYNRQKDIYLAHRVAQAWELAQFIHTTSKK ADVVLLCGGLINMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKEPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHEGY\ARS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPPQLYALL\LGCQCEGDTKEQ EAVLSADPALHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFODKLLLGYSDIETPSVVSVQSVQKIIDFMVSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFFGIQDSQDTPRG TPESGTSGSSDTESGYLQSHPQHSVDRIYSALYACSMQMSGSE RSFYSGAVVSHETALGLPRDHMMEDPSWITRIHERSQCMENYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQGFGAARDSQAETPTQPEQAAEAPAEGGPQTNQLETGASSPE EQQFGPGAARDSQAETPTQPEQAAEAPAEGGPTTYLETSSPE	6961	340	1646	RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRIGDET.
LCVPSKHPJQELTQHITTINGYPYMIHHGDWFSGKAVGLLVIHL SGMVINAYVTHLHAEVPRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDINMHPEDLGCCLLKEWTGLHDAYLETRDPKGSEGG NTMVPKNCYVSQQELKPPPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQHPSSTHGP\AERS PL/MCVCLKEALDGSLGIGMA\QARWWA\TFA\SYVIGIGI\LL LALLCULAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRYKEQ 6962 340 1646 RPWSSPTMKPNFSIRLR IFNLNCWGIPYLSKHRADRWRELGDFL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVPSKHPIQELTQHITTLNGYPYMIHHGDWFSGKAVGLLVIHL SGMYLNAVYTHLHAPVRQKDIYLAHRVAQAMELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMYPKNCYVSQQELKFFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGI\LL LALLCVLAAGGAGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDTKKQ PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGI\LL LALLCVLAAGGAGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDTKKQ PL/MCVCLKEALDGSLGLGMKYQTVTWHAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDTKKQ PL/MCVCLKEALDGSLGLGMKYQTVTWHAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDTKKQ PL/MCVCLKEALDGSLGLGMKYCTVTHIGSMLRAQRCVLAAGS PL/MCVCLKEALDGSLGLGMKYCTVTHIGSMLRAQRCVLAAGS PFFQDKLLLGYSDIETPSVVSVQSVQKI.IDEWYSGLCRVLAAGS PFFQDKLLLGYSDIETPSVVSVQSVQKI.IDEWYSGLCRVLAAGS PFFGDKLLLGYSDIETPSVVSVQSVQKI.IDEWYSGLCRVLAAGS PFFGDKLLLGYSDIETPSVVSVQSVQKI.IDEWYSGLCRVLAAGS STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTBTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE				NQESFDLALLEEVWSEQDFQYLROKLSPTYPAAHHFRSGITGSG
SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCTVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSIGLGMA\QARWWA\TFA\SYVIGLGI\LL LALLCVLAAGGGAGFAAILLMTPSVGLIVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ NQESFDLALLEEVWSEQDPGYLRQKLSPTYPAAHHFRSGIGSG LCVPSKHPIQELTCHIYTLNGYPYMIHHGDWFSGKAVGLLVHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLMMHPEDLGCCLLKEWTGLHDAYLETRDPKGSEEG NTMYPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGIGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG PPL/MCVCLKEALDGSLGIGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG EAVLSPDPALIHSTHSLINSHAHTGSSDCDISCKGMTERHSIN LHNFSNSLETLINEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LOILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSQDTPRG TPESGTSGQSSDTESGYGSPTGNGVSTVACSMQNGSGE TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHIMEDPSWITRIHERSQOMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQABGTESSPKGSSTDSGVSSSIGTEPDSV ILERNESEECTEDTDQABGTESSPKGGSFDSGVSSSIGTEPDSV EQQFGFGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNVENDSTUTTVSNSSDKSVLQQPSVMTSIGQPLFSTQLLYLR	1			LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL
ADVVILCGDINMHEDLGCCLLKENTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRCTPLSDHEALMATLFVRHSPPQONPSSTRGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRWRRLGGFL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVPSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHABYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVILCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLG\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LVRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALITSHTSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFODKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGGSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV STPPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQBEGGBGPQTNQLETGASSPE RSNVEMDSTVITVSNSSDKSVLQQPSVMTSIGQPLFSTQLYLR	1			SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAOFIHHTSKK
NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSIGIGMA\QARWWA\TFA\SYVIGIGI\\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ 1480 1646 RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL NQESFDLALLEEVWSEQDFQYLRQKLSFTYPAAHHFRSGIGSG LCVPSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAVYTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADDVVLLCGDLMMHPEDLGCCLLKEWTGLHDAYLETRDPKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGIGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ 1480 RVYPLILKLLKKPKTAENQKRSEENETTOPGGSSAKPGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCULAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMVSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFFGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQMGRFL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGGAARADSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSKSVLQQDSVNTSIGQPLPSTQULYR				ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG
TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCULAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVPSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLMMHPEDLGCCLLKEWTGLHDAYLETRDPKGSEEG NIMWYKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCULAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGFEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLIMSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSQDTPRG TPESGTSGGSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYYYGQQRVQ ILERNESEECTEDDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQFGPGARARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVWTSIGQPLETGASSPE				NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET
PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGIGL\LL LALLCVLAAGGGAGEAAILUTPSVGLVLWAGAFYLFHYQEVIG LYRAQAELQHVLGRAREAQDLGPEPPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPPQLYALL\LGQQEGDRTKEQ RPWSSPTMKPNFSLRIRIFNLINCWGIPYLSKHRADRMRRLGDFL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIGSG LCVPSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQABELAQFIHHTSKK ADVVLLCGDLMMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFFFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLG\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELOHVLGRAREAQDLGPEPQLVALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETINEQRNRGHFCDVTVR HGSMLRAQRCVLAAGS PFFODKLLLGYSDIEIPSVVSVQSVQKLIDFMVSQVLSQEEA LQILTAASTLQIKTVIDECTRIVSQNVGDVFPGIQDSQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILLERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGARRDSQAEPTQPEQAAEAPAGGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS
LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ RPWSSPTMKPNFSLRIFINLNCWGTPYLSKHRADRMRRLGDFL NQESPDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVPSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTWYPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTESVGLVLWAGAFYLFHVQEVMG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVUSPDPALHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETINEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFGDKLLLGYSDIEIPSVVSVQSVQKI.IDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHIMEDPSWITRIHERSQQMERYL STTPETTHCKQRPPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	i i			PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL
RPWSSPTMKPNFSLRIRIFNLNCWGIFYLSKHRADRMRRLGDFL NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHLL SGMVULAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\ARRS PL\MCVVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILLERNESEECTEDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	1			LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG
NQESPILALEEVWSEQDFQYLRQKLSPTYPAAHHFRSGI IGSG LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHIL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSIGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQOMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILLERNESEECTEDTDQAEGTESEPKGESFDSGVSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	6053			LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEO
LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSPYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	0362	340	1646	RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL
SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK ADVVLLCGDLMMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG NTMVPKNCYVSQQELKPFFFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR				NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG
ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDPKGSEEG NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL\MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSPYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	1			LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL
NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFPPHRGTPLSDHEALMATLFVRHSPPQONPSSTHGP\AERS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	1 1			SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK
TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS PL/MCVCLKEALDGSLGLMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMVSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPFTTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR]]		ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG
PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETINEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSPYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNOLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	1	1		NIMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET
LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ EVTPLILKLKKKKTAENQKASEENEITQPGGSSAKFGLPCINF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNOLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	Į į	}		TIGEDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS
LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ RVTPLILKLLKKPKTAENQKASEENEITQPGGSSAKPGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSPYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR		ļ	İ	PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL
RVTPLILKLLKKPKTAÉNQKASEENEITQPGGSSAKPGLPCLNF EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETINEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PPFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR		l	i	LANDON DI CHE CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROLL CONTROL CO
EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGOSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSPYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNOLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	6963	374	2610	DIRAYALLUHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ
LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQMGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR		-7.3	2019	RVIPLINKLEKKPKTAENQKASEENEITQPGGSSAKPGLPCLNF
PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEFTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	i			EAVES PER AND THE
LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG TPESGTSGQSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSPYSGAVVSHHETALGLPRDHIMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEFTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	1	į		DEFORM I GUARANTE TENERAL TENE
TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	1 1	ł		FEETONYPHYSZNIETBSAASAÖSAÖKI'IDŁWASGAIBASÖSEV
RSFYSGAVVSHHETALGLPRDHIMEDPSWITRIHERSQQMERYL STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR		Ì		DQIDIAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG
STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR		İ		TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE
ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR	[ľ	ľ	
EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR			1	
RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR			1	ILEKNESECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV
	ļ		ì	EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE
QTETLTSNLRMPLTLTSNTQVIGTAGNTYLPALFTTQPAGSGPK			1	
	L			QTETLTSNLRMPLTLTSNTQVIGTAGNTYLPALFTTQPAGSGPK

			I have the second and
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
(location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	-	\=possible nucleotide insertion)
ļ	Bequeinee		PFLFSLPQPLAGQQTQFVTVSQPGLSTFTAQLPAPQPLASSAGH
į	1	}	STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEKPHQCSI
İ		1	CWRSFSLKDYLIK\HMVTHTGVRAYQCSICNKRFTQKSSLNVHM
1	1	1	RLHRGEKSYECYICKKKFSHKTLLERHVALHSASNGTPPAGTPP
I	I)	GARAGPPGVVACTEGTTYVCSVCPAKFDQIEQFNDHMRMHVSDG
			GARAGPPGVVACTEGTTTVCSVCPARFDQTEQFNDAFIRMIVSDG
6964	1	178	SGRPFFFFFSNTDVYFIKKVTNRWTAGSSYKMTRMKSIGKILLL
ł]		QIFIG\NCSMFVLVI
6965	757	208	NVFIEPRIQGFMKTSAHPGQKHPDFSMGLLFPLLAALEVCSCGS
}	,	}	SGSLGYNLPQNH\GLLGRNTLVLLGQMRRISPFLCLKDRSDFRF
		1	PQEKVEVSQLQKA\QAMSFLYDVLQQVFNFSHKALL\CCMEHDL
1	1	ľ	PGPTPHFTSSAAGTPGDLLGAGDGRRRSWGQWVIEGSTLALRRY
	i	1	FOESISTLE
6966	820	1867	IITALGVRGMPGCPCPGCGMAGPRLLFLTALALELLGRAGGSQP
9000	020	1	ALRSRGTATACRLDNKESESWGALLSGERLDTWICSLLGSLMVG
1			LSGVFPLLVIPLEMGTMLRSEAGAWRLKQLLSFALGGLLGNVFL
1			HLLPEAWAYTCSASPGGEGQSLQQQQQLGLWVIAGILTFLALEK
İ	Į.	ļ	HPPEAMATICSASPGGEGGSTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
j	1 .)	/HVPGQQGGDQPGPQQRPHCCCRRAQWRPLSGPAGCRARPRCR
			GP\DIKVSGYLNLLANTIDNFTHGLAVAASFLVSKKIGLLTTMA
ì	1	Į.	ILLHEIPHEVGDFAILLRAGFDRWSAAKLQLSTALGGLLGAGFA
ł	1	i	ICTQSPKGVEETAAWVLPFTSGGFLYIALVNVLPDLLEEEDPW
6967	162	633	GFLPFKYWILDLSASSRMETDCNPMELSSMSGFEEGSELNGFEG
1		1	TDMKDMRLEAEAVVNDVLFAVNNMFVSKSLRCADDVAYINVETK
1	l		ERNRYCLELTEAGLKVVGYAFDQVDDHLQTPYHETVYSLLDTL\
1	1	1	SPAYREAFGKR\LLQRLEALKRDGQS
6968	1	2265	RGGGGGRGGPGARERERPGEPERTMEAAAGGRGCFQPHPGLQKT
6568	1 -	1 2233	LEQFHLSSMSSLGGPAAFSARWAQEAYKKESAKEAGAAAVPAPV
	i	1	PAATEPPPVLHLPAIQPPPPVLPGPFFMPSDRSTERCETVLEGE
1	ł	1	TISCFVVGGEKRLCLPQILNSVLRDFSLQQINAVCDELHIYCSR
1	1	1	CTADQLEILKVMGILPFSAPSCGLITKTDAERLCNALLYGGAYP
	Į.	1	CTADQUETERVMGTEPFSAFSCGETTRIDAERGCRAEGIGGATZ
1		1	PPCKKELAASLALGLELSERSVRVYHE\CFGKCKGL\LVPELYS
		1	SPSAACIQCLD\CRLMYPPHKFVVHSHKALENRTCHWGF\DSA\
ļ		Í	NWRAYILLSQDYTGKEEQARLGR\CLDDVKEKFDYGNKYKRRVP
1		ì	RVSSEPPASIRPKTDDTSSQSPAPSEKDKPSSWLRTLAGSSNKS
1			LGCVHPRQRLSAFRPWSPAVSASEKELSPHLPALIRDSFYSYKS
1	1		FETAVAPNVALAPPAQQKVVSSPPCAAAVSRAPEPLATCTQPRK
j		1	RKLTVDTPGAPETLAPVAAPEEDKDSEAEVEVESREEFTSSLSS
1	1		LSSPSFTSSSSAKDLGSPGARALPSAVPDAAAPADAPSGLEAEL
1			EHLRQALEGGLDTKEAKEKFLHEVVKMRVKQEEKLSAALQAKRS
1			LHQELEFLRVAKKEKLREATEAKRNLRKEIERLRAENEKKMKEA
1			NESRLRLKRELEQARQARVCDKGCEAGRLRAKYSAQIEDLQVKL
1			OHAEADREOLRADLLREREAREHLEK\VVK\ELQEQLWPRARPE
1	1		* -
L_			AAGSEG\AAELEP
6969	1855	118	AGTMHGRLKVKTSEEQAEAKRLEREQKLKLYQSATQAVFQKRQA
1	1		GELDESVLELTSQILGANPDFATLWNCRREVLQQLETQKSPEEL
1 .			AALVKAELGFLESCLRVNPKSYGTWHHRCWLLGRLPEPNWTREL
1			ELCARFLEVDERNFHCWDYRRFVATQAAVPPAEELAFTDSLITR
-	1	1	NFSNYSSWHYRSCLLPQLHPQPDSGPQGRLPEDVLLKELELVQN
1	(1	AFFTDPNDQSAWFYHRWLLGRADPQDALRCLHVSRDEACLTVSF
1	1 .		SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDLP
1			AASLNDQLPQHTFRVIWTAGDVQKECVLLKGRQEGWCRDSTTDE
1	}		QLFRCELSVEKSTVIQSELESCKELQELEPENKWCL\LTIILLM
ļ	1	1	QLFRCELSVEKSTVLQSELESCREDQEDEFERANCE (LITTIDE)
	1		RALDPLLYEKETLQYFQTLK\AWDPKRATY\LDDLRSKFLLENS
ĺ	1	Į.	VLKMEYAEVRVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRTL
1	1	}	PPALAALRCLEDPPPRT\VLQASDNAIESLDGVTNLPRLQELLL
1	1		CNNRLQQPAVLQPLASCPRLVLLNLQGNPLCQAVGILEQLAELL
	1	ł	PSVSSVLT
1	ľ	1	[52/22/DI

C CEO	I 5 31		
SEQ ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ĺ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
i	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	ocquence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6970	3	1528	CERRILLEGRENCECKANA DESCRIPTION)
	_	1320	SFPPLLSSPSAVGEGKVAVAAPCPGRSECARAKMAYIQLEPLNE
ł			GFLSRISGLLLCRWTCRHCCQKCYESSCCQSSEDEVEILGPFPA QTPPWLMASRSSDKDGDSVHTASEVPLTPRTNSPDGRRSSSDTS
1			KSTYSLTRRISSLESRRPSSPLIDIKPIEFGVLSAKKEPIQPSV
Į.	,		LRRTYNPDDYFRKFEPHLYSLDSNSDDVDSLTDEEILSKYQLGM
	j		LHFSTQYDLLHNHLTVRVIEARDLPPPISHDGSRQDMAHSNPYV
	1		KICLLPDQKNSKQTGVKRKTQKPVFEERYTFEIPFLEAQRRTLL
			LTVVDFDKFSRHCVIGKVSVPLCEVDLVKGGHWWKALIPSSONE
1			VELGELLLSLNYLPSAGRLNVDVIRAKQLLQTDVSQGSDPFVKI
	!		QLVHGLKLVKTKKTSFLRGTIDPFYNESFSFKVPQEELENASLV
ł	1		FTVFGHNMKSSNDFIGRIVIG\QYSSGP\SEPNHWRRMLNTHRT
Ł			AVEQWHSLRSRAECDRVSPASLEVT
6971	37	3702	ACFYVPGSRSFKLIPRHGLVNMGRSGKLPSGVSAKLKRWKKGHS
			SDSNPAICRHRQAARSRFFSRPSGRSDLTVDAVKLHNELQSGSL
1			RLGKSEAPETPMEEEAELVLTEKSSGTFLSGLSDCTNVTFSKVQ
1			RFWESNSAAHKEICAVLAAVTEVIRSQGGKETETEYFAALIRKA
			AQHGVCSVLKGSEFMFEKAPAHHPAAISTAKFCIOEIEKSGGSK
1			EATTTLHMLTLLKDLLPCFPEGLVKSCSETLLRVMTLSHVLVTA
1			CAMQAFHSLFHARPGLSTLSAELNAQIITALYDYVPSENDLOPL
			LAWLKVMEKAHINLVRLQWDLGLGHLPRFFGTAVTCLLSPHSQV
			LTAATQSLKEILKECVAPHMADIGSVTSSASGPAQSVAKMFRAV
			EEGLTYKFHAAWSSVLQLLCVFFEACGRQAHPVMRKCLQSLCDL
			RLSPHFPHTAALDQAVGAAVTSMGPEVVLQAVPLEIDGSEETLD
			FPRSWLLPVIRDHVQETRLGFFTTYFLPLANTLKSKAMDLAQAG
			STVESKIYDTLQWQMWTLLPGFCTRPTDVAISFKGLARTLGMAI
			SERPDLRVTVCQALRTLITKGCQAEADRAEVSRFAKNFLPILFN
í I			LYGOPVAAGDTPAPRRAVLETIRTYLTITDTQLVNSLLEKASEK
			VLDPASSDFTRLSVLDLVVALAPCADEAAISKLYSTIRPYLESK AHGVQKKAYRVLEEVCASPQGPGALFVQSHLEDLKKTLLDSLRS
} [1		TSSPAKRPRLKCLLHIVRKLSAEHKEFITALIPEVILCTKEVSV
j	Į.		GARKNAFALLVEMGHAFLRFGSNQEEALQCYLVLIYPGLVGAVT
1	Ĭ		MVSCSILALTHLLFEFKGLMGTSTVEQLLENVCLLLASRTRDVV
	ŀ		KSALGFIKVAVTVMDVAHLAKHVQLVMEAIGKLSDDMRRHFRMK
1 1	ı		LRNLFT\KFIPK\FGILTWGKKAVGPKEYHRVLVNIRKABARAK
1 1			RHRALSQAAVBEEEEEEEEEEPAQGKGDSIEEILADSEDEEDNE
1 1			EEERSRGKEQRKLARQRSRAWLKEGGGDEPLNFLDPKVAQRVLA
			TQPGPGRGRKKDHSFKVSADGRLIIREEADGNKMEEEEGAKGED
1	1		EEMADPMEDVIIRNKKHQKLKHQKEAEEEELEIPPQYOAGGSGI
1	ľ		HRPVAKKAMPGAEYKAKKAKGDVKKKGRPDPYAYIPLNRSKLNR
6033			RKKMKLQGQFKGLVKAAQRGSQVGHKNRRKDRRP
6972	2179	973	PGGAILLPLWRRTRPREATVPRGAAQRGRARSAEGRIPSSQSPS
, !			PAEAGGATRSPPPRPPRPARPPGPSAPPLLRSDAGPGATVSAAA
į (AAATERARRGATMGAQLSTLGHMVLPPVWFLYSLLMKLFORSTP
[]			AITLESPDIKYPLRLIDREIISHDTRRFRFALPSPQHILGLPVG
			QHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKDTHPK
1			FPAGGKMSQYLESMQIGDTIEFRGPSGLLVYQGKGKFAIRPDKK
1		l	SNPIIRTVKSVGMIAGGTGITPMLQVIRAIMKDPDDHTVCHLLF
i	i		ANOTEKDILLRPELEELPNKHSARFKLWYTLDRAFEAWDYGQG\
	ļ		FVNEEMIRDHLPPPE\EEPLVLMCGPPPMIQYACLPNL\DHVGH
6973	1	1964	PTERCFVF
/-	-	1364	LQPRCAHRGLRAQKCGRPAPGVDAMVLCPVIGKLLHKRVVLASA
1	[SPRROEILSNAGLRFEVVPSKFKEKLDKASFATPYGYAMETAKQ
ļ ŀ	İ		KALEVANRLYQKOLRAPDVVIGADTIVTVGGLILEKPVDKQDAY
ľ	1		RMLSRFE/SGREHSVFTGVAIVHCSSKDHQLDTRVSEFYEETKV
	ŀ		KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDFL
·			NVVGFPLNHFCKQLVKLYYPPRPEDLRRSVKHDSIPAADTFEDL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	***************************************	\=possible nucleotide insertion)
		<u> </u>	SDVEGGGSEPTQRDAGSRDEKAEAGEAGQATAEAECHRTRETLP
			PFPTRLLELIEGFMLSKGLLTACKLKVFDLLKDEAPQKAADIAS
ſ			KVDASACGMERLLDICAAMGLLEKTEQGYSNTETANVYLASDGE
]		YSLHGFIMHNNDLTWNLFTYLEFAIREGTNOHHRALGKKAEDLF
1			QDAYYQSPETRLRFMRAMHGMTKLTACQVATAFNLSRFSSACDV
1	1		GGCTGALARELAREYPRMQVTVFDLPDIIELAAHFQPPGPQAVQ
1	i		IHFAAGDFFRDPLPSAELYVLCRILHDWPDDKVHKLLSRVAESC
ľ	1		KPGAGLLLVETLLDEEKRVAQRALMQSLNMLVQTEGKERSLGEY
[ſ		QCLLELHGFHQVQVVHLGGVLDAIL\PPKWPPEAQAACSL
6974	3082	2172	RSCAAFASFASRPPLELFAPPGSHRSPPGRGVATSAQCALSVRK
1	1		LLAARPGLGTKYQATMVYKTLFALCILTAGWRVQSLPTSAPLSV
[[SLPTNIVPPTTIWTSSPONTDADTASPSNGTHNNSVLPVTASAP
1	1		TSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVH
			LTTTLEEHSLGTPEAGVAATLSQSAAEPPTLISPQAPASSPSSL
	i		STSPPEVFSASVTTNHSSTVTSTQPTGAPTAPESPTEESSSDHT
1	}		PTSHATAEPVPQEKTPPTTVSGKVMCELIDMET\PPPFPG
6975	2	500	RPRPTVHCCKWALKLETAMETLINVFHAHSGKEGDKYKLSKKEL
1			KELLQTELSGFLDVKELML*ATEALKTFEEA*KSPIIQCSSSRS
1	1		SLPPAPQPPPYL*LSAVPFPIHLPLPLLPPQAQKDVDAVDKVMK
	<u> </u>		ELDENGDGEVDFQEYVVLVAALTVACNNFFWENS
6976	1216	970	GCQL*VAYGTTENSPVTFAHPPEDTVEQKAESVGRIMPHTEARI
j	1		MNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEBAVDQDKW
}	Į i		YWTGDVATMNEQGFCKIVGRSKDMIIRGGENIYPAELEDFFHTH
1			PKVQEVQVVGVKDDRMGEEICACIRLKDGEETTVEEIKAFCKGK
1			ISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL+IKQQ
			ACPGRLA
6977	1298	588	SLFINTNLLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R
			ANKKSKHHVNGNRTVEPFPEGTQMAVFGMGCFWGAERKFWVLKG
1	ł i		VYSTQVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVYQPEHMSFE
			ELLKVFWENHDPTQGMRQGNDHGTQYRSAIYPTSAKQMEAALSS
	1		KENYQKVLSEHGFGPITTDIREGQTFYYAEDYHQQYLSKNPNGY
6978	3	242	CGLGGTGVSCPVGIKK
) "		242	SFPFRDSRRCGCCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ
6979	3917	1146	FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG
1	(351,	1140	DEARVRGEAVAAAILSRCRHWSGPPPFPPSPPDRKGLRGTEPWE
			AGPGSGATPGARAMDVRRLKVNELREELQRRGLDTRGLKTELAE
i	ľ		RLQAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE
1			NESGYERRPLEMEQQQAYRPEMKTEMKOGAPTSFLPPEASOLKP
]			DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPQPPAEEDEDDFD
j i			
1			DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTOL
j l			GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN
)			DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF
			GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV
]			GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR
	1		NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR
			RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL
			EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP
	ļ .		PPEKRFDNRGGGGFRGRGGGGGFQRYENRGPPGGNRGGFQNRGG
	İ		GSGGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA
			PQQQPPPQQPPPPQPPPQQPPPPPSYSPARNPPGASTYNKNSNI
! !	1		PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNOGGYSO
]		GYTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY
			NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTQGGTSTQ
6980	1	420	GTRGRKTGRVAAPSTRRRTGNMOKLOTRSPAMSLSDPGLGYHPT

CEC	I Broods at a 3		
SEQ	Predicted beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
No.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
		 	CWTLRWPPLCSLHALHVFHCLFSSRLGTPVSPRLAMDPNCSCEA
i			GGSCACAGSCKCKKCKCTSCKKSCCSCCPLGCAKCAQGCICKGA
	1		SEKCSCCA
6981	10	1054	PGRGFRRASLRPAFAARGVFQGGLGQAKQARTRACAALPTPHPS
1	ì		APRLLEPQGVFSLFPPPPGPWPNMILTKAQYDEIAQCLVSVPPT
}		,	RQSLRKLKQRFPSQSQATLLSIFSQEYQKHIKRTHAKHHTSEAI
ì			ESYYQRYLNGVVKNGAAPVLLDLANEVDYAPSLMARLILERFLQ
1	1		EHEETPPSKSIINSMLRDPSQIPDGVLANQVYQCIVNDCCYGPL
	ļ	[VDCIKHAIGHEHEVLLRDLLLEKNLSFLDEDQLRAKGYDKTPDF
1			ILQVPVAVEGHIIHWIESKASFGDECSHHAYLHDQFWSYWNRFG
			PGLVIYWYGFIQELDCNRERGILLKACFPTNIVTLCHSIA
6982	153	1285	FPQQDCSAPAAPGLAGSEPRRLRAYRRRRQRARGLKRVAWLAPP
1		İ	PSLLQGLQGWAQAPVDGTLGPEDSRASSPMIQNSRPSLLQPQDV
1	1		GDTVETLMLHPVIKAFLCGSISGTCSTLLFQPLDLLKTRLQTLQ
1			PSDHGSRRVGMLAVLLKVVRTESLLGLWKGMSPSIVRCVPGVGI
1	ł.		YFGTLYSLKQYFLRGHPPTALESVMLGVGSRSVAGVCMSPITVI
l			KTRYESGKYGYESIYAALRSIYHSEGHRGLFSGLTATLLRDAPF SGIYLMFYNQTKNIVPHDQVDATLIPITNFSCGIFAGILASLVT
1			QPADVIKTHMQLYPLKFQWIGQAVTLIFKDYGLRGFFQGGIPRA
1		•	LRRTLMAAMAWTVYEEMMAKMGLKS
6983	82	773	EMSFLQDPSFFTMGMWSIGAGALGAAALALLLANTDVFLSKPOK
Ī	ì	}	AALEYLEDIDLKTLEKEPRTFKAKELWEKNGAVIMAVRRPGCFL
	•		CREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQPYFKGE
1	}		IFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLE
1		ł	GEGFILGGVFVVGSGKQGILLEHREKEFGDKVNLLSVLEAAKMI
			KPQTLASEKK
6984	1845	1282	GGRSAYSLPAGSLPRVPATAAAKMASGVQVADEVCRIFYDMKVR
1		ĺ	KCSTPEEIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTIT
1	Ì	ļ	DPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELA
			PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLG
6985	1887	1324	GSLIVAFEGCPV
1000	1007	1324	RRTAGIYPCFPKPGRTRHALCSVVLLLLTGQLAFDDFQESCAMM WQKYAGSRRSMPLGARILFHGVFYAGGFAIVYYLIQKFHSRALY
1		j	YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLK
1			IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFK
1			LSGENGDEVKKE
6986	642	1350	YHLYFKMGDPNSRKKQALNRLRAQLRKKKESLADQFDFKMYIAF
1			VFKEKKKKSALFEVSEVIPVMTNNYEENILKGVRDSSYSLESSL
			ELLQKDVVQLHAPRYQSMRRDVIGCTQEMDFILWPRNDIEKIVC
	ļ		LLFSRWKESDEPFRPVQAKFEFHHGDYEKQFLHVLSRKDKTGIV
			VNNPNQSVFLFIDRQHLQTPKNKATIFKLCSICLYLPQEQLTHW
			AVGTIEDHLRPYMPE
6987	1623	341	LEAAEKASRAFKESQRQTDSKNYETENWSPQKSQRRYDMYNTAC
			FLGEIEVGLYTIQILQLTPFFHKENELSKKHMVQFLSGKWTIPP
	İ		DPRNECYLALSKFTSHLKNLQSDLKRCFDFFIDYMVLLKMRYTQ
1			KEIAEIMLSKKVSRCFRKYTELFCHLDPCLLQSKESQLLQEENC
			RKKLEALRADRFAGLLEYLNPNYKDATTMESIVNEYAFLLQQNS
!			KKPMTNEKQNSILANIILSCLKPNSKLIQPLTTLKKQLREVLQF
			VGLSHQYPGPYFLACLLFWPENQELDQDSKLIEKYVSSLNRSFR
			GQYKRMCRSKQASTLFYLGKRKGLNSIVHKAKIEQYFDKAQNTN
[[SLWHSGDVWKKNEVKDLLRRLTGQAEGKLISVEYGTEEKIKIPV
6988	3	600	ISVYSGPLRSGRNIERVSFYLGFSIEGPPGL
5,55	,	689	TOLLRRPAVFVGSAASGIRSGLWSASSGHWCAPAAGRAHAPVPR
]			LVRGLGAASTAAPQDAQTGPQPMPRADCIMRHLPYFCRGQVVRG FGRGSKQLGIPTANFPEQVVDNLPADISTGIYYGWASVGSGDVH
j j			KMVVSIGWNPYYKNTKKSMETHIMHTFKEDFYGEILNVAIVGYL
			1101 TO TOWN THE THE THE PROPERTY OF THE THE VALUE OF THE THE THE THE THE THE THE THE THE THE

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
1			RPEKNFDSLESLISAIQGDIBEAKKRLELPEHLKIKEDNFFQVS
6989	2	1110	KSKIMNGH
0303		1118	LMPSDRPLSPSTHASAGSHCHAPPTTARRAFPIPFGSKSNMATL
			KDQLIYNLLKEEQTPQNKITVVGVGAVGMACAISILMKDLADEL
		İ	ALVDVIEDKLKGEMMDLQHGSLFLRTPKIVSGKDYNVTANSKLV IITAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPNCKLLIV
{	{		SNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGV
1			HPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDKDK
1	ľ		EQWKEVHKQVVESAYEVIKLKGYTSWAIGLSVADLAESIMKNLR
1	1		RVHPVSTMIKGLYGIKDDVFLSVPCILGQNGISDLVKVTLTSEE
L			EARLKKSADTLWGIQKELQF
6990	719	258	THASGMASVVLALRTRTAVTSLLSPTPATALAVRYASKKSGGSS
1			KNLGGKSSGRRQGIKKMEGHYVHAGNIIATQRHFRWHPGAHVGV
[(GKNKCLYALEEGIVRYTKEVYVPHPRNTEAVDLITRLPKGAVLY
	<u> </u>		KTFVHVVPAKPEGTFKLVAML
6991	169	451	RRSSDFHNPGFLSRPVSLRENIHHQVICSTKNKRRNPKKIAYLL
j]		SSLLMTNLNPNESTENQPVDAYWAFTLDQEFLTYACVEGTGCLF
6992	944		CGRHVH
0992	941	510	ROAPGCSSLALRQVRQVYCGLVRAPQVQTRPLSSRFVERRGALY
1			RSPMNQENPPPYPGPGPTAPYPPYPPQPMGPGPMGGPYPPPQGY
1			PYQGYPQYGWQGGPQEPPKTTVYVVEDQRRDELGPSTCLTACWT ALCCCCLWDMLT
6993	1	374	QWCVTCPQHNARQGPAVPPGIQAYGAAPFEDLQVDFTEMSKCRG
	i - i	3,4	DRVWIKNWNVASLCPLWKGPQTVVLSPPTAVKVEGIPAWIHHSH
1	ļ		VKPAARETWEARPSPDNPFRVTLKKTTSPAPVTPGS
6994	346	1100	QWPEKDPVMAASSISSPWGKHVFKAILMVLVALILLHSALAOSR
1		•	RDFAPPGQQKREAPVDVLTQIGRSVRGTLDAWIGPETMHLVSES
	· .		SSQVLWAISSAISVAFFALSGIAAQLLNALGLAGDYLAQGLKLS
1			PGQVQTFLLWGAGALVVYWLLSLLLGLVLALLGRILWGLKLVIF
}			LAGFVALMRSVPDPSTRALLLLALLILYALLSRLTGSRASGAQL
6995	144		EAKVRGLERQVEELRWRQRRAAKGARSVEEE
6393	144	1346	GSVAVGLSGIMAAQKDLWDAIVIGAGIQGCFTAYHLAKHRKRIL
			LLEQFFLPHSRGSSHGQSRIIRKAYLEDFYTRMMHECYQIWAQL
1]		BHEAGTQLHRQTGLLLLGMKENQELKTIQANLSRQRVEHQCLSS
1			EELKQRFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIRQLG GIVRDGEKVVEINPGLLVTVKTTSRSYQAKSLVITAGPWTNQLL
}			RPLGIEMPLQTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH
			HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL
1			SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKYDNIVI
1			GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG
			KAHL
6996	543	1942	BTANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE
1]		MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR
1	ļ		EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN
			YENFLKVGEKAGAKCKQFFTAKVFAKLLHTDSYGRISIMQFFNY
1 1	İ		VMRKVWLHQTRIGLSLYDVAGQGYLRESDLENYILELIPTLPQL
j i			DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD
]	1		LLELRDEELSKESQETNWFSAPSALRVYGQYLNLDKDHNGMLSK
]	ĺ		EBLSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDFVLALEN
1 1	{	_	RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKIHGQD
j l	Ī	·	PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTTILIDL NGFWTYENREALVANDSENSADLDDT
6997	370	1104	AMELTIFILRLAIYILTFPLYLLNFLGLWSWICKKWFPYFLVRF
			TVIYNEQMASKKRELFSNLQEFAGPSGKLSLLEVGCGTGANFKF
]			YPPGCRVTCIDPNPNFEKFLIKSIAENRHLQFERFVVAAGENMH
			THE OCCUPANT OF THE PARTY OF THE ANALYSIS OF THE PARTY OF

		1 50 - 32 - 42 - 31 - 42	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	location	to first	L=Leucine, M=Methionine, N=Asparagine,
į	corresponding	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	to first	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of		Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence	<u> </u>	QVADGSVDVVVCTLVLCSVKNQERILREVCRVLRPGGAFYFMEH
		1	VAAECSTWNYFWQQVLDPAWHLLFDGCNLTRESWKALERASFSK
		1	LKLQHIQAPLSWELVRPHIYGYAVK
			FVSRALLRVRSRRHPAEERAAPGRPEDAPIECPGATNCPEPLWC
6998	2	616	SHLPVPYAPPTMESRGKSASSPKPDTKVPQVTTEAKVPPAADGK
		1	APLTKPSKKEAPAEKQQPPAAPTTAPAKKTSAKADPALLNNHSN
		· I	LKPAPTVPSSPDATPEPKGPGDGAEEDEAASGGPGGRGPWSCEN
		1	LKPAPTVPSSPDATPEPKGPGDGAEEDEAA3GGFGGKGFW3CIII
	1		FNPLLVAGGVAVAAIALILGVAFLVRKK
6999	14	1591	GRAGACSRRDTAMSIEIESSDVIRLIMQYLKENSLHRALATLQE
	1	1	ETTVSLNTVDSIESFVADINSGHWDTVLQAIQSLKLPDKTLIDL
	}	Į.	YEQVVLELIELRELGAARSLLRQTDPMIMLKQTQPERYIHLENL
		į.	LARSYFDPREAYPDGSSKEKRRAAIAQALAGEVSVVPPSRLMAL
	·	l .	LGQALKWQQHQGLLPPGMTIDLFRGKAAVKDVEEEKFPTQLSRH
		ł	IKFGQKSHVECARFSPDGQYLVTGSVDGFIEVWNFTTGKIRKDL
		1	KYQAQDNFMMMDDAVLCMCFSRDTEMLATGAQDGKIKVWKIQSG
	Ì		QCLRRFERAHSKGVTCLSFSKDSSQILSASFDQTIRIHGLKSGK
		,	TLKEFRGHSSFVNEATFTQDGHYIISASSDGTVKIWNMKTTECS
	.	\$	NTFKSLGSTAGTDITVNSVILLPKNPEHFVVCNRSNTVVIMNMQ
		· l	GQIVRSFSSGKREGGDFVCCALSPRGEWIYCVGEDFVLYCFSTV
	1		TGKLERTLTVHEKDVIGIAHHPHQNLIATYSEDGLLKLWKP
7000	2	827	GPGVVFLELMESEGPPESERSEFFSQREEENEEEEAQEPEETGF
7000	1	1	KNDLLOPALTGDVEGLOKIFEDPENPHHEQAMQLLLEEDIVGRN
	1		LLYAACMAGOSDVIRALAKYGVNLNEKTTRGYTLLHCAAAWGRI
		j	ETI.KAI.VELDVDIEALNFREERARDVAARYSQTECVEFLDWADA
	,	}	RLTLKKYIAKVSLAVTDTEKGSGKLLKEDKNTILSACRAKNEWI
		1	ETHTEASINELFEQRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH
		1	DOKRSODDISN
	2056	844	PROLITAFIKGCFIFIYFIFIFETEFLSCCPGWSAVAQSRLIAN
7001	2030	1	FASOVOATETI.PKDSOVGPDVKSEAAPKRALYESVFGSGEICGE
	Į.	·	TSPKRLCIRPSEPVDAVVVVSVKHDPLPLLPEANGHRSTNSPT
		1	VSDATVSPTODSRPNMSRPLITRSPASPLNNQGIPTPAQLTKS
	1	1	ADVITTOVCCHMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLK
	1	1	HYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQI
			QPMLLEMERWKQDRETGRFSRPCECLVVRVAPDLGERITLSGD
	į.		SLIEEVFPEIGDVMCNSVNAGWNHDSTHVIRFPLNGYCHLNSV
	1		VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSV
	1		RIKQEPLD
			PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWW
7002	1043	498	TPCSRHQSRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASS
	1		TPCSRHQSRRRLTCWCSISRPCGR-GGLCVRTAPIRFITSASSISWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSS
		1	PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLP.
	i ·	l l	
}			RGAEVC CALLAY ACKITT DRIVENCES
7003	818	61	QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSP
		1	GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILEGKD
	1		GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEA
	1		LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKP
1		1	FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEA
1			GIKETR\NTRRSIGIEPGAEQLLPNFCPSLEG
7004	121	2285	FLLPVLTSRSLRQPAVPHARLGGVKPAAMKSARAKTPRKPTVK
7004	1		G/PKRTLKTOLG/YYCRVRPLGFPDQECCIEVINNTTVQLHTP
l	1	1	GVRINRNGDVKETOYSFKOVFGTHTTQKELFDVVANPLVNDLI
Į.		1	GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGS
	Į.	1	GKNGLLFTYGVIGSGKIHIMIGSFGEGGHER KEEDIIII KEE
			OAKRYVEKSNDRNSMDIOCEVDALLERQKREAMPNPKTSSSKR
			OAKRYVEKSNDRNSMDIOCEVDALLERQKREAMPNPKTSSSKR
			QKRGLLFTYGYTGSGKTHTWTGSFERDER QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKR VDPEFADMITVQBFCKAEEVDEDSVYGVFVSYIBIYNNYIYDL EEVPFDPINPNLHNLNCFVKIKNHNMYVAGCTEVEVKSTEEAF VFWRGQKKRRIANTHLNRESSRSHSVFNIKLVQAFLDADGDNV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1		i	QEKEQITISQLSLVDLAGSERTNRTRAEGNRLREAGNINQSLMT
			LRTCMDVLRENQMYGTNKMVPYRDSKLTHLFKNYFDGEGKVRMI
(1	VCVNPKAEDYEENLQVMRFAEVTQEVEVARPVDKAICGLTPGRR
1			YRNQPRGP\IGNEPLVTDVVLQSFPPLPSCEILDINDEQTLPRL
			IEALEKRHNLRQMMIDEFNKQSNAFKALLQEFDNAVLSKENHMQ GKLNEKEKMISGOKLEIERLEKKNKTLEYKIEILEKTTTIYEED
[}	KRNLQQELETQNQKLQRQFSDKRRLEARLQGMVTETTMKWEKEC
	}	}	ERRVAAKQLEMQNKLWVKDEKLKQLKAIVTEPKTEKPERPSRER
			DREKVTQRSVSPSPVPVSYL
7005	63	876	RNMALYQRWRCLRLQGLQACRLHTAVVSTPPRWLAERLGLFEEL
		· -	WAAQVKRLASMAQKEPRTIKISLPGGQKIDAVAWNTTPYQLARQ
}		1	ISSTLADTAVAAQVNGEPYDLERPLETDSDLRFLTFDSPEGKAV
		ŀ	FWHSSTHVLGAAAEQFLGAVLCRGPSTEYGFYHDFFLGKERTIR
			GSELPVLERICQELTAAARPFRRLEASRDQLRQLFKDNPFKLHL
1	ļ	1	IEEKVTGPTATVYGCGTLVDLCQGPHLRHTGQIGGLKLLSNSSS
			LWRSSG
7006	22	898	NAFGRHSTAVKMAAAAWLQVLPVILLLLGAHPSPLSFFSAGPAT
{		Ì	VAAADRSKWHIPIPSGKNYFSFGKILFRNTTIFLKFDGEPCDLS
	}		LNITWYLKSADCYNEIYNFKAEEVELYLEKLKEKRGLSGKYQTS
]]		SKLPQNCSELFKTQTFSGDFMHRLPLLGEKQEAKENGTNLTFIG
			DKTAMHEPLQTWQDAPYIFIVHIGISSSKESSKENSLSNLFTMT
		ļ	VEVKGPYEYLTLEDYPLMIFFMVMCIVYVLFGVLWLAWSACYWR DLLRIQFWIGAVIFLGMLEKAVFYAGFQ
7007	2	1001	AMTVSGPGTPEPRPATPGASSVEQLRKEGNELFKCGDYGGALAA
, , , ,	•		YTQALGLDATPQDQAVLHRNRAACHLKLEDYDKAETEASKAIEK
1	ĺ		DGGDVKALYRRSQALEKLGRLDQAVLDLQRCVSLEPKNKVFQEA
]			LRNIGGQIQEKVRYMSSTDAKVEQMFQILLDPEEKGTEKKQKAS
		1	QNLVVLAREDAGAEKI FRSNGVQLLQRLLDMGETDLMLAALRTL
			VGICSEHQSRTVATLSILGTRRVVSILGVESQAVSLAACHLLQV
i i			MFDALKEGVKKGFRGKEGAIIVGEWKQVWGLLDVTVMEGMGLSQ
			PGQFFGDQTCSCRLFGIRFGDIILL
7008	70	1478	CRSALGHERPPPAHLPAGGRRLQTCPRSCRWLGRPPSGLPPGPR
1]	SPPPLAGPGQKMVQKKPAELQGPHRSFKGQNPFELAFSLDQPDH
1 1	1	1	GDSDFGLQCSARPDMPASQPIDIPDAKKRGKKKKRGRATDSFSG
		l	RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH IRSRVFREVEMLYOCOGHRNVLELIEFFEEEDRFYLVFEKMRGG
		1	SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE
		<u> </u>	NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS
1		!	AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG
[.			RCGSDCGWDRGEACPACONMLFESIQEGKYEFPDKDWAHISCAA
i :		ĺ	KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR
1			WDSHFLLPPHPCRIHVRPGGLVRTVTVNB
· 7009	1	626	ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG
ļ			RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA
1			LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH
			WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL
			GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE
7010	79	571	SHTRRAVVPETLLSPLCPLLGGGTAMSGGEQKPERYYVGVDVGT
1			GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACC
[1	VVTKKVVQGIDLNQIRGLGFDATCSLVVLDKQFHPLPVNQEGDS
1 70			HRNVIMWLDHRAVSQVNRINETKHSVLQYVGG
7011	3	994	RIQTLPNQNQSQTQPLLKTPPAVLQPIAPQTTFGVQTQPQPQSL
]			LQAQISAASITPLLQTQPQPLLQQPQQKAGLLQPPVRIVSQPQP
			ARRLDPPSRFSGRNDRGDQVPNRKDDRSRERERERRRSRERSPQ RKRSRERSPRRERERSPRRVRRVVPRYTVQFSKFSLDCPSCDMM
]	!		ELRRRYQNLYIPSDFFDAQFTWVDAFPLSRPFQLGNYCNFYVMH

		B-37-6-3	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	 		REVESLEKNMAILDPPDADHLYSAKVMLMASPSMEDLYHKSCAL
		[AEDPQELRDGFQHPARLVKFLVGMKGKDEAMAIGGHWSPSLDGP
			DPEKDPSVLIKT\AIRCCKALTG
7012	1 1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA
7012		1	AAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA
	Ļ		VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME
	ļ	1	TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER
	į.	1	NAKAEKEKKLPPPPPQAPPEEENESEPEEPSGVEGAAFQSRLPH
			DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQL
		}	
	•		TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL
	1	1	PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV
1		1	ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP
[1	LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP
Ī	l	ł.	VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV
			NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE
ì	ì	i	YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE
Ì	1	1	FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG
}	İ	1	LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL
ļ	1		PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV
İ			FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG
l		1	IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA
]	}		RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE
1	1		HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP
1			AQQSPSM
7013	1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA
1		i	AAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA
		1	VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME
l .		1	TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER
1	1		NAKAEKEKKLPPPPPQAPPEEENESEPEEPSGVEGAAFQSRLPH
Ì	1	Ī	DRMTSOEAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQL
l	1	1	TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL
1	1	1	PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV
[1	1	ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP
		ì	LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP
		1	VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV
1	}	1	NLKEKIKELHOOYKEASEVKPPRDITAEFLVKSKHRDLTALCKE
1			YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE
1		1	FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG
		1	LDIKLNTAVROVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL
1		1	PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV
1		1	
			FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG
1	1	1	IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA
1		1	RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE
1			HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP
		<u> </u>	AQQSPSM
7014	3	3950	DFEVGDKIRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE
1	1		ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEAEEPD
1			CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM
}	}	1	PLATDSPTSDPTEVVNCISSQPQVPFHPMLQKSQYYSTVGGSHP
1			HSEQYPDLLPLEARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS
			SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG
1	{	ł	POAQGLVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP
	i	Ī	DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR
1	1		PCTPVSTSPHLLVDQNLKPAPPLVVRPSRPAPLPPSAQQRTNAV
1			SPKLLSRHRPTCETLEKEGPGHMGRSLDQTSPCPLVLVRIEEME
1	1		RDLDMYSRAQEELNLMLEEKQDESSRAETLEDLKFCESNIESLN
1			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
\	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			MELQQLREMTLLSSQSSSLVAPSGSVSAENPEQRMLEKRAKVIE
}	}	1	ELLQTERDYIRDLEMCIERIMVPMQQAQVPNIDFEGLFGNMQMV
	İ	ł	IKVSKQLLAALEISDAVGPVFLGHRDELEGTYKIYCQNHDEAIA
			LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFLIKP
}	1	1	VORVMRYPLLLMELLNSTPESHPDKVPLTNAVLAVKEINVNINE
1		į	YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSHLKH
!	ì	ł	LTGFAPOIKDEVFEETEKNFRMQERLIKSFIRDLSLYLQHIRES
ł	}		ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNFKER
	ļ	1	TERLVISPLNOLLSMFTGPHKLVQKRFDKLLDFYNCTERAEKLK
	1		DKKTLEELQSARNNYBALNAQLLDELPKFHQYAQGLFTNCVHGY
l			AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSRVLQ
l			QLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYMLQSE
l]	1	ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVIKKK
Į		1	
1			DPMGSQNRWLIDNGVTKGFVYSSFLKPYNPRRSHSDASVGSHSS
1		}	TESEHGSSSPRFPRQNSGSTLTFNPN\S\MAVSFTSGSCQKQPQ
1		1	DASPPPKEWDQGTLSASLNPSNSESSPSRCPSDPDSTSQPRSGD
}			SADVARDVKQPTATPRSYRNFRHPEIVGYSVPGRNGQSQDLVKG
Ì			CARTAQAPEDRSTEPDGSEAEGNQVYFAVYTFKARNPNELSVSA
L			NQKLKILEFKNVTGNTEWWLAEVNGKKGYVPSNYIRKTEYT
7015	1842	513	RQAWHE\VAAPSWRGARLVQSVLRVWQVGPHVARERVIPFSSLL
	ļ		GFQRRCVSCVAGSAFSCPRLASASRSNGQGSALDHFLGFSQPDS
ļ	Į.		SVTPCVPAVSMNRDEQDVLLVHHPDMPENSRVLRVVLLGAPNAG
1		1	KSTLSNQLLGRKVFPVSRKVHTTRCQALGVITEKETQVILLDTP
		1	GIISPGKQKRHHLELSLLEDPWKSMESADLVVVLVDVSDKWTRN
1	j	1	QLSPQLLRCLTKYSQIPSVLVMNKVDCLKQKSVLLELTAALTEG
			VVNGKKLKMRQAFHSHPGTHCPSPAVKDPNTQSVGNPQRIGWPH
l .			FKE1FMLSALSQEDVKTLKQYLLTQAQPGPWEYHSAVLTSQTPE
ł	}	ļ.	EICANIIREKLLEHLPQEVPYNVQQKTAVWEEGPGGELVIQQKL
İ	1	l .	LVPKESYVKLLIGPKGHVISQIAQRAGHDLMDIFLCDVDIRLSV
1			KLLK
7016	167	2513	ILNAPKPPPPRDSVEAVAAKRDTGGGSWGTGMDVSGQETDWRST
	1	1	AFROKLVSQIEDAMRKAGVAHSKSSKDMESHVFLKAKTRDEYLS
1	ł	ł	LVARLIIHFRDIHNKKSQASVSDPMNALQSLTGGPAAGAAGIGM
1	1		PPRGPGQSLGGMGSLGAMGQPMSLSGQPPPGTSGMAPHSMAVVS
]	TATPOTOLOLOGOVAAAAAAATARSSSSSRRRYSSSSSSSNSKQ
i	j .	j	FOAQOSAMOO\QFQA\VVQQQQQL\QQQQQQQQHLIKLHHQNQQ
1			OTOOOOOLORIAQLOLQQQQQQQQQQQQQQQQQQALQAQPPIQQP
}			PMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQQPPVAQNQPSQ
	ļ	j	LPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQP
1	1		QVQQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTP
l		i	QSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPF
1	1	1	\QSPVTARTPQNFSVPSPGPLNTPVNPSSVMSPAGSSQAEEQQY
[LDKLKQLSKYIEPLRRMINKIDKNEDRKKDLSKMKSLLDILTDP
i	1		SKRCPLKTLQKCBIALEKLKNDMAVPTPPPPPVPPTKQQYLCQP
1			LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR
1		1	
1		1	RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC
1			KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV
		<u> </u>	HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA
7017	1	1785	INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQHL
1	1	j	FAFLAHTQREAYAPRIFFEASRPPWFTPRSQQDCSEYLRFLLDR
I	1	}	LHEEEKILKVQASHKPSEILECSETSLQEVASKAAVLTETPRTS
1	1		DGEKTLIEKMFGGKLRTHIRCLNCRSTSQKAEAFTDLSLAFWPS
			YSLEYMSCPDCSQSPSIQDGGLMQASVPGPSEEPVVYNPTTAAF
1		}	ICDSLVNEKTIGSPPNEFYCSENTSVPNESNKILVNKDVPQKPG
Į.			GETTPSVTDLLNYFLAPEILTGDNQYYCENCASLQNAEKTMQIT
]	1		EEPEYLILTLLRFSYDQKYHVRRKILDNVSLPLVLELPVKRITS
<u> </u>		<u> </u>	

Deginning Nucleotide location corresponding correspo	•			
No. nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence service uence seque	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Corresponding Correspondin	ID		B .	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence service of amino acid sequence sequenc	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid sequence sequ	ļ		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence amino acid sequence (amino acid sequence) amino acid sequence (amino acid sequence) (amino	,	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
maino acid sequence maino acid sequence maino acid sequence codon, /-possible nuclectide deletion,			amino acid	P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence codon, /-possible nucleotide deletion, -possible nucleotide dinsertion sequence results respective results sults resul		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Sequence	İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence	1	amino acid	sequence	Codon, /=possible nucleotide deletion,
FSSLSESWYDUDTTDLSENLAKKIKPSGTDEASCTKLVPYLLS SVVHYSGISSESGHYYSYRANITSTDSYNMYSGEALALASSQ SHLIGRDSPSAVFEQDLENKENSKEWFLFMDSRVFTFSFGSVQK ITSSPPKDTAVYLLYKQHSTMGLGGNGKHTMGEGALDALINGDPPLQKE IMDAITKDNKLYLQEQELNARARALQAASASCSFRPMGFDDNDP INGSGPTGGGGGGGTNTVGRLVF 7018 484 1066 SLVFRGNTWSGEAGHLGSALFRILANYHQLFVGTERIRAPEIJFO PSLIGGEQAGIAETLQYILDRYFKDVQEMLVONVFLIGGNTWYP GMKARMEKELLEMRPFRSSFQVQLASSPVULDAWYGARDWALAHL DDNEVWITRKEVEEKGGEYJKEHCASNIYVPIRLDKQASRSSDA QASSKGSAAGGGGAGEQA QASSKGSAAGGGGAGEQA AGASKGSAAGGGAGGAG GROWN AGASKGSAAGGGAGGAG GROWN AGASKGSAAGGGAGGAG GROWN AGASKGSAAGGGAGGAGA GROWN AGASKGSAAGGGAGAGAG GROWN AGASKGSAAGGGAGAGAG GROWN AGASKGSAAGGGAGAGAG GROWN AGASKGSAAGGGAGAGAG GROWN AGASKGSAAGGGAGAGAG GROWN AGASKGSAAGGGAGAGAG GROWN AGASKGSAAGGGAGAGAG GROWN AGASKGSAAGGGAGAGAG GROWN AGASKGSAAGGGAGAGAG GROWN AGASKGSAAGGGAGAGAG GROWN AGASKGSAAGGGAGAGAG GROWN AGASKGSAAGGGAGAGAG GROWN AGASKGSAAGGGGAGAGA GROWN AGASKGSAAGGGAGAGAG GROWN AGASKGSAAGGGAGAGAG GROWN AGASKGSAAGGGAGAGAG GROWN AGASKGSAAGGGAGAGAG GROWN AGASKGSAAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	f .	1 -	\=possible nucleotide insertion)
SVVVHSGISSESGHYYSYARNITSTDSSYQMYHOSEALALASSQ SHLIGROSPSAVFEODLERNENKSKEMILYDGSVUTFTSFQSVQK ITSEPPKDTAYVLLYKKQHSTMGILSGNNPTSGLMINGDPLOKE IMDAITKDNKLYLQOGGLARARAAQAASACSFROMGPDDND PGSGGPTGGGGGGGFNTVGRLVF 7018 484 1066 SLVFRGNTWSGRAGHGSALFALAANYHQLFVGTEIRAPEIIFO PSLIGBEGGAGIAETLGYILDRYPKDVGEMLVONVELTGGNTWYP GMKARMEKELLEMRPFRSSFQVQLASMPULDAWYAGABWALNHI DDNEWWITREVEEKGGGFYLKEHCASNITYPTRLDKQASRSDA QASSKGSAAGGGAGEQA ARMHIPLAPGSWRDLPNIEVPLSDGTMARKLRYTHHDRINGRS SGALRGVCSCVEAGKACDPAARPINTLGVLHTURGNINNWA GLYGRLEWDGFFSTTVTNPBEMKKGGRVLIPEGHRVVSVRECAR SGGPPTYRLFONILDKIRROVGNAVPPPLAKAIGLIKLCHLAK ARESASAKIKEEBAAKO TO20 1 2154 FADSKRKSVLLDKIRNLQVALTSKQGLETAMSFVARNTFKRVR NGFLMRKVAVFFSNPTTASPGLREAVLUKSDGGTPLFITRGE DRQLINALQINNTAVGHALVLEAGRDLTDFLENVLTCHVCLDIC NDFBCGGGSWRFSFRDRAAGSDVDIMARKLSDGGTPLFITRGE DRQLINALQINNTAVGHALVLEAGRDLTDFLENVLTCHVCLDIC NDFBCGGGSWRFSFRDRAAGSDVDIMARKLSDGGTPLFITRGE DRQLINALQINNTAVGHALVLEAGRDLTDFLENVLTCHVCLDIC NDFBCGGGSWRFSFRDRAAGSDVDIMARKLSDGGTPLFITRGE DRQLINALQINNTAVGHALVLEAGRDLTDFLENVLTCHVCLDIC NDFBCGGSWRFSFRDRAAGSDVDIMARKLSDGGTPLFITRGE DRQLINALQINNTAVGHALVLEAGRDLTDFLENVLTCHVCLDIC NDFBCGGSWRFSFRDRAAGSDVDIMARKLSDGGTPLFITRGE DRQLINALQINNTAVGHALVLEAGRDLTDFLENVLTTHVCHULDC NDFBCGGSWRFSFRDRAAGSDVDIMARKLSDGGTPLFITRGE DRQLINALQINNTAVGHALVLEAGRALTDFLAGACKAV VAVPNNVTSSPDRAVTTTRASPUDGCGGADGTALGSALTEYT ENVFSARNFALKVYFSARNFULGGTRALGSGTALASGTYTLFOYT INGFSVRPAAAARCPARAFAVAVACHARAARTATKPTTKRVT VAVPNNVTSSPTSNPVTTFKVTTTREPVTTTTREVTTTTREVT INGFSVRPAAAARCPARAFAVAXEPAARAFAATRATKATTREPVTAVRATHAV VANSFPPNOGFASTSTINMVSTEIDFPTFPTTTREVTTTTREVTT INGFSVRPAAAARCPARAFAXERVAARCHARAFARTATKATTREPVTTTREVTT INGFSVRPAAAARCPARATGSVAGGGGNRKRGSGKCKCKCA TCDFILKWYYDDTKSCARRWGGGGGNRKRGSGKCKCKCA TCDFILKWYYDDTKSCARRWGGGGGNRKRGSGKCKCCA TCDFILKWYYDDTKSCARRWGGGGGNRKRGSGKCKCKA TCSGFWSFPTGAARATGSVAGGGGNRKRGSGVLAGHDRVS CLGVYDDGMAVATGSWDFFCVVWTLTTTGAARCKKUL VANSFPNOGFASTTINMVTSTEIDFDCHTKVGAGGGGGNRKGGRACHTHOFPGGGG CHARAGGGGIDAAGWARDKWARDKRYBGGGGRACHTHOFPGGGG CHARAGGGGGGGGGRACHARHAURTRATKS TAADSKABESGGALTATUTHLMLKLCTERVANELARRRS TAADSKABESGAPTLAVFFTGFTAAV				FSSLSESWSVDVDFTDLSENLAKKLKPSGTDEASCTKLVPYLLS
SHLIGRDS PSAVFEQDLENKENSKEWFLYNDSKYTYFSCGVOK ITDSEPFENTAVULIKKKUSTNICLIGENTPSCHINGOPPLOKE LMDAITKDNKLYLORGELANARALQAASASCSFRPNGFDDNDP POSCOGPYGGGGGGGWTWYCGLVP 7018 484 1066 SLVFRGNTWSGEAGHKCSALFNLAAYHOLFVGTER IRAPELIFO PSLIGBEQAGIAETLQYILDRYPKDVQEMLVONVFLTGGTMYP GMKARMSKELLEMRPFERSSFOVOLASRPVIDAWYGARDHALNHL DDNEVWITKKEYEEKGGEYJKEHCASRIYVPIRLEKQASRSCDA QASSKSSAAGGGAGGGC GNARPWILDRAWGARDHALVANIAL RMRHIPLAGGSWRILDRIBURULSGTMARKKRYTHIDRKNORS SGALRGVCSCVEAGKACDPAARGPNTLIFWCHPTLCKROMSALVAA GLYGRLEWDGFFSTTVYNFPEPMKGGGVHIPBCHRVVSVBECAR SGGPPTYRLFGNILDKHRQVGNAVPPHLKATGLEIKLCMLAK ARESSASKIKEERAAKO TÖZO 1 2154 FADSKRIKEVYLDKIKNLOVALTSKOGGLETAMSTVANIA RAESSASKIKEERAKO SGRPPTYRLFGNILDKHRQVGNAVPPHLAKAIGLEIKLCMLAK ARESSASKIKEERAKO NGPLWRKVAVPFSNYPTTASPQURRAVLAVQHAPSESVDNAS MEPVIXVFSABNOVFFKLVDRSTTLLGSAETTTLFOP NRMKYTYLTJLVKGLDMSFDERGGGBFRAVAVQHAPSESVDNAS MEPVIXVESSITDYGSKEKLUDFISRAWGIQGGTRALTGVCLLDIC NIDBSCGFGSWRRSFGRRAAGSDVDIDMAFILDSAETTTLFOP NRMKYTYLTJLVKGLDMSFDERGGGBFRAVAVQHAPSESVDNAS MEPVIXVESHNPROLKIVULMIGRSVEPGOLBEAGRVILQAKCKGY FFVVLGIGRKVNIKKEVYTFASBINDVFFKLVDRSTELBEEPLAR FEGRLLPBSFYSSENAFYLISPDIRRCQUMPGGDGPTKNLVKRGHKQ VAVPNNVTSSPTSINPVTTTREVTTTREVTTTTREVTTTTREVTTTREVTTTREVTTTREVTTTREVTTTREVTTTREVTTTREVTTTREVTTTREVTTTREVTTTREVTTTREVTTTREVTTTREVTTTREVTTTREVTTTREVTTRESPLOKARVANTARALTEREPLAR PVAARPAAVRPPAAARAPARAKAKAKAKTATREPVAVXPATAAK PVAARPAAVRPPAAARAPARAKAKAKATATREPVAVXPATAAKA PVAARPAAVRPPAAARAPARAKAKAKATATREPVAVXPATAAKA PVAARPAAVRPPAAARAPARAKAKAKATATREPVAVXPATAAKA PVAARPAAVRPPAAARAPARAKAKAKATATREPVAVXPATAAKA PVAARPAAVRPPAAARAPARAKAKAHAKATATREPTVAVXPATAAGS TCGGTTLGWTDOGGGGGRRNKFGSQKBCEKVCA PVLARFGGVILSWMT VXASFFFRINGYAFATGSDDATCRLFDLARAGGLAGULAGHDNRVS TCCGTTLGWTDOGAAVATGSKOGGGNRKKGSQKBCEKVCA PVLARFGGVILSWMT ONDAIDIJGADULAGGTTVAVAVCVLRSQVAATHOSSS TKKSQPPPPOPASSASSSTINMAVSTEPGFTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	ļ]	ļ	SVVVHSGISSESGHYYSYARNITSTDSSYQMYHQSEALALASSQ
TISKPPKDTAYVLLYKKQHSTNAGLAGARSGSPRRGFDDMD EMDAITKONKLYLOGGENABARAGLAGARSGSSPRRGFDDMD PGSCGPTGGGGGGRYTVGRUF 7018 484 1066 SLVFRGNTWSGEAGHHCSALFNLAMYHOLFVGTERIRAPEIIFO PSLIGBEDAGIAETLOYILDRYPKDVQEMLVONVFLTGGNTWY GMKARMEKELLENRPFRSSFUVGLASNFULDAWWARDHALINHL DDNEVWITHREYBEKGGSFYLKEHCASNIVVIRLPKQASRSSDA QASSKGSAAGGGAGEQA 7019 1048 335 ARGGFLVTMVPPAPAS PPWMLGCCSHEVTAGPPTLCKDMSALVAA RNRHIPLAPGSDWRDLPNIEVRLSDGTMARKLRYTHHDRKNORS SGGALRGCSCVEAGKACDPAARGFHLYWCHPEOHRVJSVECCAR SGGARGCSCVEAGKACDPAARGFHLYWCHPEOHRVJSVECCAR SGGARGCSCVEAGKACDPAARGFHLYWCHPEOHRVJSVECCAR SGGARGCSCVEAGKACDPAARGFHLYWCHPEOHRVJSVECCAR SGGARGCSCVEAGKACDPAARGFHLYWCHPEOHRVJSVECCAR SGGARGCSCVEAGKACDPAARGFHLYWCHPEOHRVJSVECCAR SGGARGCSCVEAGKACDPAARGFHLYWCLAMIGHNIWA GLYGRLEWDGFFSTTVTNPEPMGKOGRVLHPEOHRVJSVECCAR SGGARGCSCVEAGKACDPAARGFHLYWCLHPEOHRVJSVECCAR SGGARGCSCVEAGKACDPAARGFHLYWCLHPEOHRVJSVECCAR SGGARGFTSTLYRLGGTHLAGAGGACHACHACA ARESASAKIKEEBAAKD 7020 1 2154 PFADERRKSVLLDKIRKULQVALTSKOQGLETAMSFVARWTFKRVX NGFHMKKYIAYLJVGLDMSPDPKASGHFARVAVVQHAPSESVDNAS MPVKVEGGGSWRSFFBTRAGAGSVDJUDWAFILDSAGTTTLFGF NEMKKYIAYLJVGLDMSPDPKASGHFARVAVVQHAPSESVDNAS MPVKVEGSGSWRSFBTBRAAGSVDJUDWAFILDSAGTTTLFGF NEMKKYIAYLJVGLDMSPDPKASGHFARVAVVQHAPSESVDNAS MPVKVEGSGSWRSFBTRAGAGSVDJUDWAFILDSAGTTTLFGF NEMKKYIAYLJVGLDMSPDPKASGHFARVAVVQHAPSESVDNAS MPVKVEGSTBJARGSKLUDPLSGRKULDGGARGATTTTFFVTT INQPSVKBAAKARPARKPVAARPVAAVVATTTTRVVTTTTTTTTTTTTTTTTTTTTT	ł	l	1	SHLLGRDSPSAVFEODLENKEMSKEWFLFNDSRVTFTSFQSVQK
IMDAITKONKLYLOGGCELNARARLOGASASCSFRENGFONDD PGSCGPTGGGGGGGTTVGRLVF PGSCGPTGGGGGGGTTVGRLVF PGSCGPTGGGGGGGTTVGRLVF PSLIGEBQAGIARTLQYILDRYPKDVQEHLVONVELTGGTYMP GMKARMEKELLENEPFRSSGVGLASNEVLDAWGARDMALNHL DDNEVMITRKEYBEKGGEYLKEHCASNIYVILDRYGASRSSDA QASSKGSAGGGGGQA ARGGIPUTMVPPAPSFPWHIACCSHEVTAGPPTLCKDMSALVAA ARGGIPUTMVPPAPSFPWHIACCSHEVTAGPPTLCKDMSALVAA RNRHIPLAPGSDWRDLPNIEVRLSDGTMARKLRYTHHDRKNGRS SGALRGVCSCVEAGKACDPAAROFNTLIPWCLPHTGNRINNWA GLYGRLEWDGFFSTTVTWPEPPMGGUHPPOHRVVSWECAR SGGPPTYRIFGMILDKHRQVGNAVPPPLAKAIGLEIKLCMLAK ARESASAKIKEBEARKD ARGGIPUTMVFPSTTTASPGLEEAVIKLSDAGITPLFITRGE PROLINALQINITAVCHALVEARGAUTPPOHRVVSWECAR SGGPPTYRIFGMILDKHRQVGNAVPPPLAKAIGLEIKLCMLAK ARESASAKIKEBEARKD ARGGIPTTYRIFGMILDKHRQVGNAVPPPLAKAIGLEIKLCMLAK ARESASAKIKEBEARKD ARGGIPTTYRIFGMILDKHRQVGNAVPPPLAKAIGLEIKLCMLAK ARESASAKIKEBEARKD ARGGIPTTYRIFGMILDKHRQVGNAVPPPLAKAIGLEIFLTRGE BROLINALQINITAVCHALVEAGUTFFENVITCHCULDIC NIDBSCGFGSNRSFFBDRRAAGSDVDIDMAFILDSAETTTLFGV MEMKEYTATYLVRGCLDBSPDPKASHAVVOHAPSESVONAS MPPVKVBFSITDVGSKEKLUPBLERGVATVOHAPSESVONAS MPPVKVBFSITDVGSKEKLUPBLGRGTGTALGSATETTILFGV MEMKEYTATYLVRGUNGSPPRAVOVOHAPSESVONAS MPPVKVBFSITDVGSKEKLUPBLGRGTAVOVOHAPSESVONAS MPPVKVBFSITDVGSKEKLUPBLGRGTAVOVOHAPSESVONAS MPPVKVBFSITDVGSKEKLUPBLGRGTAVOVOHAPSESVONAS MPPVKVBFSITDVGSKEKLUPBLGRGTARGSATETTLFGVI INQPSVKPAAAKPAAARPAAARPAVAVAPAVOVOHAPSESVONAS MPVKVBFSITDVGSKEKLUPBCGGGAFGATTLFGVTTTKVTTTTTKVTTTTTKVTTTTKVTTTTKVTTTTTKVTTTTKVTTTTKVTTTTKVTTTTKVTTTTKVTTTTKVTTTTKVTTTTKVTTTTKVTTTTKVTTTTTKVTTTTKVTTTTKVTTTTKVTTTTTKVTTTTKVTTTTTKVTTTTKVTTTTKVTTTTTKVTTTTKVTTTTTKVTTTTTKVTTTTKVTTTTTT	Į.	ì	1	ITSRFPKDTAYVLLYKKOHSTNGLSGNNPTSGLWINGDPPLQKE
POSCGPTGGGGGGNTVGRLUF TO18	1]	1	LMDAITKDNKLYLOEOELNARARALOAASASCSFRPNGFDDNDP
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PSLIGEEQAGIAFTLQYILDRYPKDVQEMUVONFITGATINYP GMKARMEKELEMPPRESSPOVLDANYGARDMAINHI DDNEWITTRKEYEEKGGEYLKEHCASNIYVPIRLPKQASRSSDA QASSKGSAAGGGABROA 7019 1048 335 AFGGGLTVITWPPRASPPWMLGCCSHEVTAGPPTLCKDMSALVAA RMRHIPLAPGSDWRDLPNIEVRLSDGTMARKLRYTHHDRKNGRS SGGLARGVGSCVERGKACDPAAROTLIPWCLPHTORNENNIMA GLYGRLENDGFSTTVTNDPPMGKQGRULHPEGHRVVSVVBCCAR SQGPPDTYRLPGNILDKHRQVGNAUPPPDLAKAIGLBIKLCMLAK ARESASAKIKEERAAKD 1 2154 FADSKRKSVLLDKIKNIQVALTSKQGSLETAMSFVARNTFKRVR NGPLMRKVAVPFSTATPTASPGLARGVLSLAGAGITPLETLTRGE DRQLINALQINNTAVGHALVLPAGRBLTDFLENVITCHVCLDIC NIDPSCGGSNRSPFBORRAASJOHDAMSFVARNTFKRVR NGPLMRKVAVFSTDTYGSKEKLVDPLSRGMTOLGGTBASTTTLEGP NEMKKYIAYLVROLDMS PDPKASQHFARVAVVQHAPSESVDNAS MPPVKVEFSLADVBGKEKLVDPLSRGMTOLGGTBAGSTTTLFQT NEMKKYIAYLVROLDMS PDPKASQHFARVAVVQHAPSESVDNAS MPPVKVEFSLADVBGKEKLVDPLSRGMTOLGGTBAGSTTTLFQT NEMKYIAYLVROLDMS PDPKASQHFARVAVVQHAPSESVDNAS MPPVKVEFSLADVBGKEKLVDPLSRGMTOLGGTBAGSTTTLFQT NEMKYIAYLVROLDMS PDPKASQHFARVAVQHAPSESVDNAS MPPVKVEFSLADVBGKEKLVDPLSRGMTOLGGTBAGSTTTLFQT NEMKYSAPANPARDLKIVVLMILTGEVPEQQLEEAQRVILQAKCKGY FFVVLGIGRKVNIKEVTFASBENDVFFKLUKSGTHKQV UNVPNNYTSSPTSNPVTTTKEVTTTKPVTTTTKPVTTTTRVTT NOPSVERPAARAPARPARPARPARPAKTATTATVTTKRVTTTTKPVTI NGPSVERPAARPARPARPARPARPARPARPARPARPARPARPARPA	7010	184	1066	STATERCHTWSGEAGHHCSALFNIAAYHOLFVGTERIRAPEIIFO
GMKARMEKELLEMRPFESSGVULASNPVLDAWGARDMALMHLDDNEWTTRKEYERGEVIKEHCASNIYVPIRLPKQASRSDA QASSKGSAAGGGAGEQA 7019 1048 335 APGGFLVTMVPPABSPEWMIGCCSHEVTAGPPTLCKOMSALVAA RNRHIPLAPGSDMEDLPNIEVLSSOTMARKLEYTHDRKNORS SGALRGVCSCVERGKACOPARAGPNTLIPGCLPHTONRHINWA GLYGRLEMOGPFSTTVTNEPEMSKGRVLHPEOHRVVSVHECAR GLYGRLEMOGPFSTTVTNEPEMSKGRVLHPEOHRVVSVHECAR GLYGRLEMOGPFSTTVTNEPEMSKGRVLHPEOHRVVSVHECAR GLYGRLEMOGPFSTTVTNEPMSKGRVLHPEOHRVVSVHECAR GLYGRLEMOGPFSTTVTNEPMSKGRVLHPEOHRVVSVHECAR GLYGRKSVLLDKKRNLQVALTSKQGSLETAMSFVARNTFKRVR ROMENKAYTH GAN THE AREA ARESASAKI KEERAAKD TO20	7018	484	1080	DEL TERRODETARTI OVIL DRVPKDVORMI VONVET TEGNTMYP
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MPPVKVBFSLTDVGSKEKLVDFLSRGMTQLQGTRALGSAIEYTI ENVFESAPNPRDLKIVVLMLTGEVPEQQLEEAQRVILQAKCKGY FFVVLGIGRKVNIKEVYTFASBPNDVFKLVDKSTELNEEPLMR FGRLLPSFVSSENAFYLSPDIRKQCDWFQGDQPTKNLVKFGHKQ VMVPNNVTSSPTSNPVTTTKPVTTTKPVTTTTKPVTTTTKPVTI INQPSVKPAAAKARPAKPVAAKFPATATVAPPVAVKPATAAK PVAAKPAAVRPPAAAAKPVATKTATVAPPVAVKPATAAK MVMMSREVQVFETTENSAKLHWERPEPFGPYFYDLTVTSAHDQS LVLKQNLTVTDRVIGGLLAGQTYHVAVVCYLRSQVRATYHGSFS TKKSQPPPPQPARSASSSTINLMVSTEPLALTETDICKLPKDEG TCRDFILKWYYDPNTKSCARFWYGGCGGNENKFGSQKBCEKVCA PVLAKPGVISVMGT 7021 2 338 VNAVSFFPMGYAFATGSDDATCRLFDLRADQELLLYSHDNIICG ITSVAFSKSGRLLLAGYDDFNCNVWDTLKGDRAGVLAGHDNRVS CLGUTDDGMAVATGSWDSFLRIWN CLGUTDDGMAVATGSWDSFLRIWN 7022 2 856 VYIGSFWSHPLLIPONRKLFEAEEQDLFRDIQSLPRNAALRKIN GRIEREHQISPGDFPNLKKMQDQLQAOPFSKPQPLKSKLLEVVD DMLAHDIAQLMVLVRQEESQRPIQMVKGGAFEGTLHGPFGHGYG GRAGGGIDDAEWVVARDKFWYDEIFYTLSPVDGKITGANAKERW VRSKLPNSVLGKIWKLADIDKDGMLDDDEFALANHLIKVKLEGH ELPNELPAHLLPPSKKVAE 7023 2 748 AMVFGGVPYVPQVRDIRRTQNADGFSTVCLVLLVANILRILE WFCRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRSE TAADSKDEBVKVAPRRSFLDFDPHHFWQMSSFSDYVQCVLAFTG VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST EGMS IKMVLWWTSGDAFKTAYFLLKGAFLQFFSVCGLLQVLVDLF LIGQAYAFARHPQKPAPHAVHPTGTKAL		1		NIDPSCGFGSWRPSFRDRRAAGSDVDIDMAFILDSAETTTLFQF
ENVFESAPMPRDLKIVVLMLTGEVPEQQLEEAQRVILQAKCKGY FFVVLGIGRKVNIKEVYTFASEPNDVFFKLVDKSTELMEEPLMR FGRLLPSFVSSENAFYLSPDITRKQCDWFQGDQPTKNIVKFGHKQ VMVPNNVTSSPTSNPVTTTKPVTTTTKPVTTTTKPVTTTTKPVTIT INQPSVKPAAAKPAARKPVAAKRVATKTATVRPVVAVKPATAAK PVAAKPAAVRPPAAAAKPVATKPEVPRPQAAKPAATKPATTKP MVKMSREVQVFEITENSAKLHWERFEPPGFYFYDLTVTSAHDQS LVLKQNLTVTDRVIGGLLAGQTYHVAVVCYLRSQVRATYHGSFS TKKSQPPPPQPARSASSSTINLMVSTEPLALTETDICKLPKDEG TCRDFILKWYYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCA PVLAKPGVISVMGT 7021 2 338 VNAVSFFPNGYAFATGSDDATCRLFDLRADQELLLYSHDNIICG LITSVAFSKSGRLLLAGYDDFNCNVWDTLKGDRAGVLAGHDNRVS CLGVTDDGMAVATGSWDSFLRIWN 7022 2 856 VYIGSFWSHPLLIPDNRKLFEAEEQDLFRDIQSLPRNAALRKLN GRIEREHQISPGDFPNLKRWQDQLQAQDFSKFQPLKSKLLEVVD DMLAHDIAQLMVLVRQEESQRPIQMVKGGAFEGTLHGPFGHGYG EGAGEGIDDAEWVVARDKPMYDEIFYTLSPVDGKITGANAKKEM VRSKLPNSVLGKIWKLADIDKDGMDDDEFALANHLIKVKLEGH ELPNELPAHLLPPSKRKVAE 7023 2 748 AMVEGGVVPYVPQVRDIRRTQNADGFSTYVCLVLLVANILRILE WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRSE TAADSKDEBVKVAPRRSFILDFDHHFWQWSSFSDYVQCVLAFTG VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST TAADSKDEBVKVAPRRSFILDFDHHFWQWSSFSDYVQCVLAFTG VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST LEGMSIKMVLMWTSGDAFKTATFLLKGAFLQFSVCGLLQVLVDLF LIGQAYAFARHPQKPAPHAVHPTGTKAL		1	1	NEMKKYIAYLVRQLDMSPDPKASQHFARVAVVQHAPSESVDNAS
FFVVLGIGRKVNIKEVTFASBPNDVFFKLVDKSTELNEEPLMR FCRLLPSFVSSENAFYLSPDIRKQCDWFQGDQPTKNLVKFGHKQ VNVPNNVTSSPTSNPVTTTKPVTTTKPVTTTKPVTTTKPVTT INQPSVKPAAAKPAPAKPVAAKPVATKTATVRPPVAVKPATAAK PVAAKPAAVRPPAAAAKPVATKPEVPRPQAAKPATKPATKAA PVAAKPAAVRPPAAAAKPVATKPEVPRPQAAKPATKPATKAA PVAKKPAAVRPPAAAAKPVATKPEVPRPQAAKPATKPATKAA PVAKKPAVVFEITENSAKLHWERPEPPGPYPJLTVTSAHDQS LVLKQNLTVTDRVIGGLLAGQTYHVAVVCYLRSQVRATYHGSFS TKKSQPPPPQPARSASSSTINLMVSTEPLALTETDICKLPKDEG TCRDFILKWYYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCA PVLAKPGVISVMGT 7021 2 338 VNAVSFFPNGYAFATGSDDATCRLFDLRADQELLLYSHDNIICG ITSVAFSKSGRLLLAGYDDFNCNVWDTLKGDRAGVLAGHDNRVS CLGVTDDGMAVATGSWDSFLRIWN 7022 2 856 VYIGSFWSHPLLIPDNRKLFEAEEQDLFRDIQSLPRNAALRKLN DLIKRARLAKVHAYIISSLKKEMPSVFGKDNKKKELVNNLASIY GRIEREHQISPGDFPNLKRMQDQLQAQDFSKPQPLKSKLLEVVN DMLAHDIAQLMVLVRQEBSQRPIQMVKGGAFEGTLHGPFGHGYG EGAGEGIDDAEWVVARDKFMYDEIFYTLSPVDGKITGANAKKEM VRSKLPNSVLGKIWKLADIDKDGMLDDDEFALANHLIKVKLEGH ELPHELPPSKRKVAE 7023 2 748 AMVEGGVVVPVPQYRDIRRTQNADGFSTVVCLVLVANILRILE WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRRSE TAADSKDEBVKVAPRRSFIDFDPHHFWQMSSFSDVVQCVLAFTG VAGYITYLSIDSALFVETLGFLAVITEAMLGVPQLYRNHRHQST EGMSIKMVLMWTSGDAFRTAYFLLKGAPLQFSVCGLLQVLVDLF ILGQAYAFARHPQKPAPHAVHPTGTKAL		1	ì	MPPVKVEFSLTDYGSKEKLVDFLSRGMTQLQGTRALGSALEYTI
FGRLLPSFVSSENAFYLSPDIRKQCDWFQGDQPYKNLVKFGHKQ VNVPNNVTSSPTSNPVTTTKRVTTTTKPVTTTTKPVTT INQPSVKPAAAKPAPARPVAAKPVATKTATVRPVVAVKPATAAK PVAAKPAAVRPPAAPAVRPVAKPVATKTATVRPPVAVKPATAAK PVAAKPAAVRPPAAAAKPVATKPEVPRPQAAKPAATKPATTKP MVKMSREVQVFEITENSAKLHWERPEPEGPYFYDLTVTSAHDQS LULKQNLTVTDRVIGGLLAGQTYHVAVVCYLRSQVRATYHGSFS TKKSQPPPPPQPARSASSTINLMVSTEPLALTETDICKLPKDEG TCRDFILKWYYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCA PVLAKPGVISVMGT 7021 2 338 VNAVSFPPNGYAFATGSDDATCRLFDLRADQELLLYSHDNIICG LISVAFSKSGRLLLAGYDDFNCNWDTLKGDRAGVLAGHDNRVS CLGUTDDGMAVATGSWDSFLRIWN 7022 2 856 VYIGSFWSHPLLIPDNRKLFEAEEQDLFRDIQSLPRNAALRKLN GRIEREHQISPGDFPNLKRMQDQLQAQDFSKFQPLKSKLLEVVD DMLAHDIAQLMVLVRQEESQRPIQMVKGGAFEGTLHGPFGHGYG EGAGEGIDDAEWVVARDKRMYDGIFYTLSFVDGKITGANAKKEM VRSKLPNSVLGKINKLADIDKDGMLDDDEFALANHLIKVKLEGH ELPNELPAHLLPPSKRKVAE 7023 2 748 AMVEGGVVPYVPQYRDIRRTQNADGFSTVVCLVLVANILRILE WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRSE TAADSKDEBVKVAPRRSFLDFDHHFWQWSSFSDYVQCVLAFST TAADSKDEBVKVAPRRSFLDFDHHFWQWSSFSDYVQCVLAFST VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST EGMSIKMVLMWTSGDAFKTAIFLLKGAFLQFSVCGLLQVLVDLF ILGQAYAFARHPQKPAPHAVHPTGTKAL	ł	1	1	ENVFESAPNPRDLKIVVLMLTGEVPEQQLEEAQRVILQAKCKGY
VNVPNNVTSSPTSNPVTTTKPVTTTTRPVTTTTRPVTT INQPSVKPAAARKPVAKKPATKTATVRPPVAVKPATAAK PVAAKPAAVRPPAAAAKPVATKPEVPRQAAKPAATKPATKRP PVAKKPAAVRPPAAAAKPVATKPEVPRPQAAKPAATKPATKPA MVKMSREVQVFEITENSAKLHWERPEPEPPYFVDLITVTSAHDQS LVLKQNLTVTDRVIGGLLAGQTYHVAVVCYLRSQVRATYHGSFS TKKSQPPPPQPARSASSSTINLMVSTEPLALTETDICKLPKDEG TCRDFILKWYYDPNTKSCARFWYGGCGNENKFGSQKECEKVCA PVLAKPGVISVMGT 7021 2 338 VNAVSFFPNGYAFATGSDDATCRLFDLRADQELLLYSHDNIICG ITSVAFSKSGRLLLAGYDDFNCNVWDTLKGDRAGVLAGHDNRVS CLGVTDDGMAVATGSWDSFLRIWN 7022 2 856 VYIGSFWSHPLLIPDNRKLFEAEEQDLFRDIQSLPRNAALRKLN GRIEREHQISPGDFPNLKRMQDQLQAQDFSKFQPLKSKLLEVVD DMLAHDIAQLMVLVRQESQRPIQMVKGGAFEGTLHGPFGHGYG EGAGGGIDDAEWVVARDKPMYDEIFYTLSPVDGKITGANAKKEM VRSKLPNSVLGKIWKLADIDKDGMLDDDEFALANHLIKVKLEGH ELPMELPAHLLPPSKRKVAE 7023 2 748 AMVFGGVVPVVQVRDIRRTQNADGFSTYVCLVLLVANILRILF WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRSE TAADSKDEEVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHGST LGGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLF ILGQAYAFARHPQKPAPHAVHPTGTKAL	1	1		FFVVLGIGRKVNIKEVYTFASEPNDVFFKLVDKSTELNEEPLMR
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7023 2 748 AMVFGGVVPYVPQYRDIRRTQNADGFSTYVCLVLLVANILRILF WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRRSF TAADSKDEBVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST EGMSIKMVLMWTSGDAFKTAYFLLKGAFLQFSVCGLLQVLVDLF ILGQAYAFARHPQKPAPHAVHPTGTKAL	1			ELPNELPAHLLPPSKRKVAE
WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRRSF TAADSKDEBVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST EGMSIKMVLMWTSGDAFKTAYFLLKGAFLQFSVCGLLQVLVDLF ILGQAYAFARHPQKPAPHAVHPTGTKAL	7023	1 2	748	AMVFGGVVPYVPQYRDIRRTQNADGFSTYVCLVLLVANILRILF
TAADSKDEBVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST EGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLF ILGQAYAFARHPQKPAPHAVHPTGTKAL	[1	WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRRSF
VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST EGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLF ILGQAYAFARHPQKPAPHAVHPTGTKAL	i			TAADSKDEEVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG
EGMS 1 KMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLF ILGQAYAFARHPQKPAPHAVHPTGTKAL	İ		1	VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST
ILGQAYAFARHPQKPAPHAVHPTGTKAL	Į.	-	-	KISMS I KMVLMWTSGDAFKTAYFLLKGAFLOFSVCGLLOVLVDLA
TWO TO THE PARTY OF THE PARTY O	1		1	TIGONYAFARHPOKPAPHAVHPTGTKAL
		1207	100	RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV
7024 1207 190 RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV	7024	1207	190	SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS
STREET VIGORITATION OF THE PROPERTY OF THE PRO	l	j	Ì	QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGGQGQPQGPGLRT
QUKPPVLPGTILGGGALIGILGRGFIB 1 GOZGGE QGFGAK.				RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD
KILLITGEFGAGLIGGAMLADKARLERLIKYYAK I BARUKATO GO	1	1	1	FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV
FHLLDHRIGHARCKADFRIGUVENITOF INTERNAD VIOLENDELLICI		,	1	VRQLEAEPGLPPVQPVFITVDPERDDVEAMARYVQDFHPRLLGL
VRQLEAEPGLPPYQPYETTVDPERDDVEAMAR I VQDFHERDDGI	Ì	1	1	AKÖPEVERGPERAGEAETTANKEKINAETTAKT AKOG HEKUNGR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
'	amino acid	sequence	Codon, /=possible nucleotide deletion,
Ĺ <u> </u>	sequence		\=possible nucleotide insertion)
ł			TGSTKQVAQASHSYRVYYNAGPKDEDQDYIVDHSIAIYLLNPDG
7025	732		LFTDYYGRSRSAEQISDSVRRHMAAFRSVLS
7025	232	832	ERNSPIGNNENL*K\HSLDCLCFRGDWEGNTQFQTLQDNQEECF
			KQVIRTCEKRPTFNQHTVFNLHQRLNTGDKLNEFKELGKAFISG
1	i	i	SDHTQHQLIHTSEKFCGDKECGNTFLPDSEVIQYQTVHTVKKTY
ì			ECKECGKSFSLRSSLTGHKRIHTGEKPFKCKDCGKAFRFHSQLS VHKRIHTGEKSYECKECGKAFSCG
7026	328	1146	NPNPSIGDIKDIKKAAKSMLDPAHKSHFHPVTPSLVFLCFIFDG
	""	1110	LHQALLSVGVSKRSNTVVGNENEERGTPYASRFKDMPNFIALEK
ł	1		SSVLRHCCDLLIGVAAGSSDKICTSSLQVQRRFKAMMASIGRLS
}			HGESADLLISCNAESAIGWISSRPWVGELMFTFLFGDFESPLHK
1			LRKSS*LPRKHR*QPINAVRMFLDQCMDGSIALRAIVSEIPVFE
			EKKNNG*KGIGEIF*VWGCTLPPHYWGAVTTNVPKLSNSGKLLG
L	.		QDEQPHIFG
7027	43	954	GRRLQQQQRPEDAEDGAEGGGKRGEAGWEGGYPEIVKENKLFEH
			YYQELKIVPEGEWGQFMDALREPLPATLRITGYKSHAKEILHCL
1			KNKYFKELEDLEMDGQKVEVPQPLSWYPEELAWHTNLSRKILRK
			SPHLEKFHQFLVSETESGNISRQEAVSMIPPLLLNVRPHHKILD
			MCAAPGSKTTQLIEMLHADMNVPFPEGFVIANDVDNKRCYLLVH
Į.			QAKRLSSPCIMVVNHDASSIPRLQIDVDGRKEILFYDRILCDVP
7028	189	608	CSGDGTMRKNIDVWKKWTTLNSLQLHGLQLRIATRGAEQL
1020.	109		SRPPPEPEPGTMVEKGSDSSSEKGGVPGTPSTQSLGSKNFIRNS KKMQSWYSMLSPTYKQRNEDFRKLFSKLPEAERLIVDYSCALOR
			EILLQGRLYLSENWICFYSNIFRWETTISIQLKEVTCLKKEKTA
			KLIPNAIO
7029	1343	40	VLESNTEAKQATGTSSKLRHGTGQEKGREGPRCPSGLAQLRLWG
1			/PCPHAGRETGPRASAPIPGS*GHGWHW*RKDGRGERSEGPSAL
			SPHSPSLLNMQQAPTHVGPGMGSQRPRSSVVPEQVGVGSQLSRE
1			RWRA*RSLPGAAASERTEMTKERSP/RPCQGYDSSNWFTQPGKK
			TRKRNSRRNTMVSRGGGCLLYPLQSIMPE*QLR*GAHASPPTQG
1		ı	R*GKGGPRSPLTKASGTTHIPTPFFGSIP/RPTRDSGPGTDNS\
1 !			AAPGQKRGHREA*QGPEPV/WGRVTTHLQGPAG*TKPLGS\RNW
1			VPGPAEGEQGEGAGLEGRP*PLKGCRSTLTFSPQLSIPMVGKKP
			PEGTTASFFP\RSCHSE*RKPPPSCPHAPALSLPHPLPLPPL
1 1	ļ		PLPLPGAGT*HSARSGRPGQSETGSLCHNCHHCPPHCPKCSPGG T
7030	2	521	FVCFSAPGSGQGKRRVNMELSAVGERVFAAEALLKRRIRKGRM
			EYLVKWKGWSQKYSTWEPEENILDARLLAAFEEREREMELYGPK
j j			KRGPKPKTFLLKAQAKAKAKTYEFRSDSARGIRIPYPGRSPODL
{ !			ASTSRAREGLRN\RVCPRQRAAPAPAAP\PRRGPSGPGPRPG+G
		·	PGLHFPGPGGPSKHGFVPASEQHQHQQHLPRRGPSGPGPRPG
7031	960	59	HCSVPGAEWPRKPPAQICPQLTSRPHLSSPRSLSPGCGHSPGPG
] }	j		/CKPS/RHCDELHEGPSRTAALPCGKPQPKHGVEECG/PCPCLA
1 1			PRRLTEPPALTVSPVGRAAPSGAL*PSGRACSACSHRLAPEAAL
1	j		SAAAPRPSLGSGQNASGLPAASLPPQDSSQPHKTVPSPARSVPP
	1		LGAQARAAPPRLWCPRALVSG*EASPEAVSVAAGPPVPGPTPST
1 1	ì		SGSTASHSRRGC*SPR*TPAPPRRDHGRSAAFEVLTAAASAQPC
7032	1393	2102	ASQGGPRPTGAGRTPSPLGLPFSRGPPAASARPFCRHPSL
	1333	2104	RRPGRTEPVEPPPVPPPPRASNSKSRCR*RNLHLAPL*QSPLRK
	1		SRQIGTSSLPFGRSAGERPRPAATFCLSRGGSSPVFL+PSSSSL
[Í		EPWMKRQFGRLHSLFWKSWQKMNSFLLTPKLDTSLMSGWRYRQR
]		LPRLHTFLKKSLQMASELAPPLPTPAPLASSLPPPPPGPPPLLPV PLA*LSRSGILVPPNSGFSLSC\PLGDH*GSSGEVRGSCGSPPP
į į	i		HHCWVLPPPP*LLLPPR
7033	689	815	RSRDCLSSSATSNRARRSKCSGPKRATPLDSGPGP*APPGPSSA
للتتب			ASTUCED STATEMENT AND STATEMENT APPERSA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	p=proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
		 	LMMPSSCPWRTGALGPSPAGSRALGRCTSSVGPGSRWLTRTSSP
	1	1	GCATRTWRTMRMEPRPLRSRMGESAPGIPAELPSAAPSGPSAPS
			AAAPSAPTTPAAAGPNTL+SRRTAEWCWPPSCSCCWGWC+SWSA
	1	1	WDWRRPPLQVSPAPSSSCRASCCWCLESIT*SSSTARSRATGAS
		l	SSSTCPTSRSDRGAAWTP\SPMGAPLLPCSVPLISREEALQDPR
		Ļ	NPSP*GVCSGSSGHAGLALGKPPVACSVP
7034	92	1942	EDTSSMPFRILLIPLGLLCALLPOHHGAPGPDGSAPDPAHYRERV
,034	1		KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
]		į,	TLL\TLFYFOILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
l .	1	ļ	RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
ļ			FOTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
1			TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
i			IGAGVDSYFEYLVKGAILLODKKLMAMFLEYNKAIRNYTRFDDW
I		1	YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
1	ł	1	TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT
	1	1	GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
1	į	i	FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI
[1		FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQ
1			KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS
1			QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
1]		K K
	<u> </u>	1942	EDTSSMPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYRERV
7035	92	1942	KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
1		ļ	TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
1	ļ ·	ł	RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
1		ļ	FOTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
			TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
l		l l	IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW
1 .	1	1	YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
1	1	1	TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT
			GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
i		l	FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI
	1	Ť	FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQ
1	[1	KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS
1			QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
1			
L			K CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
7036	442	761	RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
1			
			PPPPPPPPPPRRPPRNRRPG CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
7037	442	761	CLAPLESCEQIINDHLAPSGKLKWAWDROFORN - DPGEGPSIFI
1			RNW*ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
			PPPPPPPPPPRRPPRNRRPG
7038	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL
1			QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ
ı		ļ	LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM
1		1	QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
1		{	LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR
1		ļ	LQEAASPAAERACRSSKGTSTSRTG
7039	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL
1	İ	1	QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ
1	1	1	LOEMAOLRIKHOEELTELHKKRGELAQ\RVIDLNNQMQRKDREM
- [{	1	OMNEAKIAECLOTISDLETECLDLRTKLCDLERANQTLKDEYDA
	1	i	LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR
	1		LOEAASPAAERACRSSKGTSTSRTG
7040	34	789	KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS
1]		GYESVMRDSEATGSASSAQDSTSENSSSVGGRCRSLKTPKKRSN
	•	1	

SEQ Predicted beginning nucleotide nucleotide location corresponding to first amino acid predicted end nucleotide location corresponding to first amino acid amino acid residue of Sering Tethreoning V-Valing	id, E= cine,
NO: nucleotide location Glutamic Acid, F=Phenylalanine, G=Glyc Corresponding to first L=Leucine, M=Methionine, N=Asparagine, amino acid P=Proline, Q=Glutamine, R=Arginine.	cine,
location corresponding H=Histidine, I=Isoleucine, K=Lysine, corresponding to first L=Leucine, M=Methionine, N=Asparagine, to first amino acid P=Proline, Q=Glutamine, R=Arginine.	
corresponding to first L=Leucine, M=Methionine, N=Asparagine, to first amino acid P=Proline, Q=Glutamine, R=Arginine.	
to first amino acid P=Proline, Q=Glutamine, R=Arginine,	
amino actu Fariotine, Quittamine, Ranginine,	
	=Stop
sequence \=possible nucleotide insertion)	
PGSQRRRLIPALSLDTSSPVRKPPNSTGVRWVDGPLRS	SPRGLG
EPFEIKVYEIDDVERLQRRRGGASKEAMCFNAKLKILE	HRQQRI
AEVRAKYEWLMKELEATKQYLMLDPNKWLSEPDLEQVV	ELDSLE
YLEALECVTERLESRVNFCKAHLMMITCFDIT	_
7041 1 567 SGRVAMGRRRAPAGGSLGRALMRHQTQRSRSHRHTDSW	LHTSEL
NDGYDWGRLNLQSVTEQSSLDDFLATAELAGTEFVAEI	LNIKFV
PAEARTGLLSFEBSQRIKKLHEENKQFLCIPRRPNWNC	NTTPEE
LKQAEKDNFLEWRRQL\VRLEEEQKLILTPFERNLDFW	RQLWRV
IERSDIVVQIVDA	
7042 7 345 PIHMAAAALRADI\ISPLFPHIQGYLLLSASHG\ATSI	HTKGAL
PLETVTMYTVIPKSKYVLVKPDTQYPYSENLDEFKRL	ENSASN
DDLLMAEVAISDYGDKLTLELREKY	
7043 2 2170 ARGMAARDSDSEEDLVSYGTGLEPLEEGERPKKPIPLC	GRVTOG
EKGRYKRFHGAFSGGFSAGYFNTVGSKEGWTPSTFVSS	
KSVLGPEDFMDEEDLSEFGIAPKAIVTTDDFASKTKDR	
QLAAATAP I PGATLLDDLITPAKLSVGFELLRKMGWKE	
RVKRRPRRQKPDPGVKIYGCALPPGSSEGSEGEDDDYI	
APKDVTPVDFTPKDNVHGLAYKGLDPHQALFGTSGEHF	
SERAGDLGEIGLNKGRKLGISGQAFGVGALEEEDDDIY	
KYDTVLKDEEPGDGLYGWTAPRQYKNOKESEKDLRYVG	
SLASKPLSSKKIYPPPELPRDYRPVHYFRPMVAATSEN	
LSESAGKATPDPGTHSKHOLNASKRAELLGETPIOGSA	
LSOKDKERIKEMKOATDIKAAQIKARSIAONAOSSRAC	
AGHCSWNMALGGGTATLKASNFKPFAKDPEKOKRYDEF	
GQKDALERCLDPSMTEWERGRERDEFARAALLYASSHS	
THAKEEDDSDQVEVPRDQENDVGDKQSAVKMKMFGKLT	DOUBLE
HPDKLLFQ/RLVGLPRVKRDKYSVFNFLTLPETASLPT	TOACCE
KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARS	
QOSSPLVNKEEEHAPELSAN	Master
7044 276 734 EVYLTDEFAKGRKVADLYELVQYAGNIIPRLYLLITVG	WWWC
FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRN	
EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHS	
ERERQELRILVGTNLVRLSOV	KUKEKK
	TVERSE
- DOLIGHENDOWN ON THE LIGHT OF THE PROPERTY OF	PILLECE
KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNL	VEPVNK
DLEFQLHEPFILLYRNASLSIYSIWFYDKNDCHRIAKLM	ADVVEE
ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQ	<u>ئ</u>
The state of the s	LYTFCP
KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNL	
DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLM	
ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQ	
7047 103 486 QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKN	
IMLIDVREIWEILEYQKI PESINVPLDEVGEALQMNPR	
NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYY	
7048 92 627 FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSE	
WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQ:	
RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDD	
IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QR	
EKKW	(827
7049 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARR	TVEDET.
VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAK	
NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILE	
EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRI	
ASSLWG	CTWAY
7050	77/5055
7050 393 938 KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRO	TENET

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ĺ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
ŀ	sequence		\=possible nucleotide insertion)
			VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL
•	{	1	NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT
!		1	EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX
ł	i		ASSLWG
7051	119	816	KKMNLAEICDNAKKGREYALLGNYDSSMVYYQGVMQQIQRHCQS
1		1	VRDPAIKGKWQQVRQELLEEYEQVKSIVGTLESFKIDKPPDFPV
1		}	SCQDEPFRDPAVWPPPVPAEHRAPPQIRR/RQSRSKTSEERNGR
1	j	J	SRSPGTCRPST\PISKSEKPSTSRDKDYRARGRDDKGRKNMQDG
1	1	l .	ASDGEMPKFDGAGYDKDLVEALERDIVSRNPSIHWDDIADLEEA
		ļ	KKLLREAGVLPMWM
7052	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
1	1	1	TYRNSMYHNKHVFKDKVVLDVGSGTGILSMFAARQGPRR
7053	467	715	SCPGRGKMSKLLNPEEMTSRDYYFDSYAHFGIHEEMLKDEVRTL
1 .555	1	1	TYRNSMYHNKHVFKDKVVLDVGSGTGILSMFAARQGPRR
7054	 	1036	GTSORSRETDARRRSAGAEPTARLPWPAALEEWPSCPCEPLGPG
1 ,034	†	1030	RRCRWDAMEYDEKLARFROAHLNPFNKOSGPROHEOGPGEEVPD
J		1	VTPEEALPELPPGEPEFRCPERVMDLGLSEDHFSRPVGLFLASD
1	ļ	i	VQQLRQAIEECKQVILELPEQSBKQKDAVVRLIHLRLKLQELKD
1		1	PNEDEPNIRVLLEHRFYKEKSKSVKQTCDKCNTIIWGLIQTWYT
1		Ī	CTGCYYRCHSKCLNLISKPCVSSKVSHQAEYELNICPETGLDSQ
l		1	DYRCAECRAPI/CS/DGVVPSEARQCDYTGQYYCSHCHWNDLAV
1		ì	IPARVVHNWDFEPRKVSRCSMRYLALMVSRPVLRLREIN
7055	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNQGP
1033	4	321	EYHYLHOMLG/ALCLSRASASVLNLNCSLILLPMCRTLLAYLRG
1		l .	SQKVPSRRTRRLLDKSRTFHITCGATICIFSGVHVAAHLVNALN
	ì	1	FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL
	1		M
7056	2	527	DSRRVSWRSWLANE/WGKHLCLFIWLSMNVLLFWKTFLLYNQGP
1036	4	327	EYHYLHQMLG/ALCLSRASASVLNLNCSLILLPMCRTLLAYLRG
		i	SOKVPSRRTRLLDKSRTFHITCGATICIFSGVHVAAHLVNALN
	}	i	FSVNYSEDFVELNAARYRDEDPRKLLFTTVPGLTGVCMEVVLFL
ł	1	l	M N
	1360	 	GIYLHVNEKIPRPTCIGDRQENDKENLNLENHRDQELLHASCQA
7057	1368	431	SGEVPSOASLRGFFTEDEPGCFGEGENLPEALQNIQDEGTGEQL
1.	1		SPQERISEKQLGQHLPNPHSGEMSTMWLEEKRETSQKGQPRAPM
[AQKLPTCRECGKTFYRNSQLIFHQRTHTGETYFQCTICKKAFLR
1	1		SSDFVKHORTHTGEKPCKCDYCGKGFSDFSGLRHHEKIHTGEKP
	1	1.	YKCPICEKSFIQRSNFNRHQRVHTGEKPYKCSHCGKSFSWSSSL
1		1 '	DKHQRSHLGKKPFQ*PVTKLSFPISISQPSHKNTQLHQEELCLR
1		1	
			GYPC
7058	1	469	FSGFGAVPDALGCRMSDLRITEAFLYMDYLCFRALCCKGPPPAR
1	Į.		PEYDLVCIGLTGSGKTSLLSKLCSESPDNVVSTTGFSIKAVPFQ
		1	NAILNVKELGGADNIRKYWSRYYQGSQGVIFVLDSASSEDDLEA
L	<u> </u>		ARN*SCTQLLQHPQLCTLPFLILA
7059	1	1178	WPAFPRQPAAAAMDALLGTGPRRARGCLGAAGPTSSGRAARTPA
1	1		APWARPSAWLECVCVVTFDLELGQALELVYPNDFRLTDKEKSS1
1]	i	CYLSFPDSHSGCLGDTQFSFRMRQCGGQRSPWHADDRHYNSRAP
1			VALQREPAHYFGYVYFRQVKDSSVKRGYFQKSLVLVSRLPFVRL
į		İ	FQALLSLIAPEYFDKLAPCLBAVCSETDQWPAPAPGQTLNLPVM
1		1	GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF
		1	RCFRPVLTHMQTLWELMLLGEPLLVLAPSPDVSSEMVLALTSCL
1			QPLRFCCDFRPYFTIHDSEFKEFTTRTQAPPNVVLGVTNPFFIK
ł		1	TLOHWPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP
7060	90	1670	SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ
1		-5//	YRFEHLVTQMKWRLQEGRGEAVYQIGVEDNGLLVGLAEEEMRAS
	1	1	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid		Codon, /=possible nucleotide deletion,
		sequence	
	sequence		\=possible nucleotide insertion)
		1	LKTLHRMAEKVGADITVLREREVDYDSDMPRKITEVLVRKVPDN
	j		QQFLDLRVAVLGNVDSGKSTLLGVLTQGELDNGRGRARLNLFRH
	1		LHEIQSGRTSSISFEILGFNSKGEVHGINGTQWGQTLRMGW***
	ŀ		RT*DGGRVWRLFEIV*MNALRGL*TSSAPLRKSMGNQLN*IKNG
			VKIKRQGHPGNGLGPGNSEGVGRAGRRH*GPWALGQVVNYSDSR
	ì	1	TAEEICESSSKMITFIDLAGHHKYLHTTIFGLTSYCPDCALLLV
	ł		SANTGIAGTTREHLGLALALKVPFFIVVSKIDLCAKTTVERTVR
	İ		QLERVLKQPGCHKVPMLVTSEDDAVTAAQQFAQSPNVTPIFTLS
	1	· ·	T
	Ī		SVSGESLDLLKVFLNILPPLTNSKEQEELMQQLTEFQVDEIYTV
	L		PEVGTVVGGTLSR*IDLLATLPTQPSPIYSKTSWPKGGDPGI
7061	364	710	ARMPSPLGPPCLPVMDPETTLEEPETARLRFRGFCYQEVAGPRE
	1	1	ALARLRELCCQWLQPEAHSKEQMLEMLVLEQFLGTLPPEIQAWV
	1		RGQRPGSPEEAAALVEGLQHDP*ARMPSPLGPPCLPVMDPETTL
	1		EEPETARLRFRGFCYQEVAGPREALARLRELCCQWLQPEAHSKE
		ļ ·	QMLEMLVLEQFLGTLPPEIQAWVRGQRPGSPEEAAALVEGLQHD
			PGQLLG
7062	71	744	AKAGTNLERLHWLSYFFCIPKHKLKSSOKDKVROFMACTOAGER
,	1	1	TAIYCLTONEWRLDEATDSFFONPDSLHRESMRNAVDKKKLERL
	1	1	YGRYKDPODENKIGVDGIOOFCDDLSLDPASISVLVIAWKFRAA
	1	ĺ	TOCEFSRKEFLDGMTELGCDSMEKLKALLPRLEOELKDTAKFKD
	1	1	FYQFTFTFAKNPGQKGLDL*MAGAYWKLVLSGRFKFLYLWNTFL
	į.	į.	· · · · · · · · · · · · · · · · · · ·
·	<u> </u>	·	менн
7063	2	562	LRTVPDLPGRRFRAMRTGQRR*PELPPDMNSLEQAEDLKAFERR
	1		LTEYIHCLQPATGRWRMLLIVVSVCTATGAWNWLIDPETQKVSF
]		FTSLWNHPFFTISCITLIGLFFAGIHKRVVAPSIIAARCRTVLA
	1		EYNMSCDDTGKLILKPRPHVQ*QSSLIVMGLKIAFLRISDTAKS
		İ	HKGFLLRLDM
7064	300	884	RDTGSDPSSTRRLCSTCCTGH*PAEPIASPHPSRGTCPPASSAS
	1		SRRTGCWTCPPESGHAQARRSRRASASRWGARGAVRSAVAARGC
	ì	1	SSRAGRWLETPGRRRGPPACAAAAGRLRGPAP*AAPPTASVPAR
	1	1	CRCPAARTGAPAAATWLRRRLSGLRAPALGRRRSPGPSPKSAAP
		1	PLLTPLGAGRAGGSRANS
7065	1	 	ATTTHSARRSGRGAAAEAAASAAGGROKGPDRKAWEGRRTTPGG
1000	1	555	
			RSQSEPKAPPPQKRSEAAFASMAHSPVAVQVPGMQNNIADPEEL
	1		FTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDLEEAEDEIEDI
	1.		QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLGGGSALDLL
		<u></u>	RAGPFDEFQ
7066	356	676	PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQ1CDT
		1	YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND
]	[VGVEVGGSGGCLEERTPP
7067	152	973	KENITMATEIGSPPRFFHMPRFQHQAPRQLFYKRPDFAQQQAMQ
• •	1	1	OLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWORDORDMRAIO
•	1		PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW
			TPEGRRLVTGASSGEFTLWNGLTFNFETILQAHDSPVRAMTWSH
	1	ł	
	1		NDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIP
	1	1	FSVVPIVMVKLFSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT
			HSPFCWAPF
7068	222	816	DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD
			DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
			VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY
	i		GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL
	Į.		AELRIHENKVKKIOKDTFKKK
		1	
7069	7747	1766	PDDUDDVEVINEAGGEGOWEEDIGEFFFFFGOAOSMDDETTAVA
7069	1147	1765	FRDHRRYFYVNEQSGESQWEFPDGEEEEEESQAQENRDETLAKQ TLKDKTGTDSNSTESSETSTGSLCKESFSGOVSSSSLMPLTPFW

WO 01/53312

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
)	amino acid	residue of	S≈Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
 			EKTKKGRKDKAKKSKTKMPSLVKKWQSIQRELDEEDNSSSSEED
1]		RVSTAQKRIEEWKQQQLVSGMAERNANFEA
7070	1	547	DGTMEDSEAVQRATALIEQRLAQEEENEKLRGDARQKLPMDLLV
1 /0/0	} -		LEDEKHHGAQSAALQKVKGQERVRKTSLDLRREIIDVGGIQNLI
[ELRKKRKOKKRDALAASHEPPPEPEEITGPVDEETFLKAAVEGK
1	1	1	MKVIEKFLADGGSADTCDQFRRTALHRASLEGHMEILEKLLDNG
<u> </u>	1	1	ATVDFQ
7071	2	921	ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
1 /0/1	1 2	321	VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY
1		1	FQDPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV
1		1	PESSI, PPASMPYADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPV
			PSSMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQT
1		[SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ
1	ł		IRRKPDQWAQYHTQKAPLVSSTLPVATQSPTPPSTLNRGEGS
	<u> </u>		ARGTLRALETAKKVGKVGANGQKAAGPSADSVTENKIGSPPKTP
7072	2	921	VSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPAYPPHSENIQY
1	ļ	1	FQDPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNV
1			PODPRIGIPPROPURGITPPPPINTCCPVODDDDODVCDVDDV
İ	1	1	PESSLPPASMPYADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPV
j	}	1	PSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQT
ł		1	SLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQ
ļ			IRRKPDQWAQYHTQKAPLVSSTLPVATQSPTPPSTLNRGEGS
7073	50	504	LAHGSFGVSDFPAPAAAPAHTLTSFSGSLSPQFRKPLGRAPAMP
	1	ł	LVRYRKVVILGYRCVGKTSLAHQFVEGEFSEGYDPTVENTYSKI
i	([VTLGKDEFHLHLVDTAGQDEYSILPYSFIIGVHGYVLVYSVTSL
1	1	t	HSFQVIESLYQKLHEGHGK
7074	263	1003	VCPVLCSTRQEPGHSSLVTYFGKPTRRKEFLLGHCIAAGKMNIS
1		İ	VDLETNYAELVLDVGRVTLGENSRKKMKDCKLRKKQNERVSRAM
1	1		CALLNSGGGVIKAEIENEDYSYTKDGIGLDLENSFSNILLFVPE
1	1	1	YLDFMQNGNYFLIFVKSWSLNTSGLRITTLSSNLYKRDITSAKV
ļ			MNATAALEFLKDMKKTRGRLYLRPELLAKRPRVDIQEENNMKAL
į	i	ſ	AGVFFDRTELDRKEKLTFTESTHVEI
7075	598	1005	NYINFFFRKEYPPHVQKVEINPVRLSRLQGVERIMKKTBESESQ
j	}	1	VEPEIKRKVQQKRHCSTYQPTPPLSPASKKCLTHLEDLQRNCRQ
İ	1	†	AITLNESTGPLLRTSIHQNSGGQKSQNTGLTTKKFYGNNVEKVP
1	}		IDII
7076	279	1049	LOSESSNAAEGNEORHEDEORSKRGGWSKGRKRKKPLRDSNAPK
		1	SPLTGYVRFMNERREQLRAKRPEVPFPEITRMLGNEWSKLPPEE
1	ļ	1	KQRYLDEADRDKERYMKELEQYQKTEAYKVFSRKTQDRQKGKSH
1			RQDAARQATHDHEKETEVKERSVFDIPIFTEEFLNHSKAREAEL
1		1	RQLRKSNMEFEERNAALQKHVESMRTAVEKLEVDVIQERSRNTV
1	1		LOOHLETLROVLTSSFASMPLPEXGETPTVDTIDSYM
7077	 3	1119	SSMGSNSEINGLALRKTDKYGFLGGSQYSGSLKSSIPVDVARQR
1			ELKWLDMFSNWDKWLSRRFOKVKLRCRKGIPSSLRAKAWQYLSN
1	1		SKELLEONPRKFEELERAPGDPKWLDVIEKDLHRQFPFHEMFAA
1			RGGHGOODLYRILKAYTIYRPDEGYCQAQAPVAAVLLMHMPAEQ
1	l l	1	AFWCLVQICDKYLPGYYSAGLEAIQLDGBIFFALLRRASPLAHR
1	1		HLRRORIDPVLYMTEWFMCIFARTLPWASVLRVWDMFFCEGVKI
1	1		IFRVALVLLRHTLGSVEKLRSCQGMYETMEQLRNLPQQCMQBDF
1	ļ		LVHEVTNLPVTEALIERENAAQLKKWRETRGELQYRPSRRLNGS
1	1		RAIHEERRRQQPPLGPSSS
<u></u>			FQGQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG
7078	483	767	FQGQRMAGEQKPSSNILEGFILLARGISGSANIALISQV DEAFG
Ì		İ	
			SLPELY SWEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ
7079	2	376	SVVEFKRPKEPSGSDGESDGP1DVGQEGQLSQMARPLS1PSSSQ MQARKKRRGI1EKRRDRINSSLSELRRLVPTAFEKQGSSKLEK
L	1		MQAKKKRG11EKKKKUKINSSESEEKKUVFIAFEAQGSSKHEK

- 25	1 Day 33 24 2 3	Dendier -	
SEQ	Predicted	Predicted end nucleotide	Amino acid segment containing signal peptide
ID NO:	beginning nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
I NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			AEVLQMTVDHLKMLHATGGTGTHALLFOASFIOOIF
7080	200	595	VOLPLEAPCLSLLSCRDHSGGNRDLSRRHRDCRVYGSPODGIPY
	l		LTHPLCHQDVVSVGRLQIRALATPGHTQGHLVYLLDGEPYKGPS
1			CLFSGDLLFLSGCGEFPRKREELGEEGETEVRAATVPWRALKP
7081	213	506	AVTEEMILNSLSLCYHNKLILAPMVRVGTLPMRLLALDYGADI
]	i		VYCEELIDLKMIOCKRVVNEVLSTVDFVAPDDRVVFRTCEREON
l			RVVFOMGTS
7082	3	1137	APSRNTMLMAWCRGPVLLCLROGLGTNSFLHGLGOEPFEGARSL
[CCRSSPRDLRDGEREHEAAQRKAPGAESCPSLPLSISDIGTGCL
<u> </u>	}		SSLENLRLPTLREESSPRELEDSSGDQGRCGPTHQGSEDPSMLS
i			QAQSATEVEERHVSPSCSTSRERPFQAGELILAETGEGETKFKK
(1	(LFRLNNFGLLNSNWGAVPFGKIVGKFPGQILRSSFGKQYMLRRP
}	j	j	ALEDYVVLMKRGTAITFPKDINMILSMMDINPGDTVLEAGSGSG
<u> </u>		1	GMSLFLSKAVGSQGRVISFEVRKDHHDLAKKNYKHWRDSWKLSH
l		j	VEEWPDNVDFIHKDISGATEDIKSLTFDAVALDMLNPHVTLPVF
1		ì	YPHLKHGGVCPVYVVNITQVIELLD
7083	115	541	RSNAVQLTRMEYAMKSLSLLYPKSLSRHVSVRTSVVTQQLLSEP
ì	ļ	1	SPKAPRARPCRVSTADRSVRKGIMAYSLEDLLLKVRDTLMLADK
•			PFFLVLEEDGTTVETEEYFQALAGDTVFMVLQKGQKWQPPSEQG
	L		TRHPLSLSHK
7084	3	522	NSVSVSSQSRFLASVPGTGVQRSAAADMAASTAAGKQRIPKVAK
		1	VKNKAPAEVQITAEQLLREAKERELELLPPPPPQQKITDEEELND
1			YKLRKRKTFEDNIRKNRTVISNWIKYAQWEESLKEIQRARSIYE
			RALDVDYRNITLWLKYAEMEMKNRQVNHARNIWDRAITTL
7085	243	1499	RQLARLRRRGWRSPFGGAPMAHITINQYLQQVYEAIDSRDGASC
[1	j	AELVSFKHPHVANPRLQMASPEEKCQQVLEPPYDEMFAAHLRCT
f		}	YAVGNHDFIEAYKCQTVIVQSFLRAFQAHKEENWALPVMYAVAL
ŀ			DLRVFANNADQQLVKKGKSKVGDMLEKAAELLMSCFRVCASDTR
]		İ	AGIEDSKKWGMLFLVNQLFKIYFKINKLHLCKPLIRAIDSSNLK
[· ·	DDYSTAQRVTYKYYVGRKAMFDSDFKQAEEYLSFAFEHCHRSSQ
]]		KNKRMILIYLLPVKMLLGHMPTVELLKKYHLMQFAEVTRAVSEG
		ĺ	NLLLLHEALAKHEAFFIRCGIFLILEKLKIITYRNLFKKVYLLL KTHQLSLDAFLVALKFMQVEDVDIDEVQCILANLIYMGHVKGYI
i			SHQHQKLVVSKQNPFPPLSTGC
7086	256	525	ILAARMGKQNSKLRPEVMQDLLESTDFTEHEIQEWYKGFLRDCP
1 /500	230	323	SGHLSMEEFKKIYGNFFPYGDASKFAEHVFRTFDANGDGTIDFR
	1		EF
7087	166	723	LSGSSAGKVAAPCVPPSNHELVPITTENAPKNVVDKGEGASRGG
, , , ,	1	123	NTRKSLEDNGSTRVTPSVQPHLQPIRNMSVSRTMEDSCELDLVY
			VTERIIAVSFPSTANEENFRSNLREVAQMLKSKHGGNYLLFNLS
	1		ERRPDITKLHAKVLEFGWPDLHTPALEKICSICKAMDTWLNAHP
١		1	HRCRVLHNKG
7088	104	759	GTSAASPSSLLEMAGEITETGELYSSYVGLVYMFNLIVGTGALT
00	103	159	MPKAFATAGWLVSLVLLVFLGFMSFMTTTFVIEAMAAANAQLHW
			KRMENLKEEEDDDSSTASDSDVLIRDNYERAEKRPILSVORRGS
	1		PNPPEITDRVEMGQMASMFFNKVGVNLFYFCIIVYLYGDLAIYA
	i		AAVPFSLMQVTCSATGNDSCGVEADTKYNDTDRCWGPLRRVD
7089	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
	[1	HYTLPPGIMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG
			SPIHTSVOFOASYLPKPGAOLYOFRYVNROGOVCGOSPPFOFRE
			PRPMDELVTLEBADGGSDILLVVPKATVLQNQLDESQQERNDLM
	1		QLKLQLEGQVTELRSRVQELERALATARQEHTELMEQYKGISRS
			HGEITEERDILSRQQGDHVARILELEDDIOTISEKVLTKEVELD
			RLRDTVKALTREQEKLLGQLKEVQADKEQSEABLQVAQQENHHL
			NLDLKEAKSWOEEQSAQAQRLKDKVAQMKDTLGQAQQRVAELEP
	1	Ī	1 ************************************

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
j	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
. 1	residue of	amino acid	Codon, /=possible nucleotide deletion,
'	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	<u></u>	\=possible nucleotide insertion)
			LKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIAELHRSR
		£ .	LEVAEVNGKLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILK
1		l	LSAETLRLEKAVOEERTONOVFKTELAREKDSSLVQLSESKREB
		1	TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
l l		1	EDATTEDERAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETQ
	Į.	1	ASLLIGLE
_ 1		J	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
7090	33	1775	SVCWEDRYLKARMEESPLSKAPSRGGVNFLWVAKTITFNTKVEC
		1	HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG
; !	!	l	SPIHTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE
,	ì	1	PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM
1	1		OLKLOLEGOVTELRSRVQELERALATARQEHTELMEQYKGISRS
1	1		HGEITEERDILSRQQGDHVARILELEDDIQTISEKVLTKEVELD
1 1			RLRDTVKALTREQEKLLGQLKEVQADKEQSEAELQVAQQENHHL
i			NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVAELEP
1	1	}	NLDLKEAKSWQEEQSAQAQKIKDKVAQMRDIIGQAQQXVASHEF LKBQLRGAQELAASSQQKATLLGEELASAAAARDRTIAELHRSR
	1		LKKQLKGAQELAASSQQKATLLGEELASAAAARDRITAEDRKSK
1	Į	ł	LEVAEVNGKLAELGLHLKEEKCOWSKERAGLLQSVEAEKDKILK
}	<u></u>	i	LSAEILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKREL
	ì		TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
1	l .	1	EDATTEDEBAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETQ
i	}	1	ASLLLGLE
	186	1076	EGMLTREHRCGRSEEQELEPWPSPKKARSGRWLRNGFKRKMEEP
7091	186	1 10/6	EEPADSGQSLVPVYIYSPEYVSMCDSLAKIPKRASMVHSLIEAY
	ļ	1	ALHKQMRIVKPKVASMEEMATFHTDAYLQHLQKVSQEGDDDHPD
ł	1	1	ALHKOMRIVKPAVASMEEMAIPHIDAIDQIIDQXVSQBSSSSIID
1	1	İ	SIEYGLGYDCPATEGIFDYAAAIGGATITAAQCLIDGMCKVAIN
1	1	1	WSGGWHHAKKDEASGFCYLNDAVLGILRLRRKFERILYVDLDLH
i	•		HGDGVEDAFSFTSKVMTVSLHKFSPGFFPGTGDVSDVGLGKGRY
1	j	1	YSVNVPIQDGIQDEKYYQICERYEPPAPNPGL
7092	522	809	KQGINEDQEESQKPRLGEGCEPISKRQMKKLIKQKQWEEQRELR
,032	, 522	}	KOKRKEKRKKKLERQCOMEPNSDGHDRKRVRRDVVHSTLRLII
1	1		DCSFDXLM
	1		NFGVSGVELAQQASMVRMSFVIAACQLVLGLLMTSLTESSIQNS
7093	454	655	
1	<u> </u>	_ }	ECPQLCVCEIRPWFTPQSTYREA
7094	2	508	FVRSMHWGVGFASSRPCVVDLSWNQSISFFGWWAGSEEPFSFYG
1	j	J	DIIAPPLQDYGGIMAGLGSDPWWKKTLYLTGGALLAAAAYLLHE
1			LLVIRKQQEIDSKDAIILHQFARPNNGVPSLSPFCLKMETYLRM
Į.		1	ADLPYQNYFGGKLSAQGKMPWIEYNHEKVSGTEFII
7095	1	411	IASSLPKMASLLOSDRVLYLVQGEKKVRAPLSQLYFCRYCSELR
1035	1	1	SLECVSHEVDSHYCPSCLENMPSAEAKLKKNRCANCFDCPGCMH
1	1	1	TLSTRATSISTQLPDDPAKTTMKKAYYLACGFCRWTSRDVGMAD
	1		
1		j	
			KSVGE
7096	224	2067	KSVGE ETRSLAVOEKPSOAGRRRSSRISFAGALFLTRFLLQELLLNNFC
7096	224	2067	KSVGE ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLLNNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR
7096	224	2067	KSVGE ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLLNNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE
7096	224	2067	KSVGE ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLLNNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE OREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS
7096	224	2067	KSVGE ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLLNNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE OREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS
7096	224	2067	KSVGE ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLINNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQQQF
7096	224	2067	KSVGE ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLINNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGGF LYAYRCVLGPHQDPPREAELLLQNLQSKGPRDCVVLMAAAGHPA
7096	224	2067	KSVGE ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLINNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF LYAYRCVLGPHQDPPBEAELLLQNLQSKGPRDCVVLMAAAGHFA GAIFOGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN
7096	224	2067	KSVGE ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLINNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF LYAYRCVLGPHQDPPEEAELLLQNLQSKGPRDCVVLMAAAGHFA GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF
7096	224	2067	KSVGE ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLINNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF LYAYRCVLGPHQDPPEEAELLLQNLQSKGPRDCVVLMAAAGHFA GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF FGGKGAPLORGDPRLWDIPLATRRPTFQELQRVLHKLTTLHVYE
7096	224	2067	KSVGE ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLINNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF LYAYRCVLGPHQDPPEEAELLLQNLQSKGPRDCVVLMAAAGHFA GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF FGGKGAPLQRGDPRLWDIPLATRRPTFQELQRVLHKLTTLHVYE EDPREAVELHSPQTHWKTVREERKKPTEEEIRKICRDEKEALGQ
7096	224	2067	KSVGE ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLINNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF LYAYRCVLGPHQDPPEEAELLLQNLQSKGPRDCVVLMAAAGHFA GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN LRRYNBATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF FGGKGAPLQRGDPRLWDIPLATRRPTFQELQRVLHKLTTLHVYE EDPREAVRLHSPQTHWKTVREERKKPTEEEIRKICRDEKEALGQ NEESPKOGSGSEGEDGFQVELELVELTVGTLDLCESEVLPKRRR
7096	224	2067	KSVGE ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLINNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF LYAYRCVLGPHQDPPEEAELLLQNLQSKGPRDCVVLMAAAGHFA GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF FGGKGAPLORGPPRLWDIPLATRRPTFQELQRVLHKLTTLHVYE EDPREAVRLHSPQTHWKTVREERKKPTEEEIRKICRDEKEALGO NEESPKQGSGSEGEDGFQVELELVELTVGTLDLCESEVLPKRRR PKPNKKEKSRDOFAGAHRTILOOTOEEEPSTQSSQAVAAPLGPL
7096	224	2067	KSVGE ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLINNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF LYAYRCVLGPHQDPPEEAELLLQNLQSKGPRDCVVLMAAAGHFA GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF FGGKGAPLORGPPRLWDIPLATRRPTFQELQRVLHKLTTLHVYE EDPREAVRLHSPQTHWKTVREERKKPTEEEIRKICRDEKEALGO NEESPKQGSGSEGEDGFQVELELVELTVGTLDLCESEVLPKRRR PKPNKKEKSRDOFAGAHRTILOOTOEEEPSTQSSQAVAAPLGPL
7096	224	2067	KSVGE ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLINNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF LYAYRCVLGPHQDPPEEAELLLQNLQSKGPRDCVVLMAAAGHFA GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF FGGKGAPLQRGDPRLWDIPLATRRPTFQELQRVLHKLTTLHVYE EDPREAVKLHSPQTHWKTVREERKKPTEEEIRKICRDEKEALGQ NEESPKQGSGSEGEDGFQVELELVELTVGTLDLCESEVLPKRRR RKRNKKEKSRDQEAGAHRTLLQQTQEEEPSTQSSQAVAAPLGPL LDEAKAPGOPELWNALLAACRAGDVGVLKLQLAPSPADPRVLSL
			KSVGE ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLINNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQEPMDISEKLFCSTCDQTFQNHQE QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF LYAYRCVLGPHQDPPEEAELLLQNLQSKGPRDCVVLMAAAGHFA GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF FGGKGAPLQRGDPRLWDIPLATRRPTFQELQRVLHKLITTLHVYE EDPREAVRLHSPQTHWKTVREERKKPTEEEIRKICRDEKEALGQ NEESPKQGSGSEGEDGFQVELELVELTVGTLDLCESEVLPKRRR RKRNKKEKSRDQEAGAHRTLLQQTQEEEPSTQSSQAVAAPLGPL LDEAKAPGQPELWNALLAACRAGDVGVLKLQLAPSPADPRVLSL LSAPLGSGGFTLLHAAAAAGRGSVVRLILLEAGADPTVQCQDH
7096	224	2067	KSVGE ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLINNFC SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF LYAYRCVLGPHQDPPEEAELLLQNLQSKGPRDCVVLMAAAGHFA GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF FGGKGAPLQRGDPRLWDIPLATRRPTFQELQRVLHKLTTLHVYE EDPREAVKLHSPQTHWKTVREERKKPTEEEIRKICRDEKEALGQ NEESPKQGSGSEGEDGFQVELELVELTVGTLDLCESEVLPKRRR RKRNKKEKSRDQEAGAHRTLLQQTQEEEPSTQSSQAVAAPLGPL LDEAKAPGOPELWNALLAACRAGDVGVLKLQLAPSPADPRVLSL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
{	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
1	sequence		\=possible nucleotide insertion)
			SNSFSRLHCRNANEDWMSALCPRLNDVPLHHLSIPGSHDTMTYC
	-	i .	LNKKSPISHEESRLLQLLNKALPCITRPVVLKWSVTQALDVTEQ
ļ	1		LDAGVRYLDLRIAHMLEGSEKNLHFVHMVYTTALVEDTLTEISE
	i		WLERHPREVVILACRNFEGLSEDLHEYLVACIKNIFGDMLCPRG
Į.	1	}	EVPTLRQLWSRGQQVIVSYEDESSLRRHHELWPGVPYWWGNRVK
	L		TEALIRYLETMKSCGR
7098	82	956	SSFLKRCRKVLGCWGIPSEQSLFSTLEEPRDKEIDNYCVMRLQT
		ļ	EARSGFWAPNRFPVNICRMTAVDGDRGGSSRETCRCHFHPSLEA
1]	LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLPSKPLLG
		İ	LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFLGLWLVL
j	Į		LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAEGRTRGR
	1		AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPVGCGCPF
7099	992		LGLALRLVYYHWLHPSCCWKPDPDQVD
1 '''	334	210	LFRLAPGFLRSLARQGYHQIWAFPFLPSGATATWPAASRSRSLA
1			ARSLPRSPARPGPNDALLGEHDFRGOGVRAQRFRFSEEPGPGAD GAVLEVHVPQIGAGVSLPGILAAKCGAEVILSDSSELPHCLEVC
			ROSCOMNNLPHLQVVGLTWGHISWDLLALPPQDIILASDVFFEP
1			EDFEDILATIYFLMHKNPKVQLWSTYQVRSADWSLEALLYKWDM
			KCVHIPLESFDADKEDIAESTLPGRHTVEMLVISFAKDSL
7100	205	671	ANGGFWEAAPGSEVSLPLWVPTASHSKTTALGIGSAPPPHLSVL
1]	V.2	FLFSFPPQLGDPLEAFPVFKKYDRNGLNVSIECKRVSGLEPATV
1			DWAFDLTKTNMQTMYEQSEWGWKDREKREEMTDDRAWYLIAWEN
1			SSVPVAFSHFRFDVERGDEVLYW
7101	2	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD
1			VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEEITIPADVTP
1			ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDK
			VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR
7102	2	503	WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRAADMKKD
1	}		VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEEITIPADVTP
1	1		ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDK
7103			VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR
/103	119	438	GSQSSVAVNIRSGTDEESMDLMNGQASSVNIAATASEKSSSES
1	ì	•	LSDKGSELKKSFDAVVFDVLKVTPBEYAGQITLMDVPVFKAIQP
7104	1670	795	DELSSCGWNKKEKYSSAP
,104	10/0	135	RLWEHRSVSAGASGWGLSSPGCLLLHPSLPEEBRVDILINNAGV
1]		MRCPHWITEDGFEMQFGVNHLGEAWAGAAPWVQAILPRRPPKVL
			GF*V*VKSDLFIILNPGHFLLTNLLLDKLKASAPSRIINLSSLA HVAGHIDFDDLNWQTRKYNTKAAYCOS\KLAIVLFTKELSRRLO
}	}		GSGVTVNALHPGVARTELGRHTGIHGSTFLQHHN\WAHLLAAWS
			KSPRSWPAPAQHNTLAVAEELA\VISGKYFDGLKOKAPAPEAED
1	,		EEVARRLWAESARLVGLEAPSVREQPLPR
7105	765	143	GQMCRRPSPKSTSCLSMTCDLP/RGLQDPQCLALFRVAVDKHQA
1] - 1	_ 	LLKAAMSGGGVDRHLFALYIVSRFLHLQSPFLTQVHSEQWOLST
			SQIPVQQMHLFDVHNYPDYVSSGGGFGPADDHGYGVSYIFMGDG
1			MITFHISSKKSSTKTDSHRLGQHIEDALLDVASLFQAGQHFKRR
j l	[FRGSGKENSRHRCGFLSRQTGASKASMTSTDF
7106	14	1064	GLQAGHPHPRSASRIPEADTH\YSKLQRAFDSIVNKDHKRMFGT
1	[,	YFRVGFFGSKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGQCF
1			GAEFVEVIKDSTPVDKTKLDPNKAYIQITFVEPYFDEYEMKDRV
			TYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTTMHAF
1 !			PYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINQEPPD
			AKMLQMVLQGSVGATVNQGPLEVAQVFLAEIPADPKLYRHHNKL
}			RLCFKEFIMRCGEAVEKNKRLITADQREYQQELKKNYNKLKENL
	L		RPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGS
7107	1145	591	*I*WLQTGKKK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, P=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
j	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ţ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1		sequence	\=possible nucleotide insertion)
	sequence		VKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLNSSTFYIAF
7108	1	942	FLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLCMQMGIIMVLK
Į.	1	1	FLGRFTGHPGAYLRLINKWRLEECHPSGCDIDDCHQMGIIMVDK
1	\		QTWNNFMELGYPLIQNWWTRRKVRQEHGPERKISFPQWEKDYNL
ì		[QPMNAYGLFDEYLEMILQFGFTTIFVAAFPLAPLLALLNNIIEI
		Į.	RLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITNAFVI
ł	,	,	AITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYVNASLSVFRIS
(İ	1	DFENRSEPESDGSEFSGTPLKYCRYRDYRDPPHSLVPYGYTLQF
i		ĺ	WHYLAW
	 	102	WDQRKRNSLVPGPAHGPAQEEPWEKKESLGAAQEALSIQLQPKE
7109	964	102	TOPPPKSEQVYLHFLSVVTEDGPEPKDKGSLPQPPITEVESQVF
1	1	}	SEKLATDISTFEATSEGTLELQQRNPKAERLRWSPAQEESFRQM
1	1		VVIHKEIPTGKKDHECSECGKTFIYNSHLVVHQRVHSGEKPYKC
	i	1	VVIHKEIPTGKKDHECSECGKIFIINSHEVVNQRVNSGKPIKC
1		1	SDCGKTFKQSSNLGQHQRIHTGEKPFECNECGKAFRWGAHLVQH
i	1	1	QRIHSGEKPYECNECGKAFSQSSYLSQHRRIHSGEKPFICKECG
1	1	1	KAYGWCSELIRHRRVHARKEPSH
7110	96	697	RLDNFSGFLVEVTKEERHIVKPLYDRYRLVKQMLTRASITPVLG
	į	i	SPSTKRRGQMLQPIIEGETAHFFEEIKEEEEDGVNLSSELGDML
			KTAVOVOSSLKNSESDVEENQEKLALDLRLSSSRAASMPELLEQ
1	1		LWKARAEKKKLRKTLREFEEAFYQQNGRNAQKEDRVPVLEEYRE
1		Į.	YKKIKAKLRLLEVLISKQDSSKSI
 22.2.	1 2	414	GSGLYRGPTPGGQCIWKPNSMPPDHERNFGFTQFALELNELTAE
7111	2	3.13	LKRSLPSTDTRLRPDQRYLEEGNIQAAEAQKRRIEQLQRDRRKV
i	l l	ì	MEENNIVHQARFFRRQTDSSGKEWWVTNNTYWRLRAEPGYGNMD
1	ļ	ì	GAVLW
L		<u> </u>	PRCFPVADRGRLIGGLPDVVTIMEGKTLNLTCTVFGNPDPEVIW
7112	103	495	PRCKPVADRGRLIGGLPDVVIIINGRIGGRDCCVVCINIVN
1	1	Į.	FKNDQDIQLSEHFSVKVBQAKYVSMTIKGVTSEDSGKYSINIKN
1	}		KYGGEKIDVTVSVYKHGEKIPDMAPPQQAKPKLIPASASAAGQ
7113	1	824	KCLRQAWHEAPSSLAFTRWCSREERAEGGGNLHRSITRDPKPPG
1	1	1	LRPSQRPMDDKKKKRSPKPCLAQPAQAPGTLRRVPVPTSHSGSL
1	1	1	ALGLPHLPSPKQRAKFKRVGKEKCRPVLAGGGSGSAGTPLQHSF
· F	ì	l	LTEVTDVYEMEGGLLNLLNDFHSGRLQAFGKECSFEQLEHVREM
İ		1	QEKLARLHFSLDVCGEEEDDEEEEDGVTEGLPEEQKKTMADRNL
1	1	1	DQLLSNLGSCLGALVPGGMRGGEGTYSQSHSWALGEKVGVHGSK
1	1	1	SSGPLNLPRR
1-833	3	1492	VWEVDEQIDHYKESQDKFLWQAAFIGKETLKDESGQECKICRKI
7114	1 3	1434	IYLNTDFVSVKQRLPKYYSWERCSKHHLNFLGQNRSYVRKKDDG
1			CKAYWKVCLHYNLHKAQPAERFFDPNQRGKALHQKQALRKSQRS
ı			QTGEKLYKCTECGKVFIQKANLVVHQRTHTGEKPYECCECAKAF
1	1		GIGENTIKCIRCEKA E INVANTA ANDATUTORUL I RICORCANAL
1			SQKSTLIAHQRTHTGEKPYECSECGKTFIQKSTLIKHQRTHTGE
	1		KPFVCDKCPKAPKSSYHLIRHEKTHIRQAFYKGIKCTTSSLIYQ
1		1	RIHTSEKPQCSEHGKASDEKPSPTKHWRTHTKENIYECSKCGKS
1			FRGKSHLSVHQRIHTGEKPYECSICGKTFSGKSHLSVHHRTHTG
1	I	1	EKPYECRRCGKAFGEKSTLIVHQRMHTGEKPYKCNECGKAFSEK
1			SPLIKHORIHTGERPYECTDCKKAFSRKSTLIKHQRIHTGEKPY
1			KCSECGKAFSVKSTLIVHHRTHTGEKPYECRDCGKAFSGKSTLI
1	1		KHORSHTGDKNL
		047	NAAHGYNWGLWCMYIIPPQDWLDRGDESAPIRTPAMIGCSPVVD
7115	1	947	REYFGDIGLLDPGMEVYGGENVKLGMRVWQCGGSMEVLPCSRVA
1	!	Į.	REYFGDIGLLDPGMEVYGGENVKBBRVWQCGGSHEVDFCSKVA HIERTRKPYNNDIDYYAKRNALRAAEVWMDDFKSHVYMAWNIPM
1	ĺ	1	HTEKLIKKANNDIDA JAKKMATKAWE AMINDE WOU A LIMMITEN
- {			SNPGVDFGDVSERLALRQRLKCRSFKWYLENVYPEMRVYNNTLT
l			YGEVRNSKASAYCLDQGAEDGDRAILYPCHGMSSQLVRYSADGL
1	1	1	LQLGPLGSTAFLPDSKCLVDDGTGRMPTLKKCEDVARPTQRLWD
1	4	1	FTQSGPIVSRATGRCLEVEMSKDANFGLRLVVQRCSGQKWMIRN
1		1	NTKHARH
7116	866	95	RVRMRRNAEVIEEKLSMKSWAKFRPGEPWKGYPNIDPETDPYVT
1 /118	1	1	PGSVINNLSINTVREVDHLRDRNSGSSSSLNTTLPSTSAWSSIR
	ŀ	1	}

SEQ	I fired at ad	Predicted end	
ID	Predicted beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
[residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
j	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence	0044000	\=possible nucleotide insertion)
			ASNYNVPLSSTAQSTSARNSDSKLTWSPGSVTNTSLAHELMKVP
l l	<u> </u>		LPPKNITAPSRPPPGLTGQKPPLSTWDNSPLRIGGGWGNSDARY
i	1		TPGSSWGESSSGRITNWLVLKNLTPQIDGSTLRTLCMQHGPLIT
1	l .		FHLNLPHGNALVRYSSKEEVVKAQKSLHISDLFLLTL
7117	695	1261	LLISTPGGCHPPPSSIEFTYTGAWGKALPAPHMPCAPGALPOGA
/ / / /	0,5	1201	FVSQAARAIPLLOPSQAAQAEGLSOPARACGALCSLPWPLRNWG
Į.	1		
į	Į		SPILRLPGGLRTPTNDRKTRTRSAMACWARAQWDTLGPLKLSHR
1	1		GKVCLRHPRPTGVRGGPGAAGRQGGMGTRRRGTFTSGARDPGGL
7118	4.6	3,063	RVKHRCQPTGHLP
1 '118	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE
	1		ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR
j	1		LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI
{	†		LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD
I	l .		NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT
ł			YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG
			MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS
ł	1		ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF
[1		SEVPTSVFGEKLREQUEERLSFYETGEIPRKNLDVMKRAMVQAE
j	J		EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE
	}		
į			EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPBEAGHRSGSKKKRK
ŀ	1		FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED
J			
7119	49	1963	
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELMEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLITDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLITDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGRKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKKSPSKEEL
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGRKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE
7119	1991	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELMEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLITDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGBKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLITDLSACKAQLGLGHSYSRAKVKFNVRRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEBTVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVRRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSPSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQQQGP
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQQGGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELMEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVBERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLITDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSPSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERKFGPLGFNIPY
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLITDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGBKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RAEAMMSSIERGKWFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERKKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLITDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQQQGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERKKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQPIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE BMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSPSKEEL MSSDLEETAGSTSIPKRKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQQGGP RAEAMMRSSIERGKWVFFONCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKKK FSKEEPVSSGPEEAAGKSSSKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKPPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNIGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELMEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSPSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSGGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLKKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGBKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYHGLFLEGARWDPEAFQLAESQPKELYTEM
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNIGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELMEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSGGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE
			PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLITDLSACKAQLGLGHSYSRAKVKFNVRRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTPIGRAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGBKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP RAEAMMRSSIERGKWFFQNCHLAPSWMPALERLIEHINDDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLKALKGLVVMSSQLELMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPRELYTEM AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI
7120	1991	64	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLITDLSACKAQLGLGHSYSRAKVKFNVRRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGBKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSPSKEEL MSSDLEETAGSTSIPKRKKSTPKEBTVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQQQGP RAEAMMRSSIERGKWVFFONCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLEIMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQDWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWILIPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY
7120	1991	64	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELMEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSKKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQQQGP RAEAMMRSSIERGKWVFFQNCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLEMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLGARWDEAFGLAESQPRELYTEM AVENITYPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY RPLRPWVLSLGSMVGLMTYGRQFQSLDTTMRRLIPPFREASAK LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV
7120	1991	64	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCQTGGVIAEI LRGVRLHFHNLVKGLITDLSACKAQLGLGHSYSRAKVKFNVRRVD NMIIQSISLLDQLDKDINTFSMRVREWYGYHPPELVKIINDNAT YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF SEVPTSVFGBKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSPSKEEL MSSDLEETAGSTSIPKRKKSTPKEBTVNDPEEAGHRSGSKKKRK FSKEEPVSSGPEEAAGKSSSKKKKFHKASQED QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQQQGP RAEAMMRSSIERGKWVFFONCHLAPSWMPALERLIEHINPDKVH RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS LGEDFLNSCHKVMEFKSLLSLCLFHGNALERRKFGPLGFNIPY EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK SSSAGSQGREEIVEDVTQNILLKVPEPINLQWVMAKYPVLYEES MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLEIMA ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQDWIQDG IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM AVIWILIPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI AVEIPTHQPQRHWIKRGVALICALDY

SEQ Predicted predicted end nucleotide (A=Alanine, C=Cysteine, D=Aspartic Acid, Glutamic Acid, F=Phenylalanine, G=Glycin (Corresponding to first amino acid residue of amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, Glutamic Acid, F=Phenylalanine, G=Glycin H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=S (Codon, /=possible nucleotide deletion, \qu	E= e,
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residue of amino acid w=Tryptophan, Y=Tyrosine, X=Unknown, *=S Codon, /=possible nucleotide deletion, \ sequence = ETRQE	top
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sequence \=possible nucleotide insertion) ETROE 7122 2 546 RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFRE	1
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MSKIQVSERPLMFLLDTPGVLAPRIESVETGLKLALCGTV	
VGBETMADYLLYTLNKHQRFGYVQHYGLGSACDNVERVLI	CSVAV
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7126 1 733 CRDMAAFIVPSPARRCSQKGSLGHLPTQPWLWAAMSPRG	QERGT
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PSPVLPSWLLEGPPPWLSIISDSGTQRPSPRRCPARPSP	
WRGGRIASAEASST*TPGSGSRARSGRRSPGSRRRSASA	PSPTP
PTDACA*SCVARPAGSRSSRPAAA	
7127 1311 277 GLPAMCST*KAGYYEETEGDCIPKDR*IEKRPFKEI*RR	
AKQKQI+S+NSQKIGASEIDRGRKEADCSDAPAAARIGA	VSVFR
RSTQEARVSPRSNAKSANLRAVRAD*WEHFVLLFHTPEQ	FLAEC
ICRST**K*WHQLC*PLSSL*TGLKRKLLL*VLFRI*WL	KDCDV
*FCQKIFATNFCNWQNLIQ*EE*KPVEYSVEN*HIMNLL	TbW+r
CQSSLRDQTIVTWRM*RNYSMFRINMISSL*DGSIHIPL	
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LTYFODERHPYRVEYADCVDKLEKELVSKYRQQFEELYK	TEAPT
WETHGNLMTERQVSRWFVQCLREQSMLLEIIFLYYAYFE	MAPSD
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APVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYL	ATOTA
APVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYL SLASGGNDCITSTACMCVYGLLSFVLTSLELHTLGNQQD	LIOU
APVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYL SLASGGNDC:TSTACMCVYGLLSFVLTSLELHTLGNQQD CEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP	LLQLL
APVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYL SLASGGNDCITSTACMCVYGLLSFVLTSLELHTLGNQQD CEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP RALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHED	LLQLL GTLWR
APVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYL SLASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQQD CEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP RALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHED RQTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEY	LLQLL GTLWR SYSSW
APVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYL SLASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQQD CEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP RALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHED RQTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEY TLFTCEIEMLLHVVSTADVIQHCQRVKPIIDLVHKVIST	CLLQLL GTLWR SYSSW DLSIA
APVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYL SLASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQQD CEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP RALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHED RQTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEY TLFTCEIEMLLHVVSTADVIQHCQRVKPIIDLVHKVIST DCLLPITSRIYMLLQRLTTVISPPVDVIASCVNCLTVLA	CLLQLL GTLWR SYSSW DLSIA ARNPA
APVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYL SLASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQQD CEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSP RALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHED RQTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEY TLFTCEIEMLLHVVSTADVIQHCQRVKPIIDLVHKVIST	CLLQLL GTLWR SYSSW DLSIA ARNPA LMNSE

SEQ Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence sequenc	E= , op TPS AEG GAH CLG TQP SQQ NLT DQP YQM LLV LLEG LNV RDQ LEV LPL
NO: nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence	OP TPS AEG GAH CLG TQP SQQ NLT DQP YQM LLV LLEG LNV RDQ LEV LPL
Corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence P=Proline, Q=Glutamine, R=Arginine, R=Gunine amino acid sequence P=Proline, Q=Glutamine, R=Arginine, R=Gunine amino acid sequence P=Proline, Q=Glutamine, R=Arginine, R=Gunine amino acid sequence P=Proline, Q=Glutamine, R=Arginine, R=Gunine amino acid sequence P=Proline, Q=Glutamine, R=Arginine, R=Gunine,	OP TPS AEG GAH CLG TQP SQQ NLT DQP YQM LLV LEG LEG RDQ LEV LPL
Corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence S-Serine, T-Threonine, N-Asparagine, amino acid sequence Codon, /-possible nucleotide deletion, \- possible nucleotide deletion \- possible nucleotide deletion \- possible nucleotide deletion \- possible nucleotide deletion \- possible nucleotide deletion \- possible nucleotide deletion \- possible nucleotide deletion \- possible nucleotide dele	TPS AEG GAH CLG IQP SQQ NLT DQP YQM LLV LEG LNV RDQ LEV LEV LEV
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, amino acid sequence Codon, /=possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide deletion, \possible nucleotide insertion) PSYMKWRYNSHGVREQIGCLILELIHALIMICHETDLHSSI LQFLCICSLAYTEAGGYTVINIMGIGVDTIDMVMAQPRSD QGGGQLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQN GNNLIAVLAKY1YHKHDPALPRLAIQLKRLATVAPMSVYY, NDAAAIRDAFLTRLQSK, INDMRIK\VMIL\EFLITVA\VV GLIELINLEVKDG\SDGSKEFSLGMW\SCLHAV\VWELIU ODRYWCPPLLHRAAIAPLHAQDRRDSAMLVLRTKPKFWN SPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSI LKDTLKKFSIEKRFAYWSGYVKSLAWVAETEGSSCTSLLI LUSAMRMLIITATHADIHTDSVVKRQLFLDVLDGTKAI PASVNCLRLGSMKCTLLLILLRGWKRELGSVDEILGPLTE: VLQADQQLMEKTKAKVFSAFITVUQMKEMKVSDIPQYSQLV CETLQEEVIALFPOQTRRISLAIGSATEDKDSMETDDCSRSR RDGVCVLGHHAARELCEVDEDGDSWLQVTRRLPILPTLLT: SLRMKONLHFTEATLHLILARTQQGATAVAGAGITQST LSVVQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQI LRVNFLPEALDFVGVHQERTLQCLMAVRTVQSLACLERADI LRVNFLPEALDFVGVHQERTLQCLMAVRTVGSLACLERADI LRVNFLPEALDFVGVHQERTLQCLMAVRTVGSLACLERADI LRVNFLPEALDFVGVHQERTLQCLMAVRTVGSLACLERADI EPLTQAVGLSTQAEGTTLKSLLMFTTMENCFYLLISQAMWX ASEQQALHTVQYGLKLKILSKTLARFTTPDVCQTLLDQSI ENNFLPALSFTTPTFDSEVAPSGTLLATVNVALNMIGGLE EPLTQAVGLSTQAEGTTLKSLLMFTMENCFYLLISQAMWX PAVHPRBKGRMKGELSSELTLLSSLSSFYRRGAPSSPATA SPQGKSTSLSKASPESQEDLIQLVQAFVRHMQR FREFREWRRAKYIVDSAFHPDTGEKMILIGRNSAQVPM TGCMMFFYRTTPAVLFWQMINQSFNAVVNYTNRSGDAPLTV MOOSTFIGRANHFFTTTDPRNILLITMEQLESARKIVDFYR PPGLTENELWRAKYIVDSAFHPDTGEKMILIGRNSAQVPM TGCMMFFYRTTPAVLFWQMINQSFNAVVNYTNRSGDAPLTV GTAYVSATTGAVATAIGLNALTHVSPBLIGRFVPFAAVAAA NTPLMRGRELKVGIPTDEMGNALGSANAKQAITQVVVW MAAPGMAIPFFINNTLEKKRFLKRFPKMSAPIQVGLVGFCT TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNM AAPGMAIPFFINNTLEKKRFLKRFFRWRSAPIQVGGFCT TPLCCALFPQKSSMSVTSLEAELGAKIQESHPELRRVYFNM AAPGMAIPFFINNTLEKKRFLKRFFFWRSAPIQUGGFCT TPLCCALFPQKSSMSVTSLEAELGAKIQESHPELRRVYFNM AEPGSSSSSVULNKSMDSINYPSDVGKQQLISLE	TPS AEG GAH CLG IQP SQQ NLT DQP YQM LLV LEG LNV RDQ LEV LEV LEV
residue of amino acid sequence	TPS AEG GAH CLG IQP SQQ NLT DQP YQM LLV LEG LNV RDQ LEV LEV LEV
amino acid sequence Codon, /=possible nucleotide deletion,	TPS AEG GAH CLG IQP SQQ NLT DQP YQM LLV LEG LNV RDQ LEV LEV LEV
- possible nucleotide insertion	AEG GAH CLG IQP SQQ NLT DQP YQM LLV LEG LNV RDQ LEV LEV LPL
PSYHKWRYNSHGVREQIGCILLELHATINLCHETDLHSSI LQFICICSLAYTEAGQTVINIMGIGVDTIDMVMAAQPRSX QGGQLLIKTVKLAFSVTRNVIRLKPPSNVVSFBLEQALSQ GNNLIAVLAKYIYHKIDPALPRLAJQLLKRLATVAPMSVYX NDAAAIRDAFLTRLQSK/IE\DMRIK\VMIL\EFLTVA\VII GLIELFILNLEVKDQ\SDGSKEFSLGMW\SCLHAV\VWELII QDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTRKPKFWII SPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSI LKDTLKKFSIEKRFAYWGGVKSLAVHVAETEGSSCTSLLLI LVSAWRMILIITATTHADIMHILTDSVVRRQLFLDVLDGTKAI PASVNCLRLGSMKCTLLILLRQWKRELGSVDEILGELTEI VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLV CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRI RDGVCVLGIHLAKELGEVDEDGDSWLQVTRRLPILTPILTT SLRMKQNLHFTEATLHLLTLARTQQGATAVAGAGITQSIC LSVYQLSTNGTAQTPSASRKSLDAPSWEGVYRLSMSLMEQI LRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADD FILQLSNFMKEWHFHLPQLMRDIQVNLGYLCOACTSFLHSH QHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSKQPAI ASSQQALHTVQYGLKKILSKTLAALRHFTPDVCQILLDQSI EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELI EYLTQAVGLSTOAEGTRILKSLLMFTMENCFYLLISQAMRY PAVHPRKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATC SPQGKSTSLSKASPESQEPLIQLVQAFVHMQR PAVHPRKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATC SPQGKSTSLSKASPESQEPLIQLVQAFVHMQR PAVHPRKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATC SPQGKSTSLSKASPESQEPLIQLVQAFVHMQR PROLITEMELWBAKYIYDSAFHDDTGEKMILIGRMSAQVPM TGCMMTFYTTPAVLFWQMINQSFNAVNVNYTNSGDAPLT GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAF NIPLMRQRELKVGIPVTDENGRLGESANANAQAITQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFPMMSDFIQVGLUSGFG TPLCCALFPQKSSMSVTSLEABELQAKIQSHPELRRVYFMK MAAPGMAIPPFIMNTLEKKAFLKRFPMMSDFIQVGLUGFUGFGT TPLCCALFPQKSSMSVTSLEABELQAKIGSHPELRRVYFMK 15AKSQPYHRSQSSSSVLINKSMDSINYPSDVGKQQLLSLKI LSAKSQPYHRSQSSSSVLINKSMDSINYPSDVGKQQLLSLK	AEG GAH CLG IQP SQQ NLT DQP YQM LLV LEG LNV RDQ LEV LEV LPL
LOFICICSLAYTEAGOTVINIMGIGVDTIDMYMAAQPRSDA QGQQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQI GRNLIAVLAKYIYHKHDPALPRLAIQLKRLATVAPMSVY NDAAAIRDAFLIRLQSK\IR\DMRIK\VMIL\EFLTVA\VI GLIELFLNLEVKDG\SDGSKEFSLGMW\SCLHAV\VWELII QDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLIRTKPKFWI SPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSI LKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTSLLE LVSAWRMLLIIATTHADIMHLTDSVVRRQLFIDVLDGTKAI PASVNCLRLGSMKCTLLLILRQWKRELGSVDEILGPLTET VLQADQQLMEKTKAKVFSAFITVLQMKERUKVSDIPQYSQLV CETLQEEVIALFDQTHRSLALGSATEDKDSMETDDCSRSRR RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTT SLRMKQNLHFTEATLHLLLTARTQQGATAVAGAGITTQSIC LSYVQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEDG LRYNFLPBALDPVGVHQERTLQCLMAVRTVQSLACLEEADH FILQLSNFMKEWHFHLPQLMMDIQVNLGYLCQACTSFLHSE QHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPA ASSQQALHTVQYGLLKILGKTLAALRHFTPDVCQILLDQSI EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELL EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELL EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQAMRX PAVHPRKKORMKQELSSELSTLLSSLSKYFRGAPSSPATC SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR PAVHPRKKORMKQELSSELSTLLSSLSKYFRGAPSSPATC SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR PAVHPRKORMKQELSSELSTLLSCLSKAVINGYRC PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPM TGCMMTFYRTTPAVLFWQMINQSFNAVVNYTMRSGDAPLTV GTAYVSATTGAVATALGLMALTKHVSPLIGRFVPFAAVAAA NIPLMRQRELKVGIPVTDENGNRLGESANAKQAITQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVSLEG TPLCCALFPQKSSMSVTSLEAELQAKIQSSHPELRRVYFMK 15AKSQPYHRSQSSSSVLTLNKSMDSINYPSDVGKQQLLSLE	AEG GAH CLG IQP SQQ NLT DQP YQM LLV LEG LNV RDQ LEV LEV LPL
QGGGCLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQE GNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYY NDAAAIRDAFLTRLQSK\IE\DMRIK\VMIL\EFLTVA\VI GLIELFLNLEVKDG\SDGSKEFSLGMW\SCLHAV\VWELII QDRYWCPPLHHRAAIAFLHALMQDRRDSAMLVLRTKPKFWI SPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSI LKDTLKKFSIEKRFAYWSGYVKSLAVHVABTEGSSCTSLLE LVSAWRMLLIIATTHADIMHLTDSVVRRQLFILDVLDGTKAI PASVUCRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEI VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLV CETLQEEVIALFDQTRHSLALGSATERKDSMETDDCSRSRI RDGVCVLGIHLAKELCEVDEDGDSWLQVTRRLPILPTLLTI SLRMKQNLHFTEATLHLLLTLARTQQCATAVAGAGITQSIQ LRYNFLPEALDFVGVVGETLQCLNAVRTVQSLACLEEADI FILQLSNRMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSG QHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSKQPAY ASSQQALHTVQYGLKILLSKTLAALRHFTDPVCQILLDQSI EYMFLFALSFTTPTFDSEVAPSFGTLLATVNVALNNLIGELI EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQAMRY PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATC SPQGKSTSLSKASPESQEPLIQLVQAFVRHMOR PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATC SPQGKSTSLSKASPESQEPLIQLVQAFVRHMOR 7129 1 1054 FRRFRWRRLH*AGPASSAGGSPGEASGTMSGELPPNININ WDQSTFIGRANHFFTVTDPRILLITMEQLESARKIVHDYKK PPGLIENELWRARYIYDSAFHPDTGEMMILIGRMSAQVPMM TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTV GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAA NIPLMRQRELKVGIPVTDENGRNLGESANAAKQAITQVVVS GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAA NIPLMRQRELKVGIPVTDENGRNELGESANAAKQAITQVVVS MAAPGMAIPPFIMNTLEKKAPLKRFFWMSAPIQVGLVGFCI TPLCCALFPQKSSMSVYSLEABLQAKIQESHPELRRVYFMK MAAPGMAIPPFINNTLEKKAPLKRFPWSAPIQVGLVGFCI TPLCCALFPQKSSMSVYSLEABLQAKIQESHPELRRVYFMK 15AKSQPYHRSQSSSSVLINKSMDSINYPSDVGKQQLLSLE	GAH CLG IQP SQQ NLT DQP YQM LLV LEG LNV RDQ LEV LPL
GRNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYX NDAAAIRDAFLTRLQSK\IE\DMRIK\VMIL\FITVA\VII GLIELFLALEVKOG\SDGSKEFSLGMM\SCLHAV\VWELII QDRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTKPKFWI SPLFGTLSFPSETSEPSILETCALIMKIICLEIYYVVKGSI LKDTLKKFSIEKRFAYWGGYVKSLAVWIVAETEGSSCTSLLE LVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKAI PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILDGLTEI VLQADQOLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLV CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRI RDGVCVLGLHLAKELCSVDEDCDSNLQVTRRLPILPTLLTI SLKMKONLHFTEATTHLLLTLARTQQGATAVAGAGITQSII LSVYQLSTNGTAQTPSASRKSLDAPSWFGVYRLSMSLMEQII LSVYQLSTNGTAQTPSASRKSLDAPSWFGVYRLSMSLMEQII LSVYQLSTNGTAQTPSASRKSLDAPSWFGVYRLSMSLMEQII LSVYQLSTNGTAQTPSASRKSLDAPSWFGVYRLSMSLMEQII LSVYQLSTNGTAQTPSASRKSLDAPSWFGVYRLSMSLMEQII LSVYQLSTNGTAQTPSASRKSLDAPSWFGVYRLSMSLMEQII LSVYQLSTNGTAQTPSASRKSLDAPSWFGVYRLSMSLMEQII LSVYQLSTNGTAQTPSASRKSLDAPSWFGVYRLSMSLMEQII LSVYQLSTNGTAQTPSASRKSLDAPSWFGVYRLSMSLMEQII LSVYQLSTNGTAQTPSASRKSLDAPSWFGVYRLSMSLMEQII LSVYQLSTNGTAQQVAGRYVQSPSAASAPSSSKQPA ASSQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSII EYNFLFALSFTTPDEVAPSFGTLLATVNALNMLGELI EPLTQAVGLSTQAEGTRILKSLLMFTMENCFYLLISQAMRY PANHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATC SPQGKSTSLSKASPESOEPLIQLVQAPVRHMQR PANHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATC SPQGKSTSLSKASPESOEPLIQLVQAPVRHMQR PPGLTENSLWRARYIYDSAFHPDTGEKMILIGRMSAQVPM WOQSTFIGRANHFFTVTDPRNILLTMEQLESARKIVHDYRC PPGLTENSLWRARYIYDSAFHPDTGEKMILIGRMSAQVPM TGGMMTFYRTTBAVLFWQWINQSFNAVNYTNRSGDAPLTT GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAP NIPLMRQRELKVGIPVTDENGNRLGESANAAKQAITQVVVS GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAP NIPLMRQRELKVGIPVTDENGNRLGESANAAKQAITQVVVS MAAPGMAIPPFIMNTLEKKAFLKFFWMSAPIQVGLVGFCI TPLCCALFPQKSSMSVYSLEABLQAKIGSSPPELRRVYFM MAAPGMAIPPFIMNTLEKKAFLKRFFWMSAPIQVGLVGFCI TPLCCALFPQKSSMSVYSLEABLQAKIGSSPPELRRVYFM 1SAKSQPYHRSQSSSSVLINKSMDSINYPSDVGKQQLLSLE	CLG IQP SQQ NLT DQP YQM LLV LEG LNV RDQ LEV LPL
NDAAAIRDAFLTRLQSK/IE\DMRIK\VMIL\EFLTVA\VI GLIELFINLEVKDG\SDGSKEFSLGMW\SCLHAV/WELI QDRXWCPPLIHRAATAFLHALWQDRRDSAMLVLRTKPKFWI SPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSI LKDTLKKFSIEKRFAYWGGYVKSLAVHVABTEGGSCTSLLE LVSAMRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKAI PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEI VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLV CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRI RDGYCVLGHHLAKELCEVDEDGDSWLQVTRRLPILPTLLTT SLRMKQNLHFTEATHHLLTLARTQQGATAVAGAGITQSIC LSVYQLSTNGTAQTPSASKKSLDAPSWFGYVRLSMSLMEQI LRYMFLPBEALDFVGYHOERTLQCLMAVRTVQSLACLBEADI FILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSF QHYLQNKNGDGLPSAV\QRYPSAASAAPSSSKQPAR ASEQQALHTVQYGLLKILSKTLAARHFTPDVCQILLDQSI EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALIMMLGELI EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQAMRY PAVHPRDKQRMKQELSSELSTLLSSLSRYFRGAPSSPATC SPQGKSTSLSKASFESQEPLIQLVQAFVRHMQR FRRFWRRRLH*AGPASSAGGSPGBASGTMSGELPPNINTR WDQSTFIGRANHFFTVTDPRNILLTINEQLESARKIVHDYMS SPQGKSTSLSKASFPSQEPLIQLVQAFVRHMQR TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTV GTAYVSATTGAVATALGLMALTKHVSPLIGRFVPFAAVAAR NIPLMRQRELKVGIPVTDENGRILGESANAKQATTQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLUGFCI TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFFNA NIPLMRQRELKVGIPVTDENGRILGESANAAKQATTQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLUGFCI TPLCCALFPQKSSMSVTSLEAELQAKIQCSHPELRRVYFINA NIPLMRQRELKVGT PVTDENGRILGESANAAKQATTQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLUGFCI TPLCCALFPQKSSMSVTSLEAELQAKIQCSHPELRRVYFINA NIPLMRQRELKVGT PVTDENGRUGCANAAKQATTQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLUGFCI TPLCCALFPQKSSMSVTSLEAELQAKIQCSHPELRRVYFINA NIPLMRQRELKVGT PVTDENGRORTLGESANAAKQATTQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLUGFCI TPLCCALFPQKSSMSVTSLEAELQAKIQCSHPELRRVYFINA NIPLMRQRELKVGT PVTDENGRORTLGESANAKQATTQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLLSLE 15AKSQPYHRSQSSSVVLINKSMDSINYPSDVGKQQLLSLE	TQP SQQ NLT DQP YQM LLV LEG LNV RDQ LEV LEV
GLIELFLNLEVKDG\SDGSKEFSLGMW\SCLHAV/VWELII QDRYWCPPLLHRAAIAFLHALWQDRRDSAMIVLRIKPKFWI SPLFGTLSPPSGTSEPSILETCALIMKIICLEIYVVVKGSI LKDTLKKFSIEKRFAYWSGYVKSLAVHVABTEGSSCTSLLE LVSAWRMLLIIATTHADIMHLTDSVVRQLFLDVLDGTKAI PASVNCRLGSMKCTLLLILRQWKRELGSVDEILGPLTEI VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLI CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRI RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTT SLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSIC LSVYQLSTNGTAQTPSASRKSLDAPSWFGVYRLSMSLMEQI LRYMFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADD FILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSE QHYLQNKNGGLPSAV\AQRV\QRPPSAASAAPSSKQPAS ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSI EYNELFALSFTTPTFDSEVAPSFGTLLATVNVALNMLIGELI EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQAMRY PAVHPRDKQMKQELSSELSTLLSSLSRYFRRGAPSSPATG SPQGKSTSLSKASPESGEPLIQLVQAFVRHMQR 7129 1 1054 FRFFRWRRLH+AGPASSAGGSPGASGTMSGELPPNINIT WDOSTFIGRANHFFTVTDPRNILLITNEQLESARKIVHDYRC PPGLTENELWRAKYIYDSAFHPDTGEKNILIGRMSAQVING TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTV GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAF NIPLMRQRELKVGIPVTDENGRRLGESANAAKQAITQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCI TPLCCALFFQKSSMSVTSLEAELQAKIQESHPELRRVYFNK 7130 2 780 HEVPSLQTSDFGSVQRCSVVVSQPNKENWCQDHLYNSIG	SQQ NLT DQP YQM LLV LEG LNV RDQ LEV LPL
QDRYWCPPLHRRAIAFLHALWQDRRDSAMLVLRTKPKFW SPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSI LKDTLKKFSIERFAYWSGYVKSLAVHVABTEGSSCTSLLEI LVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKAI PASVNCLRLGSMKCTLLLILLRGWKRELGSVDEILGPLTEI VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLV CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRR RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTT SLRMKQNLHFTEATLHLLTLARTQQGATAVAGAGITQSIC LSVYQLSTNGTAQTPSASRKSLDAPSWFGVYRLSNSLMEQD LRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADD FILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSR QHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPAV ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSI EYNFLFALSFTTPTFDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTFDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTFDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTFDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTFDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTFDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTFDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPTDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPTDSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPTPSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPTPSEVAPSFGTLLATUNVALNMLGELI EYNFLFALSFTTPTTPTPSEVAPSAAPSFGTLATUNVALNMLGELI EYNFLFALSFTTPTTPTPSEVAPSAAPSFGTLATUNVALNMLGELI EYNFLFALSFTTPTTPTPTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT	NLT DQP YQM LLV LEG LNV RDQ LEV LPL
SPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSI LKDTLKKFSIERRFAYWSGYVKSLAVHVABTEGSSCTSLLEI LVSAMMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKAI PASVNCURLGSMKCTLLLILIRQWKEELGSVDEILGPLTEI VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLV CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRK RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTT SLRMKQNLHFTEATLHLLTLARTQQGATAVAGAGITQSIG LSYYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQI LRYNFLPBALDFVQHQERTLQCLNAVRTVQSLACLEEADI FILQLSNFMKEWHFHLPQLMRDIQVMLGYLCQACTSFLHSE QHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSKQPAF ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSI EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELL EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQAMRY PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATG SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATG SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR FRRFRWRRLH+AGPASSAGGSFGEASGTMSGELPPNINIF WDQSTFIGRANHFFTVTDFRNILLINEQLESARKIVHDYRG PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPM TGCMMTFYRTTPAVLFWQWINQSFRAVVNYTNRSGDAPLT GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAF NIPLMRQRELKVGIPVTDENGNRLGESANAARQAITQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCI TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNM AAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCI TPLCCALFPQKSSMSVTSLEABLQAKIQESHPELRRVYFNM 1SAKSQPYHRSQSSSSVLINKSMOSINYPSDVGKQQLLSLE	DQP YQM LLV LEG LNV RDQ LEV LPL
LKDTLKKFSIEKRFAYWSGYVKSLAVHVABTEGSSCTSLLI LVSAMRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKAI PASVNCLRLGSMKCTLLLILRQWKRELGSVDEILGPLTEI VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLV CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRI RDGVCVLGLHLAKELCEVDEDGDSWLQVTRLPILPTLLTT SLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSIC LSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQI LRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADI FILQLSNFMKEWHFLPQLMRDIQVNLGYLCQACTSFLHSI QHYLQNKNGGDLSAV\AQDV\QRPPSAASAAPSSSKQPAR ASEQQALHTVQVGLLKILSKTLAALRHFTPDVCQILLDQSI EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELI EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQAMRY PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATC SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR 7129 1 1054 FRRFRWRRLH*AGPASSAGGSFGEASGTMSGELPPNINIY WDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRC PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMN TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTV GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAA NIPLMRQRELKVGIPVTDENGNRLGESANAAKQAITQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCI TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNK TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNK 1SAKSQPYHRSQSSSVULNKSMDSINYPSDVGKQQLLSLE	YQM LLV LEG LNV RDQ LEV LPL
LVSAWRMLLIIATTHADIMHLTDSVVRRQLFLDVLDGTKAI PASVNCLRLGSMKCTLLLILLROWKRELGSVDEILGPLTEI VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLV CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRI RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTT SLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSII LSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQI LRYNFLPEALDFVGYHQERTLQCLNAVRTVQSLACLEEADH FILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSEI QHYLQNKNGDGLPSAV\AQRV\QRPPSASAAPSSSKQPAN ASSQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSI EYNFLFALSFTTPTTDSEVAPSFGTLLATVNVALNMLGELI EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQAMRY PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATC SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATC SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR PFRFFRWRRRLH*AGPASSAGGSFGEASGTMSGELPPNININI WDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRC PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPM TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLT GTAYVSATTGAVATALGLNALTKHVSPLIGRPVPFAAVAAA NIPLMRQRELKVGIPVTDENGRRLGESANAAKQAITQVVVS MAAPGMAIPPFINNTLEKKAFLKRFPWMSAPIQVGLVGFCI TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNG TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNG ISAKSQPYHRSQSSSVLINKSMDSINYPSDVGKQQLLSLE	LLV LEG LNV RDQ LEV LPL
PASVNCLRLGSMKCTLLILLRQWKRELGSVDEILGPLTET VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLV CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRI RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILDTLTT SLRMKQNLHFTEATLHLLTLARTQQGATAVAGAGITQSTC LSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQI LRYNFLPEALDFVGVHQBRTLQCLNAVRTVQSLACLEEADD FILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSE QHYLQNKNGGGLPSAV\AQRV\QRPPSAASAAPSSSKQPA ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLQSI EYNFLFALSFTTPTFDSEVAPSFGTLLATUNVALNMLGELI EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQAMRY PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATC SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR 7129 1 1054 FRRFRWRRLH*AGPASSAGGSPGEASGTMSGELPPNINIF WDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRC PPGLTENELWRAKYIYDSAFHPDTGEKNILIGRMSAQVPM TGCMMTYRTTPAVLFWQWINQSFNAVVYTNRSGDAPLTV GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAR NIPLMRQRELKVGIPVTDENGNRLGESANAAKQAITQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFFWMSAPIQVGLVGFCI TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNK TGLCMTTTATATATATATATATATATATATATATATATATATA	LEG LNV RDQ LEV LPL
VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLV CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRI RDGVCVLGIHLAKELCEVDEDGDSWLQVTRRLPILPTLTT SLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSIG LSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQI LRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADH FILQLSNFNKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSE QHYLQNKNGDGLPSAV\AQRV\QRPPSASAAPSSSKQPAX ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSI EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELI EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQANRY PAVHPRDKQRMKQELSSELSTLLSSLSRYFRGAPSSPATO SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR 7129 1 1054 FRRFRWRRLH*AGPASSAGGSFGEASGTMSGELPPNINIR WDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRC PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMN TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTV GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAF NIPLMRQRELKVGIPVTDENGNRLGESANAAKQAITQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCI TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNK 7130 2 780 HEVPSLQTSDPLPGSVQRCSVVVSQPNKENWCQDHLYNSIG	LNV RDQ LEV LPL
CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRI RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTT SLRMKQNLHFTEATLHLLTLARTQQGATAVAGAGITQSIC LSYYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQI LSYYGLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQI LSYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADH FILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSF QHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPAF ASSEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSI EYNFLFALSFTTPTTDSEVAPSFGTLLATVNVALNMLGELL EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQAMRY PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATC SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR 7129 1 1054 FRRFRWRRLH*AGPASSAGGSFGEASGTMSGELPPNINIF WDQSTFIRSHMAKYIYDSAFHPDTGEKMILIGRMSAQVPMN TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTV GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAF NIPLMRQRELKVGIPVTDENGNRLGESANAAKQAITQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCI TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNK 7130 2 780 HEVPSLQTSDPLPGSVQRCSVVVSQPNKENWCQDHLYNSLG ISAKSQPYHRSQSSSVLINKSMDSINYPSDVGKQQLLSLH	RDQ LEV LPL
RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTT SLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSIG LSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQI LRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADH FILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSF GHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPAF ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSI EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELI EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQAMRY PAVHPRDKQRMKQELSSELSTLLSSLSRYFRGAPSSPATC SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR 7129 1 1054 FRFFRWRRRLH+AGPASSAGGSFGEASGTMSGELPPNINIF WDQSTFIGRANHFFTVTDPRNILLITNEQLESARKIVHDYRC PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMN TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTV GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAF NIPLMRQRELKVGIPVTDENGRRLGESANAAKQAITQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFVS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFVS TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNK 7130 2 780 HEVPSLQTSDPLPGSVQRCSVVVSQPNKENWCQDHLYNSLG	LPL
SLRMKQNLHFTEATLHLLTLARTQQGATAVAGAGITQSIC LSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQI LRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADH FILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSF QHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPAV ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQILLDQSI EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELI EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQAMRY PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATC SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR 7129 1 1054 FRRFRWRRRLH+AGPASSAGGSPGEASGTMSGELPPNINIF WDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRC PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMN TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTV GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAF NIPLMRQRELKVGIPVTDENGNRLGESANAAKQAITQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCI TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNK 7130 2 780 HEVPSLQTSDPLPGSVQRCSVVVSQPNKENWCQDHLYNSLG	LPL
LSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQI LRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADH FILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSE QHYLQNKNGDGLPSAV\AQRV\QRPPSASAAPSSSKQPAF ASEQQALHTVQYGLLKILSKTLAALRHFTPDVCQTLLDQSI EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELI EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQAMRY PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATO SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR 7129 1 1054 FRRFRWRRLH*AGPASSAGGSPGEASGTMSGELPPNINIF WDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRC PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMN TGCMMTYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTV GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAF NIPLMRQRELKVGIPVTDENGNRLGESANAKQAITQVVVS MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCI TPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNK 7130 2 780 HEVPSLQTSDPLPGSVQRCSVVVSQPNKENWCQDHLYNSLG ISAKSQPYHRSQSSSSVLINKSMDSINYPSDVGKQQLLSLE	
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EILDANKQPAEAVSATEPVTFNPQKEESDCLQSNEMVLQFL	MH MS KP CL TS
RVAQDCRGTSWPKTVYFTFQFYRFPPATTPRLQLVQLDEAG	MH MS KP CL TS FP
SGALTHILVPVSRDGTFDAGSPGFQLRYMVGPGFLKPGERR	MH MS KP CL TS FP FS
RYLAVQTLQIDVWDGDSLLLIGSAAVQMKHLLRQGRPAVQA	MH MS KP CL TS FP FS

SEQ Predicted beginning nucleotide location (A=Alanine, C=Cysteine, D= location corresponding to first amino acid residue of amino acid sequence se	Aspartic Acid, E= nine, G=Glycine, K=Lysine, =Asparagine, Arginine, 'aline, X=Unknown, *=Stop de deletion, rtion) PIGVHSVVKGRLHLTLAN GASRFSGGSLLTTGSSRR GKGPQDVSRESDATRRK QSVRTQHLRDLQVIAAYR
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence codon, /=possible nucleotide inset LEVATEYEQDNMVVSGDMLGFGRVK VGHPCEQKVRGCSTLPFSRSRVISND KHVVQAQKLADVDSELAAMLLTHARD LERMRSVRIQEAGGDLGRRGTSVLAQ ERTKAESIASLLSLAITTEHTLHATI TVTVEIDNPELSVIVDSQEWRDPKGA APQLYLRPHETAHVPPKFQSFSAGQI	nine, G=Glycine, K=Lysine, =Asparagine, Arginine, faline, X=Unknown, *=Stop de deletion, rtion) PIGVHSVVKGRLHLTLAN GASRFSGGSLLTTGSSRR GKGPQDVSRESDATRRK QSVRTQHLRDLQVIAAYR
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QRLRQHTVPLEEQTELESERLWQHVI EEAQRQRARERQESLMPWKPQLFHLI	EEGSGSSALFWTPSGEVRR PRAISKGDQHRATQEKFAL PPITQEWHYRYEDHSPWDP
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Deginning nucleotide location Corresponding to first amino acid residue of amino acid sequence Serine, Despiration, , QeGlutamine, Re-Arginine, Sestine, Tethreonine, VeValine, Methodine, Neargaigne, Peroline, QeGlutamine, Re-Arginine, Sestine, Tethreonine, VeValine, Methodine, Neargaigne, Peroline, QeGlutamine, Re-Arginine, Sestine, Tethreonine, Neargaigne, Peroline, QeGlutamine, Re-Arginine, Sestine, Tethreonine, Neargaigne, Peroline, QeGlutamine, Re-Arginine, Leieucine, Methodine, Neargaigne, Peroline, QeGlutamine, Re-Arginine, Leieucine, Methodine, Neargaigne, Peroline, QeGlutamine, Re-Arginine, Leieucine, Methodine, Neargaigne, Peroline, QeGlutamine, Re-Arginine, Leieucine, Methodine, Neargaigne, Peroline, QeGlutamine, Re-Arginine, Leieucine, Methodine, Neargaigne, Peroline, QeGlutamine, Re-Arginine, Leieucine, Methodine, Neargaigne, Peroline, QeGlutamine, Re-Arginine, Leieucine, Methodine, Neargaigne, Peroline, QeGlutamine, Re-Arginine, Leieucine, Methodine, Neargaigne, Leieucine, Methodine, Neargaigne, Peroline, CeGlutamine, Re-Arginine, Leieucine, Methodine, Respondine, Neargaigne, Peroline, QeGlutamine, Re-Arginine, Leieucine, Methodine, Respondine, Neargaigne, Peroline, CeGlutamine, Re-Arginine, Leieucine, Methodine, Respon	SEO	Predicted	Predicted end	Amino acid coment containing of
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to first amino acid residue of amino acid residue of amino acid sequence P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \possible nucleotide dissertion) OAGPAEAHREPPRILPAATGCPPHLPGLLSGISVDIDPTGLQSQ WTPKGQDPPLMFSEDYQKSLLEQYHLGLDQKLRKYVVGELIWNF ADPMINOCG USBSCKLDMEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVL VTPEKPLRRGLSHRSDPNAVAPAPQCVRLSLGFLSPEKLEEILD EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP VROLLPFVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYWK EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP GRGALPPBSLSTRKGLPRPSTHSVLKEVYVSQRLNLPVM GATRSNLQPP 7142 658 839 LIFLMLMMELKMLSSVTLHIRAFLYWICLKPTSCLIFONVLINL K**SRAVGVVVVVCRT/YSSDLQVGGVKPWLLLGSQDAAHDDT LKKNKVTHILNVAYGVENAFLSDFTYKSISLDLDPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA SEMSSDEPLSRMDSBISTIMDVDSTISSGRSTPAMMINGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSHVVDGQRGG VVVCLMKGCKVVMTPSTSQSWLQRIMLTHSGDKPFKCVVGGCNA SFRAGGGLARHVPTHFSQONSKVVSQCPKAKEESSSKAGMNKRR KLKNKRRRSLARPHDFFDQATLDAIRHARAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISSLKI 7144 1 988 FRVNMODGGPSPAEHSKNEESAGMERFTGLFDAAGSSGFTPAR RCPAPRPAGVSYVIRDBVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYLASMEHHTDWVDDIVLCCNGKTLLSASS DTTVKVWNAHKGFCMSTLRTHKDYVKALLAYADKBELVASAGLDR QIFLBDVNTLTALITASNNTVTTSSLSGRKDSTYSLAMNQLGTII VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLLINDGTGTICS GSSDGTIELMSLGQQRCIATTRVUHDEGWAALQVNDAFTHVYSGG				H=HISCIQINE, I=ISOIEUCINE, K=LYSINE,
amino acid residue of amino acid sequence Seserine, T=Threonine, V=Valine, amino acid sequence Sequenc	1			L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \ Sequence			1	
amino acid sequence (Codon, /=possible nucleotide deletion, /=possible nucleotide insertion) QAGPAEAHTRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLQSQ WTPKGQDPPLMPSEDYQKSLLEQYHLGLDQKLRKYVVGELIWNF ADFMTNQCG 7141 124 1073 LDSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDSREEBDITVL VTPKKPLRGLSHRSDPNAVAPAPQGVRLSGPLSPEKLEFILD EANRLAAQLEQCALQDRESAGEGLGFRRVKPSPRREEFFVLKDSP VRDLLPTVNSLTRSTPS/LKQPDASTPE****EGVSGGSPGYIWK EALQHEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAAKSSCQLFIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSTRKGLPPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLQPP 7142 658 839 LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFONVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVAFALSDFTYKSISILDLPETNILSYFP ECFEFIEEARRKDGVVIVHCRA 7143 3 773 SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNLAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLMKGCKVVNTPSTSQSWLQRIMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSKVSSQPKAKEESPSKAGMNKRR KLKNKRRSLARPHDFFDAGTLDAIRHRAICFNLSAHIESLGKG HSVVFISTYSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVNMQDGGFSPAEHSKAEESAGMEARFLGLPDAAGSSGFTPAR RCPAPRPAGGSVYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRINSVNQHKQDPY LASMEHHTDWVNDIVLCCNGKTLISASS DTTVKVWNAHKGFCMSTLERHKDVVKALAYAKDKELVASAGLDR QIFLMPUNTLITALTASNNTVTTSSLSGNDSIYSLAMMQLGTII VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLLNRDGTQCLS GSSDSTIRMSLEGQQRCIATYRVHDEGWALQVNDAFTHVYSGG	1			
Sequence Sequence	1		····	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
QAGPAEAHTRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLQSQ WTPKGQDPPLMFSEDYQKSLLEQYHLGLDQKLRKYVVGELIWNF ADFMTNQCG 1DSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVL VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLQPP 1142 658 839 LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVNCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYDENAFLSDFTYKSISILDLPETNILSYFP ECFFIEEAKRKDGVVLVHCNA 3 773 SLEMSSDGEPLSRMDSBDSISSTIMUDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGRGG VFVCLMKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGSLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRSLARPHDFFDQATLDAIRHRAICRNLSAHIESLGKG HSVVFHSTVSILLFFQLKYKTLQKNISTIISKSLKI 7144 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYMRNGVNALQLDPALNELFTAGRD SIRRINSVNQHKQDPYLASMEHHTDWVNDLVLCCNGKTLISASS DTTVKVWNAHKGFCMSTLRTHKDYVKALAYARDKELVASAGLDR QIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLANNQLGTII VSGSTEKVLRWDPRTCAKLMKLKGHTDNVKALLLNRDGTQCLS GSDGTIRRWSLGGQRCIATYRVHDEGVWALQVNDAFTHVYSGG			sequence	Codon, /=possible nucleotide deletion,
######################################	/	sequence		\=possible nucleotide insertion)
7141 124 1073 LDSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVL VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEILD EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP VRDLLPTVNSLTRSTPS/LKQPDASTPE****EGVSQGSPGYIWK EALQHEEGVTHLQSVPCIQRPSIFSS\SRSTPPVRGRAGPSGRA AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSQRLNLPVM GATRSNLQPP 7142 658 839 LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFQNVLNLL KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEBAKRKDGVVLVHCNA 7143 3 773 SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQOMSSKVSSQPKAKESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVNMQDGGFSPAEHSKAEESAGMERRFLGLDDAAGSSGPTPAR RCPAPPRAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNGHKQDPYLASMEHHTDWVNDIVLCCNGKTLISASS DTTVKWNAHKGFCMSTLRTHKDYVKALAYAKDKELVASAGLDR QIFLWDVNTLTALTASMTVTTSSLSGNKDSIYSLAMNQLGTII VSGSTEKURWDPRTCAKLMKLKGHTDNVKALLILNRDGTQCLS GSSDGTIRLWSLGQVRCIATYRVHDEGVWALQVNDAFTHVYSGG	į.		ł	QAGPAEAHTRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLQSQ
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KK*SRAVGVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA 7143 3 773 SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVNNQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS DTTVKVWNAHKGFCMSTLRTHKDYVKALAYAKDKELVASAGLDR QIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNQLGTII VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLINRDGTQCLS GSSDGTIRLWSLGQQRCIATYRVHDEGVWALQVNDAFTHVYSGG	<u> </u>	<u> </u>		
KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP ECFEFIEEAKRKDGVVLVHCNA 7143 3 773 SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGQ GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 7144 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYLASMEHHTDWVNDIVLCCNGKTLISASS DTTVKVWNAHKGFCMSTLRTHKDYVKALAYAKDKELVASAGLDR QIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNQLGTII VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLILNRDGTQCLS GSSDGTIRLWSLGQQRCIATYRVHDEGVWALQVNDAFTHVYSGG	7142	658	839	LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFONVLNIJ.
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GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRS IHVDGQRGG VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG HSVVFHSTVSILLFFQIKYKTLQKNISTIISKSLKI 1 988 FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD SIIRIWSVNQHKQDPYLASMEHHTDWVNDIVLCCNGKTLISASS DTTVKVWNAHKGFCMSTLRTHKDYVKALAYAKDKELVASAGLDR QIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNQLGTII VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLILNRDGTQCLS GSSDGTIRLWSLGQQRCIATYRVHDEGVWALQVNDAFTHVYSGG				
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				GSSDGTIRLWSLGOORCIATYRVHDEGVWALOVNDAFTHUVSCC
				RDRKIYCTDLRNPDIRVLICE

TRADOCS:1416260.1(%CSK01!.DOC)

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- 7. An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

- (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 12. An antibody directed against the polypeptide of claim 10.
- ·13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions
 with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and
 - b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.

- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
- 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

International application No.

PCT/US00/34263

A. CLASS	IFICATION OF SUBJECT MATTER			
IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; CU/K 14/00				
US CL: 536/23.1; 435/320.1, 435, 468, 330/300, 350 According to International Patent Classification (IPC) or to both national classification and IPC				
B. FIELD	S SEARCHED			
Minimum documentation searched (classification system followed by classification symbols) U.S.: 536/23.1; 435/320.1, 455, 468, 530/300, 350				
Documentation	searched other than minimum documentation to the ex	tent that such documents are included in	the fields searched	
Electronic data MEDLINE, E	a base consulted during the international search (name of AST	of data base and, where practicable, sear	ch terms used)	
C. DOCL	MENTS CONSIDERED TO BE RELEVANT		Relevant to claim No.	
Category *	Citation of document with indication, where app	ropriate, of the relevant passages	1-11, 13-16, and 19-26	
A	WAJIMA et al. The cDNA cloning and transient expre hydroxysteroid dehydrogenase of chickens. Gene. 1999.	9, Vol.233, pages 75-82		
A	US 5,175,095 A (MARTINEAU et al) 29 December 1 columns 3-18.	992 (29.12.1992), see especially	1-11, 13-16, and 19-26	
A	Database PubMed, ID No. 2393392, FREUDENSTEI inhibitor of metalloproteinase: sequence and expressio Biophys. Res. Commun. August 1990. Vol.171. No.	n in bovine ovatian dissue. Diochem.	1-11, 13-16, and 19-26	
A,P	Database PubMed, ID No. 10919256, HENNEBOLD generation and characterization of an ovary-selective clibrary. Endocrinology. August 2000. Vol.141. No.8.	o et al. Ovary-selective genes I; the complementary deoxyribonucleic acid	1-11, 13-16, and 19-26	
A	Database PubMed, ID No. 2760883, BEIL et al. Synt the baboon (Papio anubis). J. Reprod. Fertil. July 198 Abstract.	hesis of polypeptides by the cervix of 39, Vol.86. No.2. pages 535-544, see	1-11, 13-16, and 19-26	
A,P	Database PubMed, ID No. 10830289, HINSHELWO upstream of the human CYP19 (aromatase) gene med transgenic mice. Endocrinology. June 2000. Vol.141.	iates ovary-specific expression in	1-11, 13-16, and 19-26	
	r documents are listed in the continuation of Box C.	See patent family annex.	vernational filing date or priority	
"A" documen	Special categories of cited documents: nt defining the general state of the art which is not considered to be	date and not in conflict with the appi principle or theory underlying the in	lication but cited to understand the vention	
1	ular relevance pplication or patent published on or after the international filing date	"X" document of particular relevance; the considered novel or cannot be considered movel or cannot be considered to the document is taken alone.	dered to involve an inventive step	
*L** document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combinate		tep when the document is ich documents, such combination		
1	nt referring to an oral disclosure, use, exhibition or other means nt published prior to the international filing date but later than the	"&" document member of the same pate		
priority	date claimed actual completion of the international search	Date of mailing of the international log	arch report	
C	mailing address of the ISA/US ommissioner of Palents and Trademarks	Authorizachofficer Michael Woodward	In Illen for	
W	ox PCT /ashington, D.C. 20231 No. (703)305-3230	Telephone No. (703) 308-0196		

Form PCT/ISA/210 (second sheet) (July 1998)

International application No.
PCT/US00/34263

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)
This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
1. Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)
This International Searching Authority found multiple inventions in this international application, as follows: This includes 4 invention Groups and 3572 sequence species
 As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional serch fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, udner PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containg same, respectively, and methods of making as well as the first method of use of this jubject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

Form PCT/ISA/210 (extra sheet) (July 1998)

CORRECTED VERSION

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- (51) International Patent Classification?: C07H 21/04, C12N 15/11, 15/63, 15/70, 15/82, 15/85, C07K 14/00
- (21) International Application Number: PCT/US00/34263
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(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

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- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

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[Continued on next page]

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

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- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, Fl, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

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REVISED VERSION

INTERNATIONAL SEARCH REPORT

Interrational application No.

PCT/US00/34263

IPC(7)	SSIFICATION OF SUBJECT MATTER : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 1 : 536/23.1; 435/320.1, 455, 468, 530/300, 350			
	International Patent Classification (IPC) or to both nation	onal classification and IPC		
Minimum do	DS SEARCHED cumentation searched (classification system followed by 36/23.1; 435/320.1, 455, 468, 530/300, 350	classification symbols)		
Documentation	on searched other than minimum documentation to the ex	xtent that such documents are included in	the fields searched	
Electronic da MEDLINE,	ata base consulted during the international search (name of EAST	of data base and, where practicable, sear	ch terms used)	
C. DOC	UMENTS CONSIDERED TO BE RELEVANT			
Category *	Citation of document, with indication, where app	propriate, of the relevant passages	Relevant to claim No.	
A	WAJIMA et al. The cDNA cloning and transient expr hydroxysteroid dehydrogenase of chickens. Gene. 199	ression of an ovary-specific 17beta- 99, Vol.233, pages 75-82	1-11, 13-16, and 19-26	
A	US 5,175,095 A (MARTINEAU et al) 29 December columns 3-18.	1992 (29.12.1992), see especially	1-11, 13-16, and 19-26	
A	Database PubMed, ID No. 2393392, FREUDENSTE inhibitor of metalloproteinase: sequence and expression Biophys. Res. Commun. August 1990. Vol.171. No.	on in bovine ovarian tissue. Biochem.	1-11, 13-16, and 19-26	
A,P	Database PubMed, ID No. 10919256, HENNEBOLD et al. Ovary-selective genes I: the generation and characterization of an ovary-selective complementary deoxyribonucleic acid library. Endocrinology. August 2000. Vol.141. No.8. pages 2725-2734, see Abstract.		1-11, 13-16, and 19-26	
A	Database PubMed, ID No. 2760883, BEIL et al. Synthesis of polypeptides by the cervix of the baboon (Papio anubis). J. Reprod. Fertil. July 1989. Vol.86. No.2. pages 535-544, see Abstract.		1-11, 13-16, and 19-26	
A,P	Database PubMed, ID No. 10830289, HINSHELWOOD et al. A 278 bp region just upstream of the human CYP19 (aromatase) gene mediates ovary-specific expression in transgenic mice. Endocrinology. June 2000. Vol.141. No.6. pages 2050-2053, see Abstract.		1-11, 13-16, and 19-26	
Further documents are listed in the continuation of Box C.		See patent family annex.		
Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance.		date and not in conflict with the appl principle or theory underlying the in-	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	
"E" earlier application or patent published on or after the international filing date		"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone		
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another criticion or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means		considered to involve an inventive si combined with one or more other su	ocument of particular relevance; the claimed invention cannot be onsidered to involve an inventive step when the document is ombined with one or more other such documents, such combination eing obvious to a person skilled in the art	
"P" document published prior to the international filing date but later than the priority date claimed		"&" document member of the same patent family		
Date of the actual completion of the international search		Date of mailing of the international search report 0.5 SEP 2001		
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT		Authorized officer Shi Marsh Shi Marsh Shi Marsh Shi Marsh Shi Marsh Shi Michael Woodward		
	Washington, D.C. 20231 No. (703)305-3230	Telephone No. (703)/308-0196	<i>U</i>	

Form PCT/ISA/210 (second sheet) (July 1998)

PCT/US00/34263

Continuation of Item 1 of first sheet)			
Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)			
Box I Observations where certain claims were testing the state of certain claims under Article 17(2)(a) for the following reasons: This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:			
1. Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:			
2. Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:			
3. Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).			
Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)			
This International Searching Authority found multiple inventions in this international application, as follows: This includes 4 invention Groups and 3572 sequence species			
 As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: 			
No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-11, 13-16, and 14-26 Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.			

Form PCT/ISA/210 (continuation of first sheet(1)) (July 1998)

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional serch fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group IV, claim 27, drawn to method of treatment using composition comprising polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, udner PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containg same, respectively, and methods of making as well as the first method of use of this jubject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

Form PCT/ISA/210 (extra sheet) (July 1998)

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